Protein q Bovine al Peptide # Cysteine-

Bovine se Bovine Se Novel hum

Human sec Human sec

Insulin/i Insulin/i

Hepatocel

Bovine Se Endogenou Human gra Botulinum

Adj78050
Adz86402
Adw656557
Adw656557
Adv95854
Adv78512
Adg78512
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Adg78512
Adw8706514
Adw8706515
Adw8706513
Adw87065174
Adw87074
Adw87074

Searched:

9

Run Σ

Database

Secretin S. pyogen Protected Secretin Synthetic 27-Desami Pig Secre Sequence Intermedi

Secretin-Neutrophi Porcine a Secretin Secretin Pig prote Heptacosi

Aab91263 Aab50844

Aaw71676 Aay50236 Aab70901 Aab91262

Heptacosi Human sec Secretin Secretin

Mammalian

Porcine s Secretin

Vasoactiv

Abb06679 Aae23559 Abb004451 Abb044452 Abb044523 Abb06068 Abf0608 Add6998 Add6998 Add64185 Add74133 Adw91706 Adz60126 Adz60126 Adz60126 Adz60126

Secretin Porcine s Human VIP

Secretin Recombina 27-desami Novel bon

Sequence Peptide # Peptide # Human bon Human bra

Human pep Peptide o Endometri Human imm

Result Š. liv hum

Human Novel

Aaul1782 Aap81564 Adu04520 Adu04520 Aby 100 421 Aam73455 Aam73655 Aam73655 Aam73655 Aam7365 Aby 200 41 Aby 200 41

Staphyloc Human sec Human pol

Human liv Peptide # Plant tra Synechocy Unidentif

Abg52332 Aam06070 Adj99951 Adu04355 Adu04353

Protein

Mouse T c Protein t

Human ins

Porcine s

54

Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src; tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3; cyclophilin B gene; HLA-A2402.

Antitumour peptide blk 482-494.

17-DEC-2001 (first entry)

AAG68084;

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The present invention describes peptides recognising cancer cells with tumour specific cycloxoxic T lymphocytes (CTL). The peptides recognising scancer cells with tumour specific CTLs are selected from: (1) peptides of sequences (AAG68066 to AAG68069); (2) peptides containing the above mentioned sequences; (3) peptides having 70 % or more of homogeneity with the above mentioned sequences; and (4) peptides with one or more deleted, substituted, added or inserted amino acid(6) of the above mentioned sequences, particularly those having recognising property due to HLA-A2402 binding CTL, especially having at least 5 amino acids, used for meticine, particularly anticancer agents, derived from antitumour antigenic peptides of lok, src family, SART-1, SART-3 or cyclophilin B genes. The antitumour peptides have cytostatic activities. The peptides are used for the treatment of cancer. The peptides cause activation of CTL in cancer patients. The present sequence represents a peptide from
                Peptide #
Peptide #
Peptide #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptides for recognizing cancer cells with tumor specific cytotoxic lymphocytes and for treating cancer.
                                                                                                                                                                                                                                                                                            Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src; tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3; cyclophilin B gene; HLA-A2402.
 Adx69981 F
Aam20412 E
Abb41124 E
Aam34900 E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 30; DB 4; Length 13; 30.8%; Pred. No. 2.2e+02; tive 9; Mismatches 0; Indels
                                                                                               ALIGNMENTS
                AAM20412
ABB41124
                                               AAM34900
 ADX69981
                                                                                                                                                                           AAG68082 standard; peptide; 13 AA
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                                                                                                                                                                                                                                                                       Antitumour peptide yes 508-520.
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 300
                                                                                                                                                                                                          AAG68082;
                                                                                                                                            RESULT 1
                                                                                                                                                            AAG68082
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100
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New peptides for recognizing cancer cells with tumor specific cytotoxic T lymphocytes and for treating cancer.

WPI; 2001-610076/70.

(ITOY/) ITO Y.

28-DEC-1999;

25-DEC-2000; 2000JP-00393047.

JP2001245675-A.

11-SEP-2001.

Homo sapiens.

Claim 8; Page 2; 14pp; Japanese.

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The present invention describes peptides recognising cancer cells with tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising cancer cells with tumour specific CTLs are selected from: (1) peptides of sequences (AAG68066 to AAG68069); (2) peptides containing the above mentioned sequences; (3) peptides having 70 % or more of homogeneity with the above mentioned sequences; and (4) peptides with one or more deleted, substituted, added or inserted amino acid(s) of the above mentioned sequences, particularly those having recognising property due to HLA-A200 binding CTL, especially having at least 5 amino acid(s) used for medicine, particularly anticancer agents, derived from antitumour antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B genes. The antitumour peptides have cytostatic activities. The peptides are used for the treatment of cancer. The peptides cause activation of CTL in cancer patients. The present sequence represents a peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src; tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3; cyclophilin B gene; HLA-A2402.
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Pred. No. 2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
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Best Local Similarity
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BXSXXXXX
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Gaps

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AAG68084 standard; peptide; 13 AA.

RESULT 2
AAG68084
ID AAG6

1 TFXXXXXXLXDXX 13 ||::::::|:|: TFEYIQSFLEDYF 13

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Conservative

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Local Similarity

Best Loc Matches

Query Match

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28-DEC-1999;

11-SEP-2001.

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tumour specific cytotoxic Tiymphocytes (CTL). The periods recognising cancer cells with tumour specific CTLs are selected from: (1) peptides of sequences (AAG8066 to AAG8065); (2) peptides containing the above mentioned sequences; (3) peptides having 70 % or more of homogeneity with the above mentioned sequences; and (4) peptides with one or more deleted, substituted, added or inserted amino acid(5) of the above mentioned sequences, particularly those having recognising property due to HLA-A2402 binding CTL, especially having at least 5 amino acids, used for medicine, particularly anticancer agents, derived from antitumour antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B genes. The antitumour peptides have cytostatic activities. The peptides are used for the treatment of cancer. The peptides cause activation of CTL in cancer patients. The present sequence represents a peptide from
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Pred. No. 2.2e+02;
9; Mismatches 0; Indels
                                                                  peptides recognising
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                       Claim 8; Page 2; 14pp; Japanese.
                                                                  present invention describes
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Query Match
Best Local Similarity 30.0%,
A; Conservative
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TFEYIQSVLDDFY 13
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                                                                                                                                                                                                                                                  New peptides for recognizing cancer cells with tumor specific cytotoxic T lymphocytes and for treating cancer.
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Pred. No. 2.2e+02;
9; Mismatches 0; Indels
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                                                             25-DEC-2000; 2000JP-00393047.
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100.0%; Score 30; DB 4; Length 13; 100.0%; Pred. No. 2.2e+02; ive 0; Mismatches 0; Indels

13; Conservative

Matches

New peptides for recognizing cancer cells with tumor specific cytotoxic lymphocytes and for treating cancer.

WPI; 2001-610076/70.

(ITOY/) ITO Y.

28-DEC-1999;

Homo sapiens

11-SEP-2001

17-DEC-2001

AAG68083;

RESULT

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Best Local Similarity

Query Match

Sequence 13 AA;

RESULT 6 AAB73147

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Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and polynucleotides encoding them for treatment of cancer.
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03-AUG-2000; 2000WO-JP005220.
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Best Local Similarity
Matches 4; Conserv
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                             05-AUG-1999;
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                                                               HOTI (/HOTI)
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                                                                                                                              AAB73147 standard; peptide; 13 AA.
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Length 13;

100.0%; Score 30; DB 4; 30.8%; Pred. No. 2.2e+02;

Query Match Best Local Similarity

Sequence 13 AA;

WO200111044-A1

Best Loc Matches

RESULT 7 AAB73145

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Matches

RESULT 9 AAB73146

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Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and polynucleotides encoding them for treatment of cancer.
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                  03-AUG-2000; 2000WO-JP005220
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TFEFLQSVLEDFY 13
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Best Local Similarity
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AAB73150
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30.8%; Pred. No. 2.2e+02;
iive 9; Mismatches 0;
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Best Local Similarity
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Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and polynucleotides encoding them for treatment of cancer.
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immunogenic or less immunogenic than non-modified human Factor VIII,
useful in preparing a composition for treating e.g., Gaucher's disease.
                                                                                                                                                                                                                                                                 The present invention relates to peptides which are partial sequences o src/lck family proteins. The present sequence is one such peptide. The peptides are useful for producing vaccines for the treatment of cancer, including colon cancer and small-cell lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential human MHC class II binding human Factor VIII peptide #562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human Factor VIII, non-immunogenic; immunogenic, T-cell epitope; MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.
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Pred. No. 2.2e+02;
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30.8%; I
                                  03-AUG-2000; 2000WO-JP005220.
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24-MAR-2003; 2003EP-00006554.
                                                                 99JP-00222101
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Best Local Similarity
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                                                                                                                                                          WPI; 2001-191541/19.
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                                                                                                                             Itoh K;
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                                                                                                                                                                                                                                                                                    Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
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                   Indels
   Pred. No. 2.2e+02;
; Mismatches 0;
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                                                                                                                                                          standard; peptide; 13 AA.
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30.8%;
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les 4; Conserva
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                                                                                                                                                                                                                                                                                                                                                 WO200111044-A1
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15-FEB-2001

Itoh K;

AAB73149; AAB73149

RESULT 12 AAB73149

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The invention relates to a novel modified human Factor VIII molecule. The modified human Factor VIII molecule being substantially non-immunogenic or less immunogenic than a non-modified human Factor VIII and having essentially the same biological specificity and activity when used in

WO200111044-A1

Homo sapiens

AAB73144;

Query Match

Matches

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vivo. The modified human Factor VIII molecule comprises specifically altered amino acid residues compared with the non-modified parental molecule, where the altered amino acid residues cause a reduction or an elimination of one or more of the T-cell epitopes, which act in the parental non-modified molecule as MHC class II binding activity peptide is useful for the manufacture of the modified Factor VIII molecule or a vaccine in order to reduce immunogenicity to Factor VIII in a patient. The modified Factor VIII molecule is useful in preparing a composition for treating e.g., Gaucher's disease. This sequence represents a human Factor VIII peptide with potential human MHC class II binding activity of
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13 AA;
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Pred. No. 2.2e+02;
9; Mismatches 0; Indels
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Query Match
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RESULT 15

ADD23350

ADD23350 standard; peptide; 14 AA. ADD23350;

Breast cancer membrane protein (BCMP) peptide SEQ ID NO:120

(first entry)

15-JAN-2004

breast cancer; screening; diagnosis; breast cancer therapy; breast cancer membrane protein; BCMP; cytostatic; vaccine; human.

Homo sapiens

WO2003087831-A2

23-OCT-2003.

10-APR-2003; 2003WO-GB001559.

11-APR-2002; 2002GB-00008331

(OXFO-) OXFORD GLYCOSCIENCES UK LID.

Terrett JA; Hudson LJ, Stamps AC,

WPI; 2003-845381/78.

Screening, diagnosing and/or treating breast cancer by detecting a change in expression or activity of a breast cancer membrane protein (BCMP) polypeptide or encoding nucleic acid molecule.

Claim 1; SEQ ID NO 120; 81pp; English

The present invention describes a method of screening for and/or diagnosing breast cancer in a subject, and/or monitoring the effectiveness of breast cancer therapy. The method comprises detecting and/or quantifying in a biological sample obtained from the subject a breast cancer membrane protein (BCMP) polypeptide and a nucleic acid molecule. Also described: (1) an antibody, its functionally-active fragment, derivative or analogue, that specifically binds to one or of the BCMP polypeptide, (2) a diagnostic kit comprising a capture reagent specific for an BCMP polypeptide, reagents and instructions for use; (3) a method for screening for anti-breast cancer agents that interact with the BCMP polypeptide, comprising contacting the polypeptide with a candidate agent, and determining whether or not the candidate agent interacts with the polypeptide; (4) a method for screening for anti-breast cancer agents that modulate the expression or activity of an BCMP

Sequence 16 AA;

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polypeptide or the nucleic acid molecule cited above, comprising comparing the expression or activity of the polypeptide or nucleic acid molecule, in the presence and absence of a candidate agent or in the presence of a control agent, and determining whether the candidate agent causes the control agent, and determining whether the candidate agent causes the expression or activity of the polypeptide or nucleic acid molecule to change, and (5) an agent identified by the method of (3) or 4(4), which interacts with the polypeptide or causes the expression or activity of the polypeptide, or the expression of the nucleic acid molecule to change. BCMPs have cytostatic activities, and can be used in vaccines. The BCMP polypeptide, nucleic acid molecule, antibody, agent or their derivatives, are useful in the manufacture of a medicament for the treatment of breast cancer, where the composition is a vaccine. The present sequence represents a BCMP peptide which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteomics for controlling or eliminating isotope effects during fractionation of chemically equivalent but isotopically distinct compounds. The isotope facilitates intelligent data acquisition, also the isotope effect is reduced by eliminating deuterium from. The present sequence represents a peptide used in the exemplification of the specification, used to compare the resolution caused by reagents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isotope; intelligent data acquisition; reverse phase chromatography;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to an isotope coding agent, used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 30; DB 7; Length 14; 30.8%; Pred. No. 2.4e+02; Ative 9; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR63280 standard; peptide; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2002; 2002WO-US030742.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TEXXXXXXIXDXX 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGNIER F E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-402986/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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CA; peptide sequencing; mutation identification; carbonic anhydrase II; bovine serum albumin; BSA; ubiquitin; UB; superoxide dismutase; SOD.

Sovine BSA peptide fragment

12-FEB-2004 (first entry)

AA027568;

11-MAR-2003; 2003WO-US007637. 11-MAR-2002; 2002US-0363647P. (THER-) THERMO FINNIGAN LLC.

WO2003078584-A2.

Bos sp.

25-SEP-2003

WPI; 2003-757000/71.

Maroto FM;

AAO27568 standard; peptide; 16 AA.

RESULT 18

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the protein smaller and/or make the processing more efficient. The tags remaining on the protein fragments after acidolysis have a markedly reduced molecular weight and higher isotope density. The affinity tags also have higher solubility than prior art analogs. This sequence represents a marker peptide which is used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New, preferably isotopically labeled affinity tag compounds, useful in analyzing proteins by mass spectrometry, comprise affinity ligand, protein reactive group and acid-cleavable thiourea derivative linker.
                                                                                                                                                                                                                                                                                                                                                 affinity tag; N-phenylene-thio urea; ICAT; isotope coded affinity tag.
                                       Gaps
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Score 30; DB 6; Length 16;
Pred. No. 2.9e+02;
); Mismatches 0; Indels
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Pred. No. 2.9e+02;
9; Mismatches 0; Indels
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                                       9; Mismatches
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                                                                                                                                                                                                    ADD35548 standard; peptide; 16 AA.
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   100.08;
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Best Local Similarity 30.8%;
Matches 4; Conservative
                  30.8%;
                                                                                                                                                                                                                                                                                                             Affinity marker peptide #1
                                                                                                3 TFHADICTLPDTE 15
                                                                                                                                                                                                                                                                           (first entry)
                                                                         1 TFXXXXXXLXDXX 13
                                       4; Conservative
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 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003040093-A2
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                                                                                                                                                                                                                                                                                                                                                                                     Unidentified.
                                                                                                                                                                                                                                                                           15-JAN-2004
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The invention relates to identifying a modification in a polypeptide by a method involving peptide sequencing. The method involves (a) identifying a set of one or more candidate sequencing including sequence information to potentially corresponding to an unmodified variant of the polypeptide of serious sequence; (b) sequencing at least a portion of one or more peptide of known sequence; (b) sequencing at least a portion of one or more peptide of derived from the polypeptide to identify a sequence information for the comparing the identified sequence rag with sequence information for the set of candidate sequence to identify a candidate sequence containing the identified sequence tag; and (d) calculating the difference between at least one subsequence mass of the identified andidate sequence. Modifications that may be identified include mutations, additions, deditions, and posttranslational containing modifications. Possible sample materials include cells, body fluids, and environmental samples such as soil, water and air samples. Sequences containmental samples such as soil, water and air samples. Sequences containing the dismutase (SOD), identified in an exemplary experiment
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Method for identifying modifications in a polypeptide, based on sequencing peptides to define a tag and comparing this with candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 30; DB 7; Length 16; 30.8%; Pred. No. 2.9e+02; ive 9; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEA78908 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Fig 6; Opp; English.
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Best Local Similarity
Matches 4; Conserv
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TFXXXXXXLXDXX 13

Bovine Serum Albumin indexed peptide database peptide #299

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The invention relates to a novel method of mass spectrometry. The method comprises mass analysing the first molecules in a first mixture and accurately determining the mass to charge ratio of the first molecules in the first mixture. The invention further relates to: generating an index to the first mixture. The invention further relates to: generating an index for use in identifying molecules of biological origin by mass respectivemetry by accurately determining the masses or mass to charge ratio of the comprising peptides resulting from the digestion or fragmentation of a polypeptide or protein; determining a first physico-chemical property of the molecules comprising peptides; and optionally determining a second, third, fourth and/or fifth physico-chemical property of the molecules comprising peptides; and optionally determining a mass analyser for accurately determining the mass to charge ratio of the first molecules of the basis of at least the first physico-chemical property and the accurately determined mass to charge ratio of the first molecules of the basis of the basis of the second, third, fourth and/or fifth physico-chemical property. The method and spectrometer are useful in protein dentification, protein quantitation, protein quantitation.

The pass spectrometry method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A method of mass spectrometry, useful in protein identification and quantitation, by mass analyzing the first molecules in the first mixture and accurately determining the mass to charge ratio of the first molecules in the first mixture molecules in the first mixture.
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                                                        mass spectrometry; peptide index; protein identification; protein quantitation; protease; high-resolution mass spectrometry; proteomics; genomics; bioinformatics; Bovine Serum Albumin.
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                  Bovine Serum Albumin indexed peptide database peptide #124
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                                                                                                                                                                                                                                                                                                                                                                                                              Silva J;
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14-MAR-2002; 2002US-0364847P.
                                                                                                                                                                                                                                                                   09-DEC-2002; 2002WO-GB005571
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                                                                                                                                                                                                                                                                                                                                                                                                            Geromanos S, Dongre A,
                                                                                                                                                                                                                                                                                                                                                                      (MICR-) MICROMASS LTD
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                                                                                                                                                                                 WO2003054549-A2.
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                                                                                                                                             Bos sp.
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AEA79083
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The invention relates to a novel method of mass spectrometry. The method comprises mass analysing the first molecules in a first mixture and accurately determining the mass to charge ratio of the first molecules in the first mixture. The invention further relates to: generating an index to the first mixture. The invention further relates to: generating an index of for use in identifying molecules of biological origin by mass consisting molecules of protein; determining the masses or mass to charge ratio of the comprising peptides resulting from the digestion or fragmentation of a polypeptide or protein; determining a first physicotomelar property other than mass or mass to charge ratio of the molecules comprising peptides; and optionally determining a second, third, fourth and/or fifth physicotomelar property of the molecules comprising peptides; and optionally determining a mass spectrometer comprising a mass analyser of comprising peptides; and a mass spectrometer comprising a mass analyser of the molecules and means for identifying the first molecules of the basis of at least the first physicothemical property and the accurately or determined mass to charge ratio of the first molecules and optionally on the basis of the second, third, fourth and/or fifth physicothemical property. The method and spectrometer are useful in protein dentification, protein quantitation, protein quantitation, protein quantitation, protein mass spectrometry, proteomics, genomics and bioinformatics. This sequence converted by the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quantitation, by mass analyzing the first molecules in the first mixture and accurately determining the mass to charge ratio of the first molecules in the first mixture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A method of mass spectrometry, useful in protein identification and
                                     mass spectrometry, peptide index, protein identification, protein quantitation, protease; high-resolution mass spectrometry; proteomics, genomics, bioinformatics; Bovine Serum Albumin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 7; Length 16
Pred. No. 2.9e+02;
9; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      Opiteck G,
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                                                                                                                                                                                                                                            09-DEC-2002; 2002WO-GB005571.
                                                                                                                                                                                                                                                                                  08-DEC-2001; 2001US-0340460P.
14-MAR-2002; 2002US-0364847P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.8%;
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                                                                                                                                                                                                                                                                                                                                                                                      Dongre A,
                                                                                                                                                                                                                                                                                                                                               (MICR-) MICROMASS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-569290/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                             WO2003054549-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                    Geromanos S,
                                                                                                                                                                                                    03-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-AUG-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEA78834;
                                                                                                                         Bos sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEA78834
ID AEA7
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AC AEA7
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DT 11-A
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A method of mass spectrometry, useful in protein identification and quantitation, by mass analyzing the first molecules in the first mixture and accurately determining the mass to charge ratio of the first molecules in the first mixture molecules in the first mixture
      mass spectrometry; peptide index; protein identification; protein quantitation; protease; high-resolution mass spectrometry; proteomics; genomics; bioinformatics; Bovine Serum Albumin.
                                                                                                                                                                                                                                                         Disclosure; Fig 7B; 123pp; English.
                                                                                                    09-DEC-2002; 2002WO-GB005571.
                                                                                                                       08-DEC-2001; 2001US-0340460P.
14-MAR-2002; 2002US-0364847P.
                                                                                                                                                   (MICR-) MICROMASS LTD
                                                                                                                                                                                         WPI; 2003-569290/53
                                                                WO2003054549-A2
                                                                                                                                                                      Geromanos S,
                                                                                  03-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                              Bos
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The invention relates to a novel method of mass spectrometry. The method comprises mass analysing the first molecules in a first mixture and accurately determining the mass to charge ratio of the first molecules in the first mixture. The invention further relates to: generating an index for use in identifying molecules of biological origin by mass spectrometry by accurately determining the masses or mass to charge ratios of molecules comprising peptides resulting from the digestion or fragmentation of a polypeptide or protein; determining a first physicochemical property other than mass or mass to charge ratio of the molecules comprising peptides; and optionally determining a second, third, fourth and/or fifth physico-chemical property of the molecules comprising peptides; and a mass spectrometer comprising a mass analyser of a least the first physico-chemical property of the basis of determining the mass to charge ratio of the basis of the basis of the basis of the second, third, fourth and/or fifth physico-chemical property and the accurately or the basis of the second, third, fourth and/or fifth physico-chemical property. The method and spectrometer are useful in protein capacitical in protein quantitation, proteases, high-resolution mass spectrometry, proteomics, genomics and bioinformatics. This sequence represents a peptide from an indexed peptide database created by the novel mass spectrometry method of the invention. . 0 Gaps ö Length 16; 0; Indels Score 30; DB 7;
Pred. No. 2.9e+02;
9; Mismatches 0; 100.0%; 30.8%; 1 TFXXXXXXLXDXX 13 4; Conservative Query Match Best Local Similarity Sequence 16 AA;

3 TFHADICTLPDTE 15

g

ADH11188 standard; peptide; 16 ADH11188; RESULT 22
ADH11188
ID ADH11
XX
AC ADH11
XX
DT 11-MP
XX
XX
XX
XX
YX
YX
YX
YX
YX

(first entry) 11-MAR-2004 MALDI-MS tryptic peptide #28.

biopolymer; proteome; peptidome.

Unidentified

WO2003096021-A1

20-NOV-2003

09-MAY-2003; 2003WO-EP004878

10-MAY-2002; 2002DE-01020804.

(PROT-) PROTEOME FACTORY AG.

Thies Essmann F, Scheler C,

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useful e.g. for proteome selective release, labeling Analyzing complex mixtures of polypeptides, analysis, by fragmentation, immobilization, WPI; 2004-034708/03.

Silva J;

Opiteck G,

Dongre A,

Example; Fig 2; 64pp; German.

and characterization.

This invention describes a novel method of analysing complex mixtures of biopolymers that contain peptide bonds by fragmentation, immobilisation, cselective release of bound fragments, labelling, separation of labelled fragments according to physicochemical properties and detecting the label. The biopolymers are peptides, proteins, or their derivatives; and the binding fragments are amino acids, (lipo- or glyco-)peptides, proteins, or their derivatives; and their derivatives. Typical enzymes for used in the method are compliming tragments are mino acids, (lipo- or glyco-)peptides, PNA or their derivatives. Typical enzymes for used in the method are compliming to the linker depend on the nature of the terminal amino acid, e.g. thiols are reacted through dithiols; Glu and Asp are reacted with acarbodimide; Arg is reacted with glycard and this coupled to amino in the homoserine lactone with cyanogen bromide and this coupled to amino in the linker. Reagents for blocking specific monomers are e.g. acid anhydrides or chlorides, aldehydes etc., most preferrably acetyl chloride or chlorides, aldehydes etc., most preferrably acetyl chloride or cirraconic anhydride, and the most preferrably acetyl chloride or cirraconic anhydride, and the most preferrably in the number of isothiocyanatobenzene. The method is used in proteome and peptidome analysis. The method allows a significant reduction in the number of components that need to be characterised (and thus saves time and money), without a significant loss of information. ADH11161-ADH11216 represent

Sequence 16 AA;

Gaps ö Score 30; DB 8; Length 16; Pred. No. 2.9e+02; 9; Mismatches 0; Indels 6 100.08; 30.8%; 4; Conservative Query Match Best Local Similarity Matches

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3 TFHADICTLPDTE 15 1 TFXXXXXXLXDXX 13 g ò

RESULT 23 ADJ78034

ADJ78034 standard; peptide; 16 AA.

ADJ78034;

06-MAY-2004 (first entry)

Peptide, SEQ ID 53, for analysing cysteine-containing protein expression.

Protein expression analysis; protease cleavage

Synthetic X S X Z X E X E X S X X X X

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immobilisation site-cleavage site-link, where the immobilisation site is selected from the group consisting of an epitope tag, a linker to a solid surface, a metal chelating site, and a magnetic site, or a combination thereof, and the cleavage site is selected from the group consisting of a protease cleavage site (ADJ77982), a photocleavable linker, a restriction site, a chemical cleavage site and a thermal cleavage site, or a combination thereof. The present bovine albumin peptide was used to
                                                                                                        Novel reagent for simultaneously identifying and determining levels of expression of cysteine-containing proteins in normal and perturbed cells.
                                                                                                                                                                                                           The present invention relates to reagent compounds (C1) for identifying and determining the levels of expression of cysteine-containing proteins in normal and perturbed cells. The reagent compounds have the formula:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel method for the quantitative analysis of a protein. The method involves hydrolyzing a first test sample in water containing 90% or more of 18-0 (an isotopic labeling element). hydrolyzing a second sample in water containing 90% or more of 16-0, mixing the hydrolyzed substance of the first and second samples, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quantitative analysis; HPLC; electrospray ionization; mass spectroscopy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein quantitative analysis method related tagged BSA peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quantitative analysis of protein, by hydrolyzing test sample and
in water containing labeled oxygen, mixing hydrolyzed substance
subjecting liquid mixture to liquid chromatography/electrospray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30; DB 8;
Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                       Example 11; SEQ ID NO 69; 183pp; English
                          Andon N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADZ86402 standard; peptide; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
30.8%; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-OCT-2003; 2003JP-00353574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-OCT-2003; 2003JP-00353574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUMU ) SUMITOMO SEIYAKU KK. (SUMO ) SUMITOMO CHEM CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ionization-mass spectrometry
                          Yates J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TFHADICTLPDTE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TEXXXXXXIXDXX 13
                                                                                                                                                                                                                                                                                                                                                                                                                              illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-349932/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                       Wei J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP2005121380-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
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                          Haynes P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ٦
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to reagent compounds (C1) for identifying and determining the levels of expression of cysteine-containing proteins in normal and perturbed cells. The reagent compounds have the formula: immobilisation site-cleavage site-link, where the immobilisation site is selected from the group consisting of an epitope tag, a linker to a solid surface, a metal chelating site, and a magnetic site, or a combination thereof, and the cleavage site is selected from the group consisting of a protease cleavage site (ADJ77982), a photocleavable linker, a restriction site, a chemical cleavage site and a thermal cleavage site, or a combination thereof. The present sequence was used to illustrate the
                                                                                                                                                                                                                                                                                                                                                                                Novel reagent for simultaneously identifying and determining levels of expression of cysteine-containing proteins in normal and perturbed cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for analysing cysteine-containing protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein expression analysis; protease cleavage site; bovine; albumin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 8; Length 16;
Pred. No. 2.9e+02;
3; Mismatches 0; Indels
                                         /note= "Peptag-modified cysteine residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Peptag-modified cysteine residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 53; 183pp; English
                                                                                                                                                                                                                                                                                                Andon N;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                     (SYGN ) SYNGENTA PARTICIPATIONS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ78050 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
                                                                                                                                                                28-JUL-2003; 2003WO-IB003863.
                                                                                                                                                                                                           01-AUG-2002; 2002US-00212628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-2003; 2003WO-IB003863
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                                                                                                                                                                                                                                                                                              Wei J, Yates J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.5%;
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TFHADIXTLPDTE 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                  WO2004013636-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16 AA;
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Modified-site
  Key
Modified-site
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                                                                                                                                                                                                                                                                                              Haynes P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention.
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Query Match

Best Loc Matches

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ADJ78050;

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Gaps

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Length 16; 0; Indels control

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the invention.
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                                                                                                                         Matches
                                                                                                                                                                                                                                                                 RESULT 27
                                                                                                                                                                                                                                                                                      AAW65655
    SXS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel affinity tag compounds (preferably isotopically labelled with carbon-13 and optionally nitrogen-15)

Consisting of an affinity ligand residue covalently bonded to a protein reactive group via a linking group. The linking group contains an acid-cleavable N-phenylene-thio urea derivative group. The use of the novel tag, in isotopically labelled form, is claimed as a reagent for the mass spectrometric analysis of proteins, especially for identifying proteins or protein functions in samples containing one or more proteins. The affinity tag can also be used to determine the relative protein affinity tag can also be used to determine the relative protein carpression levels in samples containing one or more proteins.

Catenopically labelled tags are designated /ICAT's' (isotope coded finity tags). An acid-labile group can serve as a pre-determined caleavage site for acid-induced cleavage of the affinity label, e.g. to facilitate release on an affinity column to make the residue attached to the protein smaller and/or make the processing more efficient. The tags reduced molecular weight and higher solubility than prior art analogs. This sequence also have higher solubility than prior art analogs. This sequence represents a fragment of bovine albumin which is used in the method of
                                                                                                                                                                                                                           ö
carrying out quantitative analysis of the liquid mixture by liquid chromatography/electrospray ionization-mass spectrometry (LC/ESI-MS). The method enables the quantification of proteins in large-scale proteomics, and trace amount of proteins present in an organism can be quantified accurately and efficiently. This sequence represents a peptide fragment used in the protein quantitative analysis method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preferably isotopically labeled affinity tag compounds, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      affinity tag; N-phenylene-thio urea; ICAT; isotope coded affinity tag; bovine; albumin.
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analyzing proteins by mass spectrometry, comprise affinity ligand, protein reactive group and acid-cleavable thiourea derivative linker.
                                                                                                                                                                                                                           ö
                                                                                                                                                                               Score 30, DB 9; Length 16;
Pred. No. 2.9e+02;
9; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Siegmund H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immler D,
                                                                                                                                                                                                                                                                                                                                                                                                           ADD35547 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 45; 65pp; German.
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                                                                                                                                                                                 100.0%;
30.8%; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-NOV-2001; 2001DE-01054753.
29-JUL-2002; 2002DE-01034416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                 1 TFXXXXXXLXDXX 13
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TFHADICTLPDTE 15
                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lerchen H, Lockhoff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine albumin fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-513527/48.
                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003040093-A2
                                                                                                                                            Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD35547;
                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                     RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                        ADD35547
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The invention relates to methods for identification of compounds which interact with the insulin receptor beta chain at specific loci; and/or after the conformation of the cytoplasmic kinase domain (KDD). In addition the invention relates to simple non-peptide compounds that behave as agonists for the insulin receptor and enhance the effect of insulin on this receptor. The processes may be used for identification of compounds which can stimulate the uptake of glucose in calls or lower blood glucose levels. The identified compounds can be used in the compound (TER16998) binds, a series of 14 peptides the CKD to which a compound (TER16998) binds, a series of 14 peptides ("ryan peptides", AAW65642-55) were synthesised. These peptides were chosen to correspond to distinct surface elements of the CKD made evident by the X-ray structure. Collectively, these 14 peptides cover 85 per cent of the surface-exposed residues. These peptides were tested for their ability to inhibit the activation of insulin receptor by TER16998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying materials which modulate insulin receptor kinase activity useful for screening for compounds which can enhance glucose uptake in cells or lower blood glucose levels.
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #14 derived from the CKD of the insulin receptor beta chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modulator;
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                                                      Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insulin receptor beta chain; cytoplasmic kinase domain; minsulin activation; glucose; conformation; diabetes; CKD.
                                                                                                                Indels
                                                ; Score 30; DB 7; L
Pred. No. 3.1e+02;
9; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                               AAW65655 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 7; Page 38; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-00784855.
97US-00784857.
97US-00825269.
                                                      100.08;
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                                                                                        30.8%;
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                                                                                                                                                                                                           3 TFHADICTLPDTE 15
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                                                                                                             4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-414253/35.
                                                   Query Match
Best Local Similarity
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Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW65655;
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100.0%; Score 30; DB 2; Length 18;

30.8%; Pred. No. 3.3e+02;

4; Conservative Best Local Similarity WO200259144-A2 11-DEC-2002 01-AUG-2002. Bos taurus. Haynes P, ABG95997; peptide Matches RESULT 셤 8

The invention discloses analytical reagents (e.g. trifunctional synthetic reagents) which can be used for reducing the complexity of peptide mixtures. The method labels peptides at a specific amino acid residue and then selectively enriches only those peptides containing the labelled amino acid. The compound have the formula of immobilisation site-cleavage site-link. The immobilisation site is chosen from an epitope tag, a linker to a solid surface, a metal chelating site, a magnetic site and a specific oligonuclectide sequence, or their combination, the cleavage site is chosen from a protease cleavage site, a photocleavable linker, a set is cite is chosen from a protease cleavage site, a photocleavable linker, a restriction enryme cleavage site, a chemical cleavage site and a thermal cleavage site, or their combination. The compounds are useful for simultaneesite, or their combination. The compounds are useful for simultaneously identifying and determining the levels of expression of cysteine-containing proteins; in normal and perturbed cells. The advantage is that these reagents allow rapid and compasses, accurate relative quantification of peptide amounts using masses spectrometry, can be achieved. The sequences given in AbG9593-AbG96244 are examples of the peptide tags used to isolate cysteine-containing the nearest electron the peptides isolated using the nearest clearage. ö specific Rabbit; bovine; analytical reagent; trifunctional; peptide mixture; enrichment; immobilisation site; cleavage site; link; epitope tag; protease; cysteine-containing; perturbed cell; mass spectrometry; peptide tag; BSA; bovine serum albumin; PEPTag; APEPTag; IPEPTag; affinity peptide encoded tag; immobilised peptide encoded tag; chicken; beta-lactogobulin; GAPDH; glyceraldehyde-3-phosphate dehydrogenase; a-lactalbumin; ovalbumin; yeast. Gaps Novel trifunctional synthetic reagents for labeling peptides at samino acid residue and selectively enriching only those peptides containing labeled amino acid, useful for proteomic analysis. ő 0; Indels Cysteine-containing peptide isolated from BSA, #17. 9; Mismatches ż (SYGN) SYNGENTA PARTICIPATIONS AG. Andon Disclosure; Page 44; 79pp; English. ABG95997 standard; peptide; 18 AA. 26-JAN-2001; 2001US-0264576P. 13-JUL-2001; 2001US-0305232P. 25-JAN-2002; 2002WO-US002487 Yates J, (first entry) ||::::::|:|: |TFLEIVNLLKDDL 15 1 TFXXXXXXLXDXX 13 WPI; 2002-599760/64. Wei J,

In the interaction describes a novel pharmaceutical composition for treating or preventing arthritis or other degenerative disease which comprises a polypeptide a collagen type IX alpha 1 chain NC4 domain or a biologically active fragment having antiarthritic, antiinflammatory and immunosuppressive activity in combination with a carrier. The invention describes two methods for recovering a polypeptide having anti-arthritic or anti-inflammatory activity. The first method comprises isolating a mixture comprising a GAG-peptide and a polypeptide having amilecular weight of less than 30000 ba yearlolysis from connective tissue, weight of less than 30000 ba yearlolysis from connective tissue, colypeptide. The second method comprises incubating connective tissue in an autolysis medium that provides a buffeeted pH range of 2.5-8.5 for a time and under conditions sufficient to release a GAG-peptide and autolysis medium, separating the GAG-peptide and polypeptide from the autolysis medium, separating the GAG-peptide from the GAG-peptide and polypeptide from the autolysis medium, separating the polypeptide from the GAG-peptide and polypeptide from the autolysis medium, separating the polypeptide from the GAG-peptide from the autolysis medium, separating the polypeptide from the GAG-peptide from the croovering in the covered anti-arthritic or anti-inflammatory polypeptides are useful for inducing cartilage formation or for preparing a medicament for the condition of arthritis or other musculoskeletal ö Pharmaceutical composition for treating or preventing arthritis or other degenerative disease in an individual, comprises a polypeptide comprising a collagen type IX alpha 1 chain NC4 domain. degenerative condition or for tolerizing an individual to at least one antigenic component of cartilage. This sequence represents a fragment of bovine serum albumin. This invention describes a novel pharmaceutical composition for treating Gaps ö arthritis; antiarthritic; antiinflammatory; immunosuppressive; musculoskeletal disease; degeneration; bovine serum albumin. Score 30; DB 5; Length 18; Pred. No. 3.3e+02; 0; Indels Pred. No. 3.3e 9; Mismatches Bovine serum albumin peptide fragment #28. (NUTR-) INST NUTRACEUTICAL RES PTY LTD. ADV95854 standard; peptide; 18 AA. Disclosure, Fig 5, 92pp; English 100.08; 17-JUN-2004; 2004WO-AU000788 17-JUN-2003; 2003AU-00903037. 30.8%; (first entry) ||::::::|:|:: 1 TEXXXXXXIXDXX 13 Conservative WPI; 2005-039981/04. Best Local Similarity Matches 4; Conserv WO2004110475-A1. 10-MAR-2005 23-DEC-2004. 4; Bos taurus. ADV95854; Query Match Ghosh P; RESULT 2 ò 셤

100.0%; Score 30; DB 9; Length 18; 30.8%; Pred. No. 3.3e+02;

Best Local Similarity

Query Match

Sequence 18 AA

Sequence 18 AA;

Search completed: June 29, 2006, 09:51:06 Job time : 201 secs

3 TFHADICTLPDTE 15

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Gaps

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ratios of molecules comprising peptides resulting the masses or mass to charge ratios of molecules comprising peptides resulting from the digestion or fragmentation of a polypeptide or protein; determining a first physico-chemical property other than mass or mass to charge ratio of the molecules comprising peptides; and and optionally determining a second, third, fourth and/or fifth physico-chemical property of the molecules comprising peptides; and a mass spectrometer comprising a mass analyser. Or accurately determining the mass to charge ratio of the first molecules, and means for identifying the first molecules of the basis of at least the first physico-chemical property and the accurately cat least the second, third, fourth and/or fifth physico-chemical property and the accurately cat least the second, third, fourth and/or fifth physico-chemical property. The method and spectrometer are useful in protein control of the first masses, high-resolution mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method of mass spectrometry. The method accurately seas mass analysing the first molecules in a first mixture and accurately determining the mass to charge ratio of the first molecules in the first mixture. The invention further relates to: generating an index for use in identifying molecules of biological origin by mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spectrometry, proteomics, genomics and bioinformatics. This sequence represents a peptide from an indexed peptide database created by the novel mass spectrometry method of the invention.
Indels
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 7B; 123pp; English.
                                                                                                                                                                                                                                                                                                                  AEA78835 standard; peptide; 19 AA.
9.
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14-MAR-2002; 2002US-0364847P.
                                                                  1 TFXXXXXXLXDXX 13
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4 TFHADICTLPDTE 16
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4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MICR-) MICROMASS LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos sp.
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ID AEA78835
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CONTROL
Matches
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Gaps

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100.0%; Score 30; DB 7; Length 19; 30.8%; Pred. No. 3.6e+02; tive 9; Mismatches 0; Indels

Query Match 100. Best Local Similarity 30.8 Matches 4; Conservative

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A method of mass spectrometry, useful in protein identification and quantitation, by mass analyzing the first molecules in the first mixture and accurately determining the mass to charge ratio of the first molecules in the first mixture.
                                                                                                     mass spectrometry; peptide index; protein identification; protein quantitation; protease; high-resolution mass spectrometry; proteomics; genomics; bioinformatics; Bovine Serum Albumin.
Bovine Serum Albumin indexed peptide database peptide #50
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P32296 bos taurus P63297 cavia porce P3299 trypanosoma O83249 tetrandom n O24kh trichostron O34m35 bacillus th O84128 treptococc O34m91 frankia sp. O80797 arabidopsis O80795 ponicillium O8160 penicillium O8161 090728 TRYCK 0913W9 HUWAN 02XKH4 9B1LA 02XKH4 9B1LA 03XN35 BACTW 08DT72 STRMU 08DT72 STRMU 08DT60 9EURO 08J160 9EURO 08J161 9EURO 08J163 9EURO 08J165 9EURO 08J165 9EURO Q8MJA7_MACMU Q87QM2_VIBPA Q4N2A0_T Q5U3C6_B 7UH49 Result

ALIGNMENTS

neisseria g pelobacter solibacter prochloroco mycobacteri homo sapien enterobacte mus musculu dictyosteli pelagibacte homo sapien dictyosteli bacillus su ralstonia m burkholderi burkholderi orange-spot rock bream caenorhabdi microcystis microcystis microcystis streptococc prochloroco silicibacte gallus gall tortoise he streptococc macaca mula mus musculu sapien ictyosteli bacillus su erwinia car human immun magnetospir clostridium monodelphis burkholderi microcystis microcystis thermoanaer anas platyr escherichia coturnix co schistosoma homo sapien homo sapien microcystis microcystis microcystis mycobacteri gallus gall rhizobium l microcystis lyngbya aer gluconobact bacteriopha escherichia microcystis arthrobacte infections plasmodium drosophila uncultured homod Q3dcj3 g Q3dcj3 g Q3dcj3 g Q3dcj3 g Q3dg28 g Q8xbv5 g Q8xbv6 g Q8x 030qu7 04nbg7 05VZEO_HUMAN 03DC73_STRAG 07U273_STRAG 07VAG3_PROMA 08TBV5_THETN 05YE66_9VIRU 05YE66_9VIRU 05YE66_9VIRU 05YE06_DVIRU 03T010_9YIRU 030T01_9YIRU 030T01_9YIRU 030F01_CHICK 03PSQ1_CHICK 03PSQ1_CHICK 03PSQ1_CHICK 03PSQ1_CHICK 03FE05_NEIG1 05FE05_NEIG1 05FE05_NEIG1 05FE05_NEIG1 05FE05_NEIG1 05FE05_NEIG1 05FE05_NEIG1 05FE05_NEIG1 05FE05_NEIG1 05FE06 07TXG9_MYCTU 07TXG9_MYCT 055TL7 SCHJA 06D381 ERWCT 041424 9H1V1 09H318 HUMAN 06NES1 9PROT 097HU6 CLOAB 04VAF8 MOUSE 085JA2 DICDI 04FLV6 PELUB 058JA2 HUMAN 09PIH8 HUMAN 099PIH8 HUMAN Q219E8 9HERP Q219F0 9HERP Q219F0 9HERP Q35C8 9HUK Q41XN2 9BURK Q5F0K6 9CYAN Q5F0K6 9CYAN MONDO
BURVI
MICAE
MICAE
9CHRO
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MICAE
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9CHRO PLABE 9CYAN G7_GLUOX BPPF3 DROME Q8VW28_M Q8VW30_9 Q8VW33_9 002709 N 002709 N 04BQ11 E 08VLH3 N 08VLJ4 N Q8VW36_5 Q4YDD3_1 Q563D9<u>_</u> 08VLJ9 08VW27 VHED

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1 TFXXXXXXLXDXX 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Stimulates formation of NaHCO(3)-rich pancreatic juice and secretion of NaHCO(3)-rich bile and inhibits HCl production by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                              Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Strongylida,
Ancylostomatoidea, Ancylostomatidae, Ancylostomatinae, Ancylostoma.
                                                                                                                                                                                Albonico M., Wright V., Bickle Q.;
"Mollecular analysis of the beta-tubulin gene of human hookworms as
basis for possible benzimidazole resistance on Pemba Island.";
Mol. Biochem. Parasitol. 134:281-284(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=81237102; PubMed=7250377; DOI=10.1016/0014-5793(81)80343-2; Carlquist M., Joernvall H., Mutt V.; "Isolation and amino acid sequence of bovine secretin."; FRBS Lett. 127:71-74(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovinae, Bovinae, Bos.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Score 30, DB 2; Length 25
Pred. No. 4.6e+02;
9; Mismatches 0; Indels
                                                                                                                                                          NUCLEOTIDE SEQUENCE.
PubMed=15003848; DOI=10.1016/j.molbiopara.2003.12.008;
                                                                                                                                                                                                                                                                         EMBL; AF453525; AAQ01173.1; -; Genomic_DNA.
GO; GO:0005874; C:microtubule; IEA.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007018; P:microtubule-based movement; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 AA; 2936 MW; 554CF1ECB60AEF4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECR BOVIN STANDARD, PRT; 27 AA. P63296; P01279; Q9TR13; 21-JUJ-1986, integrated into UniProtKB/Swiss-Prot. 11-OCT-2004, sequence version 1.
                                                    01-OCT-2003, integrated into UniProtKB/TrEMBL
                                25 AA.
                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002453; Beta tubulin.
InterPro; IPR00217; Tubulin.
InterPro; IPR003008; Tubulin Fts2.
BATHER; PTHR11588: SF9; Beta_tubulin; 1.
PANTHER; PTHR11588; Tubulin; 1.
Pfam; PF00091; Tubulin; 1.
GTP-binding; Nucleotide-binding.
                               PRT;
                                                              01-OCT-2003, sequence version 1.
07-FEB-2006, entry version 12.
Beta tubulin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.8%;
                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                  Ancylostoma duodenale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                    NCBI_TaxID=51022;
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                           Q7XXI3_9BILA
Q7XXI3;
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SECR BOVIN
                    Q7YXI3
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Distributed under the Creative Commons Attribution-NoDerivs License
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90254163; PubMed=2340284; DOI=10.1016/0167-4838(90)90248-E; Buscail L., Cauvin A., Gourlet P., Gossen D., de Neef P., Rathe J., Robberecht P., Vandermeers-Piret M.-C., Vandermeers A., Christophe J.; "Purification and amino acid sequence of vasoactive intestinal peptide, peptide histidine isoleucinamide (1-27) and secretin from the small intestine of guinea pig."; Blochim. Blophys. Acta 1038:355-359(1990).

-! FUNCTION: Stimulates formation of NaHCO(3)-rich pancreatic juice and secretion of NaHCO(3)-rich bile and inhibits HCI production by the stomach.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Hystricognathi; Caviidae; Cavia.
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Pred. No. 5e+02;
9; Mismatches 0; Indels
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Valine amide.
2D4015814ED05B78 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P63297; P01279; O9TR13; 21-JUL-1986, integrated into UniProtKB/Swiss-Prot. 11-OCT-2004, sequence version 1. 07-FEB-2006, entry version 9.
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-!- SUBCELLULAR LOCATION: Secreted protein.
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-!- SIMILARITY: Belongs to the glucagon family.
                                                                                                                                                                                 Fram, PF00123; Hormone_2; I. SMART; SM0070; GLUCA; I. PROSITE; PS00260; GLUCAGON; I. PROTIE; PS00260; GLUCAGON; I. Secretin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            5e+02;
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SMART; SM00070; GLUCA; 1.
SMOSTIE; PS00266; GLUCAGON; 1.
Amidation; Direct protein sequencing; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.8%; Pred. No. 5e+C
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                                                                                                                                                              InterPro; IPR000532; Glucagon.
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5 TFTSELSRLRDSA 17
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Distributed under the Creative Commons Attribution-NoDerivs License
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of human immunodeficiency virus type 1 in saliva and
blood plasma by V3-specific heteroduplex tracking assay and genotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses, Retro-transcibing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21211648; PubMed=11312368;
MEDLINE=21211648; PubMed=11312368;
DOI=10.1128/JVI.75.10.4936-4940.2001;
Freel S.A., Williams J.M., Nelson J.A., Patton L.L., Fiscus S.A., Swanstrom R., Shugars D.C.;
                                                                                                                                                                   EMBL; AY514756; AAT44586.1; -; Genomic_DNA.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
InterPro: IPR001806; Ras_trnsfrmng.
Pfam; PF00071; Ras; I.
GTP-binding; Nucleotide-binding.
                   Housley D.J.E., Ritzert E., Venta P.J.; "Comparative radiation hybrid map of canine chromosome 1 (CFA1) incorporating SNP and indel polymorphisms.";
                                                                                                                                                                                                                                                                                                                                                                               30.8%; Pred. No. 5e+02; Length 27; 30.8%; Pred. No. 5e+02; Ative 9; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                            27 AA; 3119 MW; 14D5E56B1C5C4731 CRC64;
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   PubMed=15233990; DOI=10.1016/j.ygeno.2004.04.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001, integrated into UniProtKB/TrEMBL.
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GO; GO:0013031; C:viral envelope; IEA.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Envelope protein. 1
NON TER 1 27 27 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analyses.";
J. Virol. 75:4936-4940(2001).
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                                                                           Genomics 84:248-264(2004).
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15 TFNHLTTWLEDAR 27
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TFYATGDILGDIR 27
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Q900E5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Purification and amino acid sequence of vasoactive intestinal peptide, peptide histidine isoleucinamide and secretin from the ovine small intestine."; Regul. Pept. 32:169-179(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11. Pept. 32:169-179(1991).
FUNCTION: Stimulates formation of NaHCO(3)-rich pancreatic juice and secretion of NaHCO(3)-rich bile and inhibits HCl production h
                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Small intestine;
MEDLINE=91229834; PubMed=2034821; DOI=10.1016/0167-0115(91)90044-H;
BOUNJOUA Y., Vandermeers A., Robberecht P., Vandermeers-Piret M.C.,
Christophe J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                         Ovis ariės (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Caprinae, Ovis.
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/FTId=PRO 0000043937.
Valine amīde.
                                                                                                                                                   integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Secreted protein.
-!- SIMILARITY: Belongs to the glucagon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004, integrated into UniProtKB/TrEMBL.
05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 10.
RAS oncogene family member RAB2 (Fragment).
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9; Mismatches
                                                                                                              27 AA
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                                                                                                              PRT;
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                                                                                                                                            01-JUL-1993, integrated into Univ
01-JUL-1993, sequence version 1.
07-FEB-2006, entry version 33.
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27 AA; 3056 MW;
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QGJDH7;
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TFTSELSRLRDSA 17
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TFTSELSRLRDSA 17
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                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE.
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MEDLINE=20381320; PubMed=10900267; DOI=10.1073/pnas.150236097;
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                                                                                                                                                                                                                                                                                    33 AA; 3519 MW;
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les 4; Conserv
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QZKKH4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pubmed=15496914; DOI=10.1038/nature03025;

Adillon O. Aury U.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

Adillon O., Aury U.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

Mancali E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Nicaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B.,

Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,

Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

A. Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Landet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                         Tetraodon nigroviridis (Green puffer).

Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/Genbank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
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                                                                                                                                                              19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 3.
Chromosome 17 SCAF14760, whole genome shotgun sequence.
ORFNames=GSTENG0024943001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; CAAE01014760; CAG05048.1; -; Genomic DNA. SEQUENCE 31 AA; 3414 MW; 780B92E08D35B525 CRC64;
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01-MAR-2001, sequence version 1.
07-FEB-2006, entry version 11.
                                                                                                                                          19-JUL-2005, integrated into UniProtKB/TrEMBL
                                                                                             31 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                             PRT;
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Q9GYZ8;
                                                                                             PRELIMINARY;
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TFMKNVQVLLDAA 18
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                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=99883;
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Name=Sm-D3;
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                                                                                           Q4S2T4_TETNG
Q4S2T4;
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Matches
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19-27

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DT 19-3

DT 1
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QGGYZB TR
QGGYZB TR
DD QGGY
AC QGGY
DT 01-M
DT 07-F
DD 07-F
DD SM-D
DC SCH
OC SCH
OC SCH
OX NCBI
RR (1)
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Distributed under the Creative Commons Attribution-NoDerivs License
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The German cDNA Consortium;
Ansorge W., Kriager S., Regiert T., Rittmueller C., Schwager B.,
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
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Palfi Z., Luecke S., Lahm H.-W., Lane W.S., Kruft V., Bragado-Nilsson E., Seraphin B., Bindereif A.; "The spliceosomal snRNP core complex of Trypanosoma brucei: cloning and functional analysis reveals seven Sm protein constituents."; Proc. Natl. Acad. Sci. U.S.A. 97:8967-8972 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 30; DB 2; Length 33; Pred. No. 6.3e+02; 9; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                       CB8FE375E0704065 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001, sequence version 1.
07-FEB-2006, entry version 13.
Hypothetical protein DKFZp5471137 (Fragment)
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Ensembl; ENSG0000103202; Homo sapiens
                                                                                                                                                                                                                                                                                                                          EMBL; AF280390; AAG00464.1; -; mRNA.
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SEQUENCE Query Match

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RESULT 11

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                                                                                                                                                                                                                              "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Frankia sp. EANlpec
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                              WUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=UA159 / ATCC 700610 / Serotype c;
MEDLINE=22259663; PubMed=12397186; DOI=10.1073/pnas.172501299;
Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.
Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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Frankineae; Frankiaceae; Frankia.
NCBI_TaxID=298653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 30; DB 2; Length 39; 30.8%; Pred. No. 7.5e+02; Live 9; Mismatches 0; Indels
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  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Larimer F., Land M.; "Annotation of the draft genome assembly of Frankia sp. Submitted (JUN-2005) to the EMBL/GenBank/DDB databases.
                                                                                                                                                                                                                                                                                                                                                        EMBL; AE014133; AANS9156.1; -; Genomic_DNA.
InterPro; IPR005121; Fdx Antic_bd.
Pfam; PF0147; FDX-ACB; I.
Complete proteome; Hypothetical protein.
SEQUENCE 39 AA; 4463 MW; 2DFAA508C2ACE89D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F60DC6D007529D17 CRC64;
                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2005, integrated into UniProtKB/TrEMBL. 11-OCT-2005, sequence version 1. 17-EB-2006, entry version 3. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US DOE Joint Genome Institute (JGI-ORNL);
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Q3WGH1;
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42 AA; 4726 MW;
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STRAIN=EAN1pec;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                            NCBI_TaxID=1309;
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                           Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                   Webster L.M.I., Johnson P.C.D., Adam A., Keller L.F.;
"Absence of Known benzimidazole resistance mutations in
Trichostrongylus tennis, a nematode parasite of avian hosts.";
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
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Trichostrongyloidea; Trichostrongylidae; Trichostrongylinae;
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                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 30; DB 2; Length 38 30.8%; Pred. No. 7.3e+02; Live 9; Mismatches 0; Indels
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30.8%; Pred. No. 7.3e+02;
tive 9; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
NCBI_TaxID=29339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van der Auwera G.A., Andrup L., Mahillon J.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                               38 AA; 4406 MW; AD916C1027FC36E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; DQ025752; AAZ06610.1; -; Genomic_DNA.
Hypothetical protein; Plasmid.
SEQUENCE 38 AA; 4373 MW; E77F652ABADDC54F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003, integrated into UniProtKB/TrEMBL. 01-MAR-2003, sequence version 1. 21-FBB-2006, entry version 15. Hypothetical protein. Offrames=SMU 1505c; Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 AA
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                                                                                                                                                                                                                                                                  EMBL; AY914052; AAX92642.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77-SEP-2005, sequence version 1.
07-FBB-2006, entry version 3.
Hypothetical protein.
ORFNames-phW63 040;
Bacillus thuringiensis subsp. kurstaki.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBDT72 STRMU PRELIMINARY; PRT; QBDT72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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18 TFCIDNEALYDIC 30
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                                                                                NUCLEOTIDE SEQUENCE.
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hes 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                          NCBI_TaxID=40351;
                         {\tt Trichostrongylus.}
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Q3YN35;
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sp. EAN1pec.";

Query Match

Matches

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STRMU

RESULT 12 08DT72 STR 1D QBDT7 AC QBDT7 DT 01-MA DT 01-MA DT 21-FE DF 12-FE GN ORFWAR

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NUCLEOTIDE SEQUENCE.
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STRAIN=RIMD 2210633 / Serctype 03:K6;
STRAIN=RIMD 2210633 / Serctype 03:K6;
MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
MAKINO K., OSHima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                     Gaps
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                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids; eurosids II, Brassicales; Brassicaceae, Arabidopsis.
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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PIR; T02348; T02348.
GO: 0005489; F:electron transporter activity; IEA.
GO: GO: 0005189; F:electron transport; IEA.
InterPro; IPR006662; Thioxed.
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Pred. No. 8.2e+02;
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01-JUN-2003, integrated into UniProtKB/TrEMBL
01-JUN-2003, sequence version 1.
07-FEB-2006, entry version 10.
Hypothetical protein VPA1310.
                                                                                                                                                                                                           43 AA.
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                     9; Mismatches
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                                                                                                                                                                                                                                                                        01-NOV-1998, sequence version 1. 07-FEB-2006, entry version 17.
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                                                                                                                                                                                                           PRELIMINARY;
30.8%;
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                                                          1 TFXXXXXXLXDXX 13
                                                                                       19 TFDLKPTPLDDVL 31
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TFGSGSSSLGDEV 39
                     4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
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O80797;
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Matches
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087645 VIB
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11jima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Penicillium.
NCBI_TaxID=189054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=NRRL 31002, and NRRL 31401;
Peterson S.W., Sigler L.;
"Four new Penicillium species having Thysanophora-like melanized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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GO; GO: 0005251 F.GTP binding; IEA.
GO; GO: 0005251 F.GTP binding; IEA.
GO; GO: 0005251 F.GTP binding; IEA.
GO; GO: 0005198; F.STructural molecule activity; IEA.
GO; GO: 0007018; F.Structubule-based movement; IEA.
INTERPRO; IPR002473; Beta tubulin.
INTERPRO; IPR002017; Tubulin.
INTERPRO; IPR00308; Tubulin.
FANTHER; PTHR11588: FYP, Beta_tubulin; 1.
PANTHER; PTHR11588; Tubulin; 1.
PFAMTHER; PTHR11589; Tubulin; 1.
                                                                                                                                                                                                                                                                              EMBL; BA000032; BAC62653.1; -; Genomic_DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 43 AA; 5048 MW; ABD923038890678F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 AA; 5020 MW; D1E9D443770CB0BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF481129; AAN86258.1; -; Genomic_DNA
EMBL; AF481132; AAN86261.1; -; Genomic_DNA
                                                                                             distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 14.
Beta-tubulin (Fragment).
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GPT-binding; Nucleotide-binding.
NON TER 45 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                            30.8%;
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14 TFKKIPFFLQDGN 26
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Distributed under the Creative Commons Attribution-NoDerivs License
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
NCBI_TaxID=189055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peterson S.W., Sigler L.; "Four new Penicillium species having Thysanophora-like melanized
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SMR; QBJ162; 1-45.

R GO; GO:0005874; C:microtubule, IEA.

R GO; GO:000525; F:GTP binding; IEA.

R GO; GO:0007166; F:mcleotide binding; IEA.

R GO; GO:0007189; F:structural molecule activity; IEA.

R GO; GO:0007189; F:structural molecule activity; IEA.

R GO; GO:0007189; F:structubulin.

InterPro; IPR002453; Beta tubulin.

InterPro; IPR003008; Tubulin.

R InterPro; IPR003008; Tubulin.

R PANTHER; PTHR11588; FP; Beta_tubulin; 1.

R PANTHER; PTHR11588; Tubulin; 1.

R PANTHER; PTHR11588; Tubulin; 1.
                                                                                   GO: GO: 0005874; C:microtubule; IEA.
GO: GO: 0005525; F:GTP binding; IEA.
GO: GO: 0000166; F:nucleotide binding; IEA.
GO: GO: 0005198; F:structural molecule activity; IEA.
GO: GO: 0007018; P:microtubule-based movement; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 AA; 5006 MW; D1E9D443720CE0BA CRC64;
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                                            EMBL; AF481130; AAN86259.1; -; Genomic_DNA.
                                                                                                                                                                                                      InterPro; IPR002453; Beta tubulin.
InterPro; IPR002453; Beta tubulin.
InterPro; IPR003107; Tubulin.
InterPro; IPR003008; Tubulin FteZ.
PANTHER; PTHR11588:SF9; Beta_tubulin; 1.
PANTHER; PTHR11588; Tubulin; 1.
Pfam; PF00091; Tubulin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 14.
Beta-tubulin (Fragment).
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PRINTS; PR01163; BETATUBULIN.
GTP-binding; Nucleotide-binding.
NON TER 1 1
NON_TER 45
                                                                                                                                                                                                                                                                                                                                                                                    GTP-binding; Nucleotide-binding.
                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01163; BETATUBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TFXXXXXXIXDXX 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=NRRL 31003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conidiophores.
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ID Q8J162 9EURO
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
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Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Penicillium.
                                                                                                                                                                                                                                                                                                                                                                             Peterson S.W., Sigler L.; "Four new Penicillium species having Thysanophora-like melanized conidiophores.";
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"Four new Penicillium species having Thysanophora-like melanized conidiophores.";
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Pred. No. 8.8e+02;
9; Mismatches 0; Indels
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GO; GO:0005874; C:microtubule; IEA.
GO; GO:0005874; C:microtubule; IEA.
GO; GO:000516; F:muclectide binding; IEA.
GO; GO:000166; F:muclectide binding; IEA.
GO; GO:0007018; F:structural molecule activity; IEA.
GO; GO:0007018; F:structubulin.
InterPro; IPR002453; Beta tubulin.
InterPro; IPR003017; Tubulin.
InterPro; IPR003008; Tubulin.
PANTHER; PTHR11588: SF9; Beta_tubulin; 1.
PANTHER; PTHR11588; Tubulin; 1.
PETM: PF00091; Tubulin; 1.
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                                                                                                      01-MAR-2003, integrated into UniProtKB/TrEMBL. 01-MAR-2003, sequence version 1. 07-FBB-2006, entry version 14. Penicululin (Fragment).
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                                                                  PRT;
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GTP-binding; Nucleotide-binding.
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QBJ161 9EURO PRELIMINARY;
QBJ161;
                                                               PRELIMINARY;
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TFCIDNEALYDIC 18
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                NCBI_TaxID=189057;
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SEQÜENCE
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Distributed under the Creative Commons Attribution-NoDerivs License
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
NCBI_TaxID=189056;
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                                                  Peterson S.W., Sigler L.;
"Four new Penicillium species having Thysanophora-like melanized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 30; DB 2; Length 45; Pred. No. 8.8e+02; 9; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  SWR; Q8J164; 1-45.

GO; GO: 0005674; C: microtubule; IEA.

GO; GO: 0005265; F: GTP binding; IEA.

GO; GO: 0005198; F: GTP binding; IEA.

GO; GO: 0005198; F: Structural molecule activity; IEA.

GO; GO: 0007018; F: structubule-based movement; IEA.

INTERPROJA53; Beta tubulin.

INTERPRO; IPRO0217; Tubulin.

INTERPRO; IPRO0308; Tubulin.

PANTHER; PTHR11588: FTBulis88: SP.

PANTHER; PTHR11588; Tubulin; 1.

PEam; PF00091; Tubulin; 1.
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GO; GO:0005525; F:GTP binding; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:0019198; F:structural molecule activity; IEA.
GO; GO:0007018; P:microtubule-based movement; IEA.
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InterPro; IPR00217; Tubulin.
InterPro; IPR002108; Tubulin. FtsZ.
BANTHER; PTHR11588:SF9; Beta_tubulin; 1.
PANTHER; PTHR11588; Tubulin; 1.
Pfam; PF00091; Tubulin; 1.
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07-FBB-2006, entry version 14.
Beta-tubulin (Fragment).
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GTP-binding; Nucleotide-binding.
NON_TER 1
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30.8%; I
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6 TFCIDNEALYDIC 18
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Best Local Similarity
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         STRAIN=NRRL 5816;
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                                                                                                                                        conidiophores.";
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Q8J165;
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SEQUENCE
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                                                  Gaps
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Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Penicillium.
NCBI_TaxID=69772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peterson S.W., Sigler L.; "Four new Penicillium species having Thysanophora-like melanized
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Eurotiales, Trichocomaceae, Eupenicillium.
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                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF481127; AAN86256.1; -; Genomic_DNA.
SMR; Q8J163; 1-45.
GO; GO:0005874; C:microtubule; IEA.
GO; GO:0005875; F:GTP binding; IEA.
GO; GO:000166; F:mcleotide binding; IEA.
GO; GO:000718; F:structural molecule activity; IEA.
GO; GO:000718; F:structural molecule activity; IEA.
GO; GO:000718; F:structural molecule activity; IEA.
InterPro; IPR00245; Beta tubulin.
InterPro; IPR00217; Tubulin.
InterPro; IPR003008; Tubulin.
InterPro; PRR11588:SF9; Beta_tubulin; 1.
PANTHER; PTHR11588; Tubulin; 1.
PANTHER; PTHR11588; Tubulin; 1.
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         Pred. No. 8.8e+02;
9; Mismatches 0;
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07-FEB-2006, entry version 14.
Beta-tubulin (Fragment).
Bupenicillium stolkiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 14.
Beta-tubulin (Fragment).
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GTP-binding; Nucleotide-binding.
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30.8%; F
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QBJ163;
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30.8%;
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6 TFCIDNEALYDIC 18
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NUCLEOTIDE SEQUENCE.
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QBJ164;
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Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases
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Q91FG1 IRV6
ID Q91FG1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sullivan M.B., Coleman M.L., Weigele P., Rohwer F., Chisholm S.W. "Three prochlorococcus cyanophage genomes: signature features and ecological interpretations."; PLS 8194.E144.E144(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sullivan M.B., Johnson Z.I., Tolonen A.C., Rohwer F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virusės; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
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OrderedLocusNames=BURPS1710b A0313;
Burkholderia pseudomallei (sfrain 1710b).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiaceae, Burkholderiaceae, Burkholderiaceae, Burkholderia; pseudomallei group.
                                                                                                                                                                                                                                              Length 45;
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30.8%; Pred. No. 8.8e+02;
tive 9; Mismatches 0; Indels
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Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                     45 45
45 AA; 5020 MW; D1E9D443770CB0BA CRC64;
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                                                                                                                                                                                                                                      100.0%; Score 30; DB 2; 30.8%; Pred. No. 8.8e+02; ive 9; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-APR-2005, integrated into UniProtKB/TrEMBL.
26-APR-2005, sequence version 1.
07-FBB-2006, entry version 4.
ORPOCHETICAL protein.
ORFNames=PSSM2_101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
    PRINTS; PR01163; BETATUBULIN.
GTP-binding; Nucleotide-binding.
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SEOUENCE 45 AA; 5197 MW;
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6 TFCIDNEALYDIC 18
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TFNRFDDYLTDDA 14
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Matches 4, Conservative
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AC (33.4)

AC (33.4)

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MEDLINE=9118242; PubMed=1475907;
Sonntag K.C., Darai G.;
"Characterization of the third origin of DNA replication of the genome of insect iridescent virus type 6.";
Virus Genes 6:333-342(1992).
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MEDILINE=94292906; PubMed=8021587;
Schnitzler P., Sonniag K.C., Muller M., Janssen W., Bugert J.J.,
Koonin E.V., Darai G.;
"Insect iridescent virus type 6 encodes a polypeptide related to the
largest subunit of eukaryotic RNA polymerase II.";
J. Gen. Virol. 75:1557-1567(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
MEDLINE=99125223; PubMed=9926400; DOI=10.1023/A:1008017820941;
Muller K., Tidona C.A., Bahr U., Darai G.;
"Identification of a thymidylate synthase gene within the genome
                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chilo iridescent virus (CIV) (Insect iridescent virus type 6). Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
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MEDILTE=98141693; Publed=9482589; DOI=10.1023/A:1007932620930;
MEDILTE=98141693; Publed=9482589; DOI=10.1023/A:1007932620930;
Bahr U., Idona C.A., Darai G.;
"The DNA sequence of Chilo iridescent virus between the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94353641; PubMed=8073636; Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.; Schnitzler P., Koonin E.V., Darai G.; "Chilo iridescent virus encodes a putative helicase belonging distinct family within the 'DEAD/H' superfamily: implications evolution of large DNA viruses."; Virus Genes 8:151-158(1994).
                                                                                                                                                                                                                                                                      100.0%; Score 30; DB 2; Length 45; 30.8%; Pred. No. 8.8e+02; ive 9; Mismatches 0; Indels
                                                                                              EMBL; CP000125; ABA51693.1; -; Genomic_DNA.
TIGR; BURPS1710b_A0313; -.
Complete proteome; Hypothetical protein.
SEQUENCE 45 AA; 4619 MW; 01C9B6229185CE49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chilo iridescent virus.";
Virus Genes 17:243-258(1998)
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                            Local Similarity
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MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
Jakob N.J., Mueller K., Bahr U., Darai G.;
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coordinates 0.101 and 0.391; similarities in coding strategy between insect and vertebrate iridoviruses."; Virus Genes 15:235-245(1997).
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MEDLINE-86174607; PubMed=3959991;
Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
"Insect iridescent virus type 6 induced toxic degenerative hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of a gene cluster within the genome of Chilo
iridescent virus encoding enzymes involved in viral DNA replication
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"Molecular cloning and physical mapping of the genome of insect
iridescent virus type 6: further evidence for circular permutation
                                                                                                       NUCLEOTIDE SEQUENCE.
Delius H., Darai G., Fluegel R.M.;
"DNA analysis of insect iridescent virus 6: evidence for circular permutation and terminal redundancy.";
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MEDLINE=99383793; PubMed=10456793; DOI=10.1023/A:1008072319875;
Muller K., Tidona C.A., Darai G.;
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MEDLINE=87321126; PubMed=2820141;
Schnitzler P., Soltau J.B., Fischer M., Reisner H., Scholz J.,
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Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
Delius H., Darai C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the genome of insect iridescent virus type 6.";
Virology 167:485-496(1988).
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Virology 160:66-74(1987).
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Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca.
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                                                                                                                                          Length 46
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47 AA; 5403 MW; 94C9D3FBEF349435 CRC64;
                                                      EMBL; AF303741; AAK82223.1; -; Genomic DNA.
SEQUENCE 46 AA; 5365 MW; 6D82076DEF12EE14 CRC64;
                                                                                                                                                                 Pred. No. 9.1e+02;
9; Mismatches 0
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Hypothetical protein.
SEQUENCE 47 AA; 5403 MW; 94C9D3FBEF3494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uncultured sulfate-reducing bacterium.
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08-NOV-2005, sequence version 1.
07-FEB-2006, entry version 4.
Hypothetical protein.
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07-FEB-2006, entry version 9.
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Macaca mulatta (Rhesus macaque).
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Best Local Similarity 30.8
Matches 4; Conservative
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NCBI_TaxID=5875;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=RIMD 2210633 / Serotype 03:K6;
MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
MAKINO K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
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NCBI_TaxID=117;
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Vibrionaceae, Vibrio.
NCBI_TaxID=670;
EMBL; AF512352; AAM75335.1; -; Genomic_DNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004713; F:proteain-tyrosine kinase activity; IEA.
GO; GO:000468; P:proteain amino acid phosphorylation; IEA.
InterPro; IPR00179; Prot kinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF07714; Pkinase_Tyr; 1.
ProDom; PD00001; Prot_kinase; 1.
                                                                                                                                                                                                                                        Length 49;
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                                                                                                                                                                                                      100.0%; Score 30; DB 2; Length 45, 30 8%; Pred. No. 9.7e+02; O; Indels
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                                                                                                                                                                                             49 AA; 6023 MW; 3FAD624A333DD54F CRC64;
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Pred. No. 9.7e+02;
9; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, BA000031; BAC59390.1; -; Genomic DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 49 AA; 5544 MW; 9F4117D411207BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003, sequence version 1.
O7-FBB-2006, entry version 12.
Hypothetical protein VP1127.
OrderedLocusNames=VP1127;
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Gardner M., Bishop R., Shah T., de Villiers B., Carlton J.M., Hall N.,
Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
Lynn J., Weaver B., Shoaibh A., Wasawo D., Crabtree J., Wortman J.R.,
Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
Utterback T., Feldblyum T., Pertea M., Allen J., Taracha B.L.,
Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
Fraser C.M., Nene V.)
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                                                                                                       MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.; "Complete genome sequence of the marine planctomycete Pirellula strain 1.";
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Complete proteome; Hypothetical protein.
SEQUENCE 50 AA; 5444 MW; 4FF2B5333D11FA48 CRC64;
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[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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    EMBL; AAGK01000004; EAN31804.1; -; Genomic_DNA.
Hypotherical protein.
SEQUENCE 54 AA; 6238 MW; 8B9494FCD89342FC CRC64;
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New immunosupressant DNA and protein - useful for inhibition and treatment of autoimmune diseases caused by lymphoid cell protein-tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein kinase homologue; human; PKH; diagnosis; therapy; cancer; AIDS; autoimmune disorder; inflammatory disorder; reproductive defect; asthma; diabetes mellitus; infertility; ovulatory defect; endometriosis;
                                                                                                                                                                                                                                                                                                        This sequence is the Lymphoid cell protein-tyrosine kinase (Lck) SH3 domain of the invention. The DNA and protein are useful as immune suppressants, and are useful for inhibition and treatment of autoimmune diseases caused by Lck analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding a human protein kinase homolog useful for preventing, diagnosing and treating cancer, autoimmune/inflammatory disorders and reproductive defects.
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                                                                                                                          GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein kinase homologue, PKH-3
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                                                                                                                                                                                                                                                                                Claim 1; Page 4-5; 6pp; Japanese.
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Guegler KJ;
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                                                                                                                          (KAGA-) KAGAKU GIJUTSU SHINK
(MITU ) MITSUBISHI CHEM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polycystic ovary syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LODNLVIAL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JL, Yue H,
Bandman O,
                                                                                                                                                                       WPI; 1999-099029/09.
N-PSDB; AAV62889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-136321/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ86794.
                                                                                                                                                                                                                                                   kinase analogues.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 126 AA;
 JP10327864-A.
                                                                                           28-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-OCT-1998;
                                                              28-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6013455-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillman JL,
                                15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY76750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
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Abu36857 Protein e
Abb62664 Drosophil
Aae20614 Protein #
Aae20624 Protein #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and polynucleotides encoding them for treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to peptides which are partial sequences of stor/lck family proteins. The present sequence is one such peptide. The peptides are useful for producing vaccines for the treatment of cancer, including colon cancer and small-cell lung cancer
                                                                                                                                                                                                                                                                                                Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lymphoid cell protein-tyrosine kinase; Lck; SH3 domain; inhibitor; immune suppressant; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 41; DB 4; Length 9; 100.0%; Pred. No. 2.1e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lymphoid cell protein-tyrosine kinase SH3 domain.
                                                                                           ALIGNMENTS
ABU36857
ABB62664
AAE20614
AAE20624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW73554 standard; protein; 126 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 69; 75pp; Japanese.
                                                                                                                                                                       ¥Ÿ.
                                                                                                                                                                       AAB73127 standard; peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000; 2000WO-JP005220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-00222101
                                                                                                                                                                                                                                                                  Tumour antigen peptide #11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100
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 73.2
73.2
70.7
70.7
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                                                                                                                                                                                                                                                                                                                                                            WO200111044-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9 AA;
                                                                                                                                                                                                                                   09-MAY-2001
                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                          15-FEB-2001
   230 330 230 230
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Best Local Si
Matches 9;
                                                                                                                                                                                                      AAB73127;
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Itoh K;

Unidentified

RESULT 2

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Gaps

expression such as cancers (e.g. lymphoma, melanoma and cancers of the breast lung and prostate), autoimmune/inflammatory disorders (e.g. AIDS, asthuma and diabetes mellitus), and reproductive defects (e.g. AIDS, infertility, ovulatory defects, endometriosis and polycystic ovary syndrome). The DNA may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PKH by expressing inactive proteins or to supplement the patients own production of PKH polypeptides. Additionally, the DNA may be used to produce PKH, according to standard recombinant DNA methodology, by inserting the mucleic acids into a host cell and culturing the cell to coppess the protein. Conversely, antisense nucleic acid molecules may be administered to down regulate PKH expression by binding with the cells own PKH genes and preventing their expression. The DNA, and antisense sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and become an expression and all and culture to the presence of similar nucleic acid sequences in samples, and become an expression and presence of similar nucleic acid sequences in samples, and become an expression and presence of similar nucleic acid sequences in samples. also be used to study the expression and function of PKH polypeptides and their role in metabolism. The PKH polypeptides may be used as antigens in the production of antibodies against PKH and in assays to identify modulators (agonists and antagonists) of PKH expression and activity. The anti-PKH antibodies and PKH argonists may also be used to down regulate PKH expression and activity. The anti-PKH antibodies may also be used as diagnostic agents for detecting the presence of PKH polypeptides in This sequence represents a human protein kinase homolog (PKH) of the invention. The PKH sequences may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PKH expression such as cancers, autoimmune/inflammacry disorders and reproductive defects. They may be used to treat disorders associated with decreased PKH Claim 1; Col 47-50; 38pp; English

Sequence 346 AA;

Gaps ö 100.0%; Score 41; DB 3; Length 346; 100.0%; Pred. No. 5.3; ive 0; Mismatches 0; Indels Query Match Best Local Similarity luv...

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61 LODNLVIAL 69

RESULT 4 AAE06208

AAE06208 standard; protein; 346 AA.

AAE06208;

(first entry)

25-SEP-2001

Human protein kinase homolog-3 (PKH-3).

breast; autoimmune disorder; multiple sclerosis; drug screening; anaemia; Crohn's disease; ectopic pregnancy; tubal disease; inflammatory disorder; reproductive disorder; polycystic ovary syndrome; asthma. Human, protein kinase homolog-3, PKH-3, cytostatic, protein therapy; vaccine; immunosuppressive; antisclerotic; antiabortive; adenocarcinoma; Acquired Immune deficiency Syndrome; AlDS; melanoma; cancer; bone; liver;

Homo sapiens

125. .333 /note= "Signature sequence" Location/Qualifiers

Region

US6264947-B1

24-JUL-2001

99US-00420915. 20-OCT-1999; 98US-00173581 15-OCT-1998;

(INCY-) INCYTE GENOMICS INC.

Corley NC; Guegler KJ, Yue H, Hillman JL, Lu DAM; Tang YT, H: Azimzai Y, Bandman O, Gorgone GA,

WPI; 2001-450728/48

N-PSDB; AAD11845.

and treating cancers, autoimmune/inflammatory disorders and Human protein kinase proteins and homologs, useful for preventing, reproductive disorders.

Claim 1; Col 47-50; 38pp; English.

The present sequence is human protein kinase homolog-3 (PKH-3). Human protein kinase homologs (PKH) and their CDNA molecules are used in the prevention, diagnosis and treatment of diseases associated with increased or decreased expression of PKH. Examples of such disorders include, cancer (e.g. adenocarcinoma, melanoma and bone, breast and liver cancer), suttoimmune/inflammatory disorders (e.g. Acquired Immune deficiency Syndrome (AIDS), anaemia, asthma, crohn's disease and multiple sclerosis) and reproductive disorders (e.g. tubal disease, ectopic pregnancy and polycyptic oversy syndrome). PKH, its catalytic or immunogenic fragment are used for screening libraries of compounds in any of the drug screening techniques. PKH nucleic acids are used to generate thyridisation probes useful in mapping the naturally occurring genomic sequences. PKH are also used as antigens in the production of antibodies gainst protein kinases (PK) and in assays to identify modulators of PKH expression and activity. PKH is also used in protein therapy

Sequence 346 AA;

Gaps ö 100.0%; Score 41; DB 4; Length 346; 100.0%; Pred. No. 5.3; ive 0; Mismatches 0; Indels 9; Conservative Query Match Best Local Similarity Matches

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RESULT 5 ABB84435

ABB84435 standard; protein; 346 AA.

ABB84435;

08-NOV-2002 (first entry)

Human protein kinase homologue from clone 507669.

W antiantlammatory; antiallergic, antiasthmatic; antiannemic; antidiabetic; antiantlammatory; antiallergic, antiasthmatic; antiannemic; antidiabetic; antianteriosolerotic; antithyroid; dermatological; nephrotropic; human; antigout; thyromimetic; notionogical; netiulcer; antiviral; antiantritic; allergy; antiprotozoal; antiparasitic; antihelmintic; ankylosing spondylitis; antiprotozoal; antiparasitic; antihelmintic; ankylosing spondylitis; which is matiprotozoal; antiparasitic; antihelmintic; ankylosing spondylitis; antiparasitic; antihelmintic; ankylosing spondylitis; which is matoimmune haemolytic anaemia; autoimmune thyroiditis; bronchitis; autoimmune haemolytic anaemia; autoimmune thyroiditis; bronchitis; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; crohn's disease; atopic dermatitis; dermatitis; diabetes mellitus; emphysema; atrophic gastritis; gout; whishing to a thyroiditis; hypereosinophilia; irritable bowel syndrome; multiple sclerosis; mysathenia gravis; myocardial inflammation; osteoporosis; pancreatitis; polymyositis; Reiter's syndrome; rheumatoid arthritis; scleroderma; SLE; thrombocytopenic purpura; ulcerative colitis; Werner syndrome; infection; haemodialysis; extracorporeal circulation; infertility; tubal disease; ovulatory defect; endometricais; osetrous; menstrual cycle; gene therapy; uterine fibroid; autoimmune disorder; polycystic ovary syndrome; enzyme; enzyme; Protein kinase homologue; PKH; cytostatic; immunosuppressive; antifungal Sjogren's syndrome; systemic lupus erythematosus; systemic sclerosis;

RESULT 6

Corley NC;

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This invention describes a novel protein kinase homologue (PKH)

polypeptides which have cytostatic, immunosuppressive, antiinflammatory,
antiallergic, antisabimatic, antianteamic, antiarteriosclerotic,
antithyroid, dermatological, antidabetic, nephrotropic, antigout,
thyromimetic, nootropic, osteopathic, antiarthritic, antirhematic,
contralmological, antidace, antivirent antirhematic, antiprocessal, antiparasitic and antihelminic activity. The polypeptide
attiprocessal, antidace, antivirent antihelminic activity. The polypeptide
is used for treating a disease or condition associated with decreased
expression of functional PKH. The polypeptide is used to screen for
agonists and antagonists of PKH which can also be used in disease
treatment. The polypeptide and polymucleotide are used for treating
acquired immunodeficiency syndrome, allergies, ankylosing spondylitis,
andidosis, ansemia, astham, atherosclerosis, autoimmune hasenolytic
contact dermatitis, crohn's disease, atopic dermatitis, dermatomyositis,
andidosis, ansemia, astham, atherosclerosis, autoimmune haemolytic
contact dermatitis, crohn's disease, atopic dermatitis, dermatomyositis,
antenia, autoimmune thyroiditis, bronchitis, cholecystitis, dermatomyositis,
contact dermatitis, crohn's disease, atopic dermatitis,
anteniamune thyroiditis, bronchitis, cholecystitis, dermatomyositis,
contact dermatitis, osteoporosis, pandrome, multiple sclerosis,
hypereosinophilia, irritable bowel syndrome, multiple sclerosis,
conteartritis, osteoporosis, pandrome, multiple sclerosis, thrombocytopenic
purpura, ulcerative colitis, uveitis, werner syndrome, complications of
cancer, haemodialysis, and extracorporeal circulation, viral, bacterial,
including tubal disease, ovulatory defects, and endometriosis,
contect haemodialysis, and extracorporeal circulation, viral, bother,
including tubal disease, ovulatory defects, and endometriosis,
contect haemodialysis, and extracorporeal circulation syndrome,
polycystic ovary syndrome, ovarian hyperstimmune disonders, endometrial
an
ovarian hyperstimulation syndrome; ectopic pregnancy; teratogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding a human protein kinase homolog useful for preventing, diagnosing and treating cancer, autoimmune/inflammatory disorders and reproductive defects.
                                                                                                                                                                                                                                                                                                                                                      Yue H, Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                         Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 47; Page 27; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                         Bandman O, Tang YT, Hillman JL
Gorgone GA, Azimzai Y, Lu DAM;
                                                                                                                                                                                             30-MAY-2001; 2001US-00870962.
                                                                                                                                                                                                                                         98US-00173581.
99US-00420915.
                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-655433/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABQ76288
                                                                                                          US2002081290-A1
                                                              Homo sapiens.
                                                                                                                                                                                                                                         15-OCT-1998;
                                                                                                                                                                                                                                                              20-OCT-1999;
                                                                                                                                                    27-JUN-2002
                       cancer.
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used for gene therapy. This sequence represents a PKH from clone ID 507669 isolated from TMLR3DT02, a library constructed using RNA isolated from non-adherent peripheral blood monounclear cells collected from a pool of male and female donors
                                                                                                                                                                                                                                                                                                              h Similarity 100.0%; Score 41; DB 5; Length 346; Similarity 100.0%; Pred. No. 5.3; 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                    Sequence 346 AA;
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71 LQDNLVIAL 79

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Gaps

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LODNLVIAL 69

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Best Local Similarity Matches 9; Conserv

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human clasmostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, gastrointestinal disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The ditup molecules may also be used in generic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germine gene therapy. The present sequence represents a ditup protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gietzen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                              gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kirton ES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerstin EH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shen F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV, Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL, Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gi Patury S, Shi X, Suarez CJ,
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                                                                                                                                       Human diagnostic and therapeutic pprotein SEQ ID NO:3229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                 ABM82980 standard; protein; 355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; Page; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                   12-SEP-2003; 2003WO-US028227.
                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-2002; 2002US-0410259P.
12-SEP-2002; 2002US-0410260P.
                                                                                              (first entry)
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ACN41632.
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                                                                                                                                                                                                                                                               WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in gene mapping.
                                                                                              18-NOV-2004
                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                          25-MAR-2004.
                                                       ABM82980;
ABM82980
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ADP48375 standard; protein; 363 AA.

RESULT 8 ADP48375

ADP48375;

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modulates Tlymphocyte activation. The method comprises contacting at Cell comprising an A-raf-1 or TCPTP/PTNN2 polypeptide with a compound, where the A-raf-1 or TCPTP/PTNN2 polypeptide is encoded by a nucleic acid that hybridises to a nucleic acid encoding a polypeptide having a sequence selected from two 606-amino acid sequence and a 415-amino acid sequence given in the specification. The method of the invention has immunosuppressive, antiasthmatic, antiallergic, and antiinflammatory activity. The method is useful for identifying compounds that modulate lymphocyte activation and migration, and for monitoring changes in cell surface marker expression, cytokine production, antibody production, proliferation and differentiation, and apoptosis, using either cell lines or primary cells. The A-raf-1 or 'TCPTP/PTN'D proteins may be used as drivation and migration, eng for the treatment of diseases in which modulation of the immune response is desired such as delayed type hypersensitivity reactions, asthma, allergies, graft versus host disease, and acute and chronic inflammation. Modulators of lymphocyte activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a compound that modulates T lymphocyte activation, useful for monitoring changes in cell surface marker expression, comprises contacting a T cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with a compound.
                                                                                                                                                                                                    Human; T lymphocyte activation; T-cell; A-raf-1; TCPTP/PTPN2; asthma; immunosuppressive; antiasthmatic; antiallergic; antinflammatory; lymphocyte activation; lymphocyte migration; cytokine production; cell surface marker expression; antibody production; apoptosis; allergy; antibody proliferation; antibody differentiation; hypersensitivity; graft versus host disease; inflammation; p561ck.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for identifying a compound that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are useful for treating disorders related T and B cell activation and migration. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 41; DB 6; Length 363; 100.0%; Pred. No. 5.6; o; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Masuda E, Pardo J, Zhao H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to a novel method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 64; 126pp; English.
                                        ABR59690 standard; protein; 363 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2002; 2002WO-US031618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-OCT-2001; 2001US-0327212P.
                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li C, Liao XC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-363276/34.
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                                                                                                                                                                                                                                                                                                                                                                                         WO2003029277-A2
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                      25-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention
                                                                                ABR59690;
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RESULT 7
ABR59690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a compound targeted to a nucleic acid molecule encoding the human lymphocyte specific tyrosine kinase (Lck) polypeptide. The compound is an antisense oligomucleotide that specifically hybridises with the nucleic acid and inhibits expression of the polypeptide. The antisense oligomucleotide comprises at least one modified internucleoside linkage i.e. a phosphorothioate linkage, at least one modified sugar moiety, preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase comprising a 5-methyloytosine. The antisense compromidiating the expression of the human Lck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide and in preparation of a composition for treating hyperproliferative disorders, e.g. cancer. This sequence represents a human Lck polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense oligonucleotide compounds, useful for diagnosing, preventing and/or treating diseases or conditions associated with aberrant expression or activity of Lck, such as hyperproliferative
                                                                                          Human lymphocyte specific tyrosine kinase (Lck) polypeptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 41; DB 8; Length 363; 100.0%; Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                      antisense oligonuclectide; phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety; 5-methylcytosine; hyperproliferative disorder; cancer; cytostatic; enzyme.
                                                                                                                         Human; lymphocyte specific tyrosine kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 17; SEQ ID NO 75; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG79672 standard; protein; 437 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                               10-DEC-2002; 2002US-00316515.
                                                                                                                                                                                                                                                                                                                                10-DEC-2002; 2002US-00316515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-NOV-2002 (first entry)
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            Freier SM;
                                                                                                                                                                                                                                                                                                                                                             (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LQDNLVIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||||||
61 LQDNLVIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADP48372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 363 AA;
                                                                                                                                                                                                                                    US2004116365-A1.
                                                                                                                                                                                                                                                                                                                                                                                          Borchers AH,
                                                           09-SEP-2004
                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                  17-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG79672;
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ABG79672
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Gaps

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9; Conservative

Matches

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Local Similarity

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pharmaceutical composition; cancer; diagnostic; tumour; gene therapy; endothelial cell; cell differentiation; cell proliferation; apoptosis;
Tumour involved gene (TIG) splice variant protein, NV-3.
           Human; splice variant; tumour-involved gene; TIG;
                                                                          13-MAR-2001; 2001US-00805020
                                                                                      14-MAR-2000; 2000IL-00135402
16-MAY-2000; 2000IL-00136154
                                                                                                       (LEVI/) LEVINE Z.
(DAVI/) DAVID A.
(ROMA/) ROMANO C.
(BERN/) BERNSTEIN J.
                                                   US2002086384-A1
                            gene therapy.
                                        Homo sapiens.
                                                              04-JUL-2002
                                                                                                                                      Z,
                                                                                                                                                                                                                                                                                                                                                                   disclosed
                                                                                                                                                                                     cancer.
                                                                                                                                      Levine
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The invention discloses isolated human nucleic acid alternative splicing variants that are all tumour-involved genes (TIGs). The nucleic acids and polypeptides are useful for determining the level of a nucleic acid or polypeptide in a biological sample, for determining the level of a nucleic acid or polypeptide sequence in a biological sample, for determining the level of variant nucleic acid or polypeptide sequences in a biological sample and for taising antibodies. A pharmance trom which the variant has been varied by alternative splicing in a second the variant has been varied by alternative splicing in a second the variant has been varied by alternative splicing in a second composition comprising antibodies. A pharmaceutical composition comprising the level of the original sequence from which treating diseases (e.g. cancer) that can be ameliorated or cured by increasing or decreasing the level of the encoded protein. The nucleic cancer or a predisposition to cancer, for evaluating the state or aggressiveness of cancer disease, in basic research, for understanding the physiological function of the original TiG in targeting or the physiological function of the original TiG in targeting or the physiological functions of the original stage in which call cycle of pharmaceuticals, for various cancer stages in which cell cycle is noncornal, for determining mutations in tumour-involved genes and in gene therapy. The polypeptides are useful for identifying compounds capable of therapy. The polypeptides are useful for identifying compounds capable of modulating endothelial differentiation and proliferation, as well as to modulate apoptosis either ex vivo or in vivo. The sequences presented in Alenghance Novel nucleic acid sequence, which is an alternative splicing variant of tumor involved genes, useful for detecting cancer, predisposition to cancer, for evaluating cancer state and in gene therapy for treating Romano C, Bernstein J; Claim 4; Page 68-69; 180pp; English. David A, 2002-635679/68 N-PSDB; ABS65202

Sequence 437 AA;

ö Gaps ; 0 100.0%; Score 41; DB 5; Length 437; 100.0%; Pred. No. 7; 0; Indels cive 0; Mismatches 0; Indels 9; Conservative Query Match Best Local Similarity Matches

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anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian; nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic; mimunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological; antidabetic; nephrotropic; antigout; thyromimetic; neuroprotective; osteopathic; antiarthritic; antigout; thyromimetic; neuroprotective; uropathic; ophthalmological; antirheumatic; antihelminthic; antipactatic; uropathic; ophthalmological; antirheumatic; hosephatase; KPP; cell proliferative disorder; athercsclerosis; cirrhosis; hepatitis; cancer; developmental; mental retardation; neurological; hepatitis; allabetics mellitus; viral; bacterial; fungal; parasitic; protozon; helminthic infection; transgenic; gene therapy; human; enzyme. ADC99048 standard; protein; 458 AA. Human KPP protein - SEQ ID 1. 19-OCT-2001; 2001US-0345474P. 02-NOV-2001; 2001US-0343910P. 13-NOV-2001; 2001US-033944P. 30-NOV-2001; 2001US-0334248P. 17-OCT-2002; 2002WO-US033723 01-JAN-2004 (first entry) WO2003033680-A2. Homo sapiens. 24-APR-2003 ADC99048; RESULT 10 ADC99048

Tang YT; Yao MG, Yue H; Lee SY; Arvizu CS; Griffin JA; Bendman O, Baughn MR, Becha SD, Borowsky ML, Duggan Emerling BM, Forsythe IJ, Gandhi AR, Gorrad AE, Grif Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Ismkumar J, Recipon SA, Richardson TW, Swarnakar A, Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Zebarjadian Y;

(INCY-) INCYTE GENOMICS INC.

WPI; 2003-403214/38. N-PSDB; ADC99100.

diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis, New human kinases and phosphatases and polynucleotides, useful for cancer or hepatitis.

Claim 1; SEQ ID NO 1; 424pp; English.

The invention relates to a novel isolated polypeptide which is a human kinase and phosphatase (KPP). The KPP polypeptides, polymucleotides, gonists and antegonists are useful for diagnosing, treating or preventing cell proliferative disorders such as atherosclerosis, cirrhosis, hepatitis and cancer, developmental disorders e.g. mental retardation, neurological disorders including Alzheimer's disease and Parkinson's disease and inflammatory disorders such as Crohn's disease and diabetes mellitus and finally, viral, bacterial, fungal, parasitic, protozoan or helminthic infections. Furthermore, the polynucleotides encoding KPP may be useful for creating transgenic animals to model human disease, as well as during gene therapy procedures. The current sequence is that of the human KPP protein of the invention.

Sequence 458 AA;

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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                   Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                              Human Protein P06239, SEQ ID NO 4689,
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                   14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                           14-AUG-2002; 2002WO-US025765
                                       (first entry)
                                                                                                                                                                                                                                                                                   (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                WPI; 2003-268312/26.
                                                                                                                                                                                                                                                                                                                       Woolf C, D'urso D,
                                                                                                                                                              WO2003016475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 508 AA;
                                                                                                                                                                                                                                                                                                                                                             GENBANK; P06239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification,
                                                                                                                                       Homo sapiens.
                                     29-JAN-2004
                                                                                                                                                                                    27-FEB-2003.
               ADE58802;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diffracts X-rays so that the atomic coordinates of the protein-ligana complex and diffracts X-rays so that the atomic coordinates of the protein-ligand complex can be determined to a resolution of greater than 5.0 Angstroms. The truncated lck used in the present invention comprises the globular core of the corresponding full-length lck. The present sequence is the full-length human lck protein. The crystal of the present invention may be used to identify kinase inhibitors in screening assays, in drug screening and drug design processes, to design, select or test inhibitors of kinase enzymes, where the inhibitors are used as therapeutics for the treatment and modulation of diseases, disease symptoms or the effect of other physiological events mediated by kinases, having one or more kinase enzymes involved in their pathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crystal of a protein-ligand complex for identifying kinase inhibitors, comprises a truncated lymphocyte kinase and a ligand, and diffracts X-rays to determine atomic coordinates at a resolution greater than 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a crystal of a protein-ligand complex
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                               Human; lymphocyte kinase; protein co-ordinate data; crystal
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            100.0%; Score 41; DB 7; Length 458; 100.0%; Pred. No. 7.4;
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                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 434-5; 438pp; English.
                                                                                                                                             AAB37700 standard; protein; 508 AA.
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                                                                                                                                                                                                                                                                                                                                              19-MAY-2000; 2000WO-US013881.
                                                                                                                                                                                                                                                                                                                                                                      99US-0134965P
                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              (KINE-) KINETIX PHARM INC.
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                       Human lymphocyte kinase.
                                                                                   61 LODNLVIAL 69
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 508 AA;
                                                                                                                                                                                                                                                                                            WO200070030-A1.
                                                                                                                                                                                                                                                                                                                                                                      19-MAY-1999;
                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                               02-MAR-2001
                                                                                                                                                                                                                                                                                                                      23-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angstroms
                                                                                                                                                                       AAB37700;
                                                                                                                                                                                                                                                                                                                                                                                                                      zhu X;
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                                                                                                                        RESULT 11
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Costigan M;

Befort K,

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal complex to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence with a subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note:

The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68
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Best Local Similarity
Matches 9; Conserv
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ADE58802 standard; protein; 508 AA.

RESULT 12

ADE58802

68

60 LODNLVIAL

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Сарв

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Indels

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Mismatches

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9; Conservative

Matches

68

9

RESULT 14 ADF4507; ID AD

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1 LQDNLVIAL LODNLVIAL

ઠ g Human; protein kinase; enzyme; inhibitor; LCK.

20-MAR-2003; 2003WO-US008725. 21-MAR-2002; 2002US-0366892P.

WO2003081210-A2

02-OCT-2003

Homo sapiens.

(SUNE-) SUNESIS PHARM INC.

Braisted A;

Prescott JC,

WPI; 2003-865136/80.

ADF45072 standard; protein; 508 AA

(first entry)

12-FEB-2004

ADF45072;

Human kinase LCK.

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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                      Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                           Human Protein P06239, SEQ ID NO 4686.
              ADE58799 standard; protein; 508 AA.
                                                                                                                                                                                                                     Befort K,
                                                                                                                                                                                                                                                                                Claim 1; Page; 1017pp; English
                                                                                                                                                                14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                   14-AUG-2002; 2002WO-US025765
                                             (first entry)
                                                                                                                                                                                               (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                                                                                                                                     Woolf C, D'urso D,
                                                                                                                                                                                                                                   WPI; 2003-268312/26.
GENBANK; P06239.
                                                                                                                      WO2003016475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.
                                                                                                        Homo sapiens
                                            29-JAN-2004
                                                                                                                                    27-FEB-2003.
                              ADE58799;
RESULT 13
        ADE58799
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Costigan M;

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or numen polynucleotices or a polynucleotice and sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a comprising the vector, a method for identifying a nucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of the polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound to a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of the compound that activity in an animal of one or more of the polymeptides or their antibodies. The polymucleotide or the compound that complying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of polymeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. spinal sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed the specification) which is differentially expressed during pain. Note:

The sequence data for this patent did not form part of the printed specification, which has a pharmaceutical did not form part of the printed specification.
The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
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DB 7; Length 508;

100.0%; Score 41; DB 7 100.0%; Pred. No. 8.4;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for identifying a ligand (L), which binds to an inactive conformation of target protein kinase (T). The method involves contacting inactive conformation of (T), which contains or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bonding to the reactive group thus forming a kinase-(L) conjugate (C). The method is useful for identifying protein kinase inhibitors that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preferentially bind to inactive conformation of a target protein kinase. The present sequence is a protein kinase which may be modified via an amino acid substitution, for use in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                        Identifying ligand binding to inactive conformation of target protein kinase (T) comprises contacting the conformation modified (T) which contains reactive group at binding site, with ligands and detecting kinase-ligand conjugate formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 41; DB 7; Length 508; 100.0%; Pred. No. 8.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lymphocyte kinase (Lck) globular core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, SEQ ID NO 41; 260pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL34479 standard; peptide; 508 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Matches 9; Conserv
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18-NOV-2004 (first entry)

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The invention describes a crystal (1) of a protein-ligand complex (C) comprising a truncated lymphocyte kinase (Lck) and a ligand, where (1) CC effectively diffracts X-rays for determination of atomic coordinates of (C) to a resolution of greater than 5.0 angstroms, and truncated Lck comprises a sequence (S1) of residues 225-508 of a 508 amino acid comprises a sequence (S1) of residues 225-508 of a 508 amino acid comprises a sequence (S1) of residues 225-508 of a 508 amino acid comprises a sequence (S1) of residues 225-508 of a 508 amino acid comprises a sequence (S1) is useful in an inhibitor screening assay and to comprise that would be useful in an inhibitor screening assay and to comprise a sequence of that would be useful as therapeutics for diseases or symptoms of diseases comprise activity of one or more enzymes. The inhibitors identified by the methods may also be useful for inhibition of kinase activity of any enzyme comprising greater than 90%, alternatively greater than 85%, or alternatively greater than 50% and thibitions the biological activity of any enzyme that binds ATP and thus for treating disease or disease symptoms mediated by any enzyme that that binds ATP. The inhibitors are useful in inhibiting kinase activity and mammal, particularly a human e.g., cancer, autoimmunological, metabolic, inflammatory, infection, (bacterial, viral, yeast, fungal, etc.), central enzyme that service of the 
                            cytostatic; immunosuppressive; antiinflammatory; antibacterial; virucide; fungicide; noctropic; neuroprotective; kinase inhibitor; crystal; protein-ligand complex; lymphocyte kinase; Lck; Lck ligand; kinase inhibitor; therapeutic; kinase-mediated physiological event; kinase inhibitor; therapeutic; kinase-mediated physiological event; cancer; autoimmunological, metabolic; inflammatory; infection; central nervous system degenerative disease; transplant rejection; human; globular core; protein co-ordinate data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crystal of protein-ligand complex useful for identifying an inhibitor of lymphocyte kinase (Lck), comprises truncated Lck and a ligand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprising the Lck globular core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1; 295pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-2001; 2001US-00862154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAY-2000; 2000US-0205510P.
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                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                       US6589758-B1
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ö Gaps ö 100.0%; Score 41; DB 7; Length 508; 100.0%; Pred. No. 8.4; 0; Indels 0; Mismatches 9; Conservative Query Match Best Local Similarity Sequence 508 AA; Matches

δ 1 LQDNLVIAL

ADS88148 standard; protein; 508 AA. RESULT 16 ADS88148 ID ADS88 XX AC ADS88

ADS88148

LODNLVIAL 68 09 ð a

This invention relates to novel protein complexes of the tumour necrosis factor-alpha (TWR-alpha) signalling pathway. Specifically, it refers to methods for preparing these complexes comprising at least two component proteins, as well as screening methods to identify modulators of the pathway, which include antibodies, agonists and antagonists thereof. The present invention describes a protein complex and kit that are useful for diagnosing, prognosing or treating chronic inflammatory diseases such as rheumatoid arthritis and inflammatory bowel disease, infectious diseases such as such as septic shock and bacterial infections; neurological diseases such for gene therapy purposes. In particular, the invention further provides stRNA-ollgomucleotides useful for inhibiting protein expression for in vitro or cell culture assays. This polypeptide is a human protein that can be used in combination with other proteins provided in the specification to form novel complexes of the TNF-alpha signalling pathway as stroke-induced inflammation in neurons; neurodegenerative diseases and cancer. Accordingly, these complexes can be used for the development of pharmaceutical compositions that exhibit antiinflammatory, antiarthritic, antirheumatic, cytostatic and antibacterial activities and can be used New protein complex comprising at least one first and second protein of the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for diagnosing or treating inflammation, neurological diseases, infectious Human protein of a TNF-alpha signalling pathway protein complex SeqID 3. protein complex; tumour necrosis factor-alpha signalling pathway; INF-alpha; chronic inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; infectious disease; septic shock; bacterial infection; neurological disease; stroke-induced inflammation; neurodegenerative disease; ancer; antiinflammatory; antiarthritic; antirheumatic; cytostatic; antibacterial; gene therapy; human. Kuester B; Ruffner H, Bauer A, Example; SEQ ID NO 3; 1980pp; English. Bauch A, 24-SEP-2003; 2003WO-EP050655. 26-SEP-2002; 2002EP-00021809. 10-FEB-2003; 2003EP-00100274. Kruse U; Huhse B, WPI; 2004-348460/32. (CELL-) CELLZOME AG. diseases or cancer. Bouwmeester T, H Superti-Furga G, WO2004035783-A2 Homo sapiens. 29-APR-2004.

Gaps ö 100.0%; Score 41; DB 8; Length 508; 100.0%; Pred. No. 8.4; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100... 9, Conservative

Sequence 508 AA;

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68 σ 60 LODNLVIAL 7 g ò

AAY49420 standard; protein; 509 AA. AAY49420; AAY49420 ID AAY4 XX AC AAY4 XX

RESULT 17

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13-MAR-2000 (first entry)

99WO-GB001680 98NO-00002419 98US-0114240P

27-MAY-1999;

02-DEC-1999.

27-MAY-1998; 30-DEC-1998;

Homo sapiens. WO9962315-A2 WPI; 2000-086801/07

N-PSDB; AAZ46491

(JONE/) JONES E L. LAUR-) LAURAS AS.

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The present invention describes an isolated nucleic acid molecule, which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
Human, cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
heart disease; atherosclerosis; endometriosis.
                                                                                                                                                                                                                                                                                                                                                 Wilson KE;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                               (EOSB-) BOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                      2001US-0350666P.
2002US-0355145P.
                                                                                                                                                                                                                                                                             12-APR-2002; 2002US-0372246P.
                                                                                                                                                       17-SEP-2002; 2002WO-US029560.
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Best Local Similarity
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                                                                                    WO2003025138-A2
                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                       Zlotnik A;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides a novel method of altering the activity of the protein kinase A (PKA) signaling pathway in a cell that comprises altering the extent of phosphorylation of one or more PKA substrates, or Ainase substrates downstream in the PKA signaling pathway. Pharmaceutical compositions containing a nucleic acid molecule that encodes a PKA substrate, or fragment, precursor or functionally equivalent variant, where the sequence is modified to alter its susceptibility to phosphorylation by PKA can be used for treating a disorder exhibiting abnormal PKA signaling activity, immunosuppressive disorder or proliferative diseases. They can be used for treating e.g. HIV infection, AIDS, common variable immunodeficiency or cancers. Conditions in which upregulation of the PKA pathway is required, such as autoimmune disease, e.g. systemic lupus erythematosus, may also be treated. The present sequence represents a PKA substrate, wherein the substrate is in the Src-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Altering the activity of protein kinase signaling pathways, used for treating immunosuppressive disorders, e.g. AIDS, proliferative disorders, e.g. cancers or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family, preferably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk, c-tkl,
                                                                 Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cance: kinase substrate; immunosuptrestare disorder; proliferative disease; HIV infection; AIDS; immunodeficiency; autoimmune disease; systemic lupus erythematosus; Src-family.
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Tasken K, Vang T, Altman A, Munshi A;
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                                  PKA substrate, Src-family protein.
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Gaps

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(first entry)

09-JUL-2003

ABR58699
ID ABR5
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AC ABR5
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DT 09-J
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DE Huma

ABR58699;

RESULT 18

Local Similarity 100.

Matches

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Query Match

Fyk, Src-1 or Src-2

Sequence 509 AA;

1 LQDNLVIAL 9

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19-SEP-2002; 2002US-0412007P.
                                            10-DEC-2002; 2002US-0432318P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a crystalline polypeptide (I), comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck) protein. Lck is a Src-family protein tyrosine kinase expressed primarily in T-cells and plays an essential role in immune response. The present sequence is the full-length sequence of human Lck (1-509). (I) is useful for identifying a compound which is an inhibitor of human Lck protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus; HIV-related disorder; differential expression; drug screening; viral replication modulation; diagnosis; prognosis; predisposition; anti-HIV; gene therapy; antisense therapy; human; proto-oncogene Tyr protein kinase LCK; enzyme.
                    Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme; Src-family protein tyrosine kinase; T-cell; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                           New crystalline polypeptide comprising ligand binding domain or cataly domain of Lck protein, for determining three-dimensional structure of catalytic domain of Lck, has predetermined unit cell parameters.
                                                                                                                                                                                                                                                                                                                                  Loew A;
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2002US-0380249P.
2002US-0391306P.
2002US-0406297P.
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                                                                                                                       WO2003020880-A2
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13-MAY-2002;
25-JUN-2002;
27-AUG-2002;
                                                                                 Homo sapiens
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ADE40449
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The invention relates to a method of identifying a compound useful in the treatment of AIDS (acquired immunodeficiency syndrome) or an HIV (human immunodeficiency virus) related disorder. The invention involves assaying the ability of a test compound to modulate the activity or expression of 26 human proteins. These proteins and nucleic acids encoding them (ADB40473) are differentially expressed in tissues relating to AIDS or an HIV-related disorder compared to their expression in normal tissues. The invention also relates to the use of the compounds condulate viral replication in a cell and to treat a patient with AIDS or an HIV-related disorder. The invention further discloses methods for the diagnostic evaluation and prognosis of various HIV-related disorders, and for the identification of individuals exhibiting a predisposition to such conditions. The modulatory compounds identified using the method of the invention may be small organic molecules, the invention are useful in diagnosing, preventing or treating AIDS or HIV-related disorders. The present sequence represents a human protein which is differentially expressed in AIDS or HIV-related disorders.
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                                                                                                                                                                                                                             Identifying a compound capable of diagnosing, preventing or treating AIDS or an HIV-related disorder comprises assaying the ability of the compound to modulate e.g. 1414, 1481 or 1553 nucleic acid expression or polypeptide activity.
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(MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-AUG-2002; 2002US-0401701P.
16-SEP-2002; 2002US-0411017P.
30-DEC-2002; 2002US-0437107P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-2003; 2003WO-US024505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
                                                                Weich NS
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                                                                                                                                 WPI; 2003-671808/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LODNLVIAL
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                                                                                                                                                               N-PSDB; ADE40448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 509 AA;
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                                                                    Powell DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADL22907;
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Belvin M;

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The present invention relates to a method of identifying a candidate p21 or p53 pathway modulating agent. This comprises providing an assay system comprising a modulator of p21 or p53 (MP2153) polypeptide or nuclaic presence the system provides a reference activity, and detecting a test agent-biased activity of the assay system, wherein a difference between the test agent-biased activity and the reference activity identifies the test agent chises a candidate p21 or p53 pathway modulating agent. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of diseases or conditions associated with abberrant expression or activity of the p21 or p53 pathway, such as a human MP2153 protein sequence of the invention.
                                                                                                                                                                                                                        Identifying a candidate p21 or p53 pathway modulating agent using an assay system having a modulator of p21 or p53 (MP2153) polypeptide or nucleic acid, useful for diagnosing or treating cancer, such as colon or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transplant rejection; immune system; rheumatoid arthritis; lupus; inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 41; DB 8; Length 509; 100.0%; Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ly N, Prentice J,
                              L, Kidd T, Roche S,
Zhang H, Amundsen CD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by mRNA of the invention #68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 94-96; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wohlgemuth J, Fry K, Woodward R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP12458 standard; protein; 509 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-2002; 2002US-00131831.
20-DEC-2002; 2002US-00325899.
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                                 Francis-Lang H, Friedman
Plowman GD, Lickteig K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-AUG-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||||||
61 LODNLVIAL 69
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                                                                                                                         WPI; 2004-180653/17.
N-PSDB; ADL22890.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 509 AA;
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                                                                                                                                                                                                                                                                                                                              breast cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-2004.
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ADP12458
ID ADP12458
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DT 12-AUC
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Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of

Morris M;

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Gaps

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0; Indels

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                                                                   The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, xenotransplant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or thugal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense oligonucleotide compounds, useful for diagnosing, preventing and/or treating diseases or conditions associated with aberrant expression or activity of Lck, such as hyperproliferative
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lymphocyte specific tyrosine kinase (Lck) polypeptide #1.
                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 41; DB 8; Length 509; 100.0%; Pred. No. 8.4; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyperproliferative disorder; cancer; cytostatic; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; lymphocyte specific tyrosine kinase; Lck;
antisense oligonucleotide; phosphorothioate linkage;
2'-O-methoxyethyl sugar moiety; 5-methylcytosine;
                                   Claim 65; SEQ ID NO 2467; 1762pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 4; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP48374 standard; protein; 509 AA.
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LQDNLVIAL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-498280/47.
                                                                                                                                                                                                                                                                                                                                           Sequence 509 AA;
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the genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 23
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The specification describes a method for identifying protein kinase inhibitors that preferentially bind to the inactive conformation of a target protein kinase. The inhibitors are identified by locking the target protein kinase in an inactive conformation, and using Tethering to identify inhibitors preferentially targeting the inactive conformation. The method of the invention is useful for identifying a ligand which binds to an inactive conformation of a target protein kinase. The present sequence represents the human Tyr kinase Lck. Lck variants were used to demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein kinase inhibitor; inactive conformation; Tethering; Tyr kinase;
                                                                   polypeptide and in preparation of a composition for treating hyperproliferative disorders, e.g. cancer. This sequence represents a human Lck polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying ligand binding to inactive conformation of target protein kinase, by contacting inactive conformation of target with ligand candidates specific to target, detecting formation of kinase-ligand conjugate and identifying ligand.
                 moiety, preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase comprising a 5-methylcytosine. The antisense compounds are useful for modulating the expression of the human Lck
linkage i.e. a phosphorothioate linkage, at least one modified sugar
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                                                                                                                                                                       100.0%; Score 41; DB 8; Length 509; 100.0%; Pred. No. 8.4;
                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of human Tyr kinase Lck.
                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 9; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                             ADZ51107 standard; protein; 509 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SUNE-) SUNESIS PHARM INC
                                                                                                                                                                                       Local Similarity 100.
                                                                                                                                                                                                                                                                            69
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                                                                                                                                                                                                                                                              LQDNLVIAL
                                                                                                                                                                                                                                          1 LODNLVIAL
                                                                                                                                      Sequence 509 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2005034840-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                ADZ51107;
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                                                                                                                                                                       Query Match
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                           RESULT 24
ADZ51107
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12-DEC-2003; 2003EP-00028713.

(SIRE-) SIRENADE PHARM AG. Obermeier A, Bieger B;

12-DEC-2003; 2003EP-00028713

note= "constant amino acid K in domain SH2" 'note= "constant amino acid T in domain SH2" /note= "constant amino acid Y in domain SH1"

Misc-difference 316 Misc-difference

Misc-difference

EP1541694-A1

15-JUN-2005.

Location/Qualifiers

Human Lck kinase amino acid sequence SEQ ID NO:8.

(first entry)

25-AUG-2005

AEA35921;

Src family kinase; Lck kinase.

.; 0

Gaps

Homo sapiens

AEA35921 standard; protein; 509 AA.

LODNLVIAL 69

61

RESULT 25 AEA3592

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characterizing a compound which modulates Streaming will be characterizing a compound which modulates Streaming whether cells, contacting cells with test compound and determining whether phenotype of cells is changed as compared with phenotype of cells not expressed with above nucleic acids, where difference in phenotype of cells is changed as compared with phenotype of cells not expressed with above nucleic acids, where difference in phenotype of cells not compound modulate SFK activity. Also described: (1) a compound modulate SFK activity. Also described: (2) a pharmaceutical composition (PC1) containing (1), and a carrier, adjuvant or vehicle. (1) is useful as a medicament, particularly for the treatment of diseases, which are at least in part caused by a Src family kinase. (1) and PC1 are useful for producing a medicament for the treatment of diseases, which are at least in part caused by a Src family kinase. (2) aparticularly by a dysfunction of a Src family kinase, in particular cancer, hypercalcemia, restenosis, osteopoxosis, osteoparthritis, symptomatic treatment of bone metastasis rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying compound which modulates Src family kinase (SFK) activity, by contacting cells expressed with SFK or mutated SFK with test compound, where change in phenotype of cells indicates that test compound modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            asthma, ischemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rejection or allergic rhinitis. The present sequence represents human Lok
kinase, which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method (M1) for identifying, selecting and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory bowel disease, multiple sclerosis, psoriasis, lupus, graft versus host disease, T-cell mediated hypersensitivity disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hashimoto's thyroiditis, Guillain-Barré syndrome, chronic obstructive pulmonary disorder, contact dermatitis, Paget's disease, asthma, ischen or reperfusion injury, allergic disease, atopic dermatitis, transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 8; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-428084/44.
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Gaps

.. 0

Query Match

100.0%; Score 41; DB 9; Length 509;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 9; Conservative 0; Mismatches 0; Indels

Sequence 509 AA;

LODNLVIAL

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Gaps

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Indels

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Mismatches

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9; Conservative

Matches

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Gaps

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08:56:40 2006

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Mon Jul

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Score 41;
Pred. No.
100.0%;
Query Match
Best Local Similarity
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DB 8; Length 539;

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Gaps

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp infections caused by virus, bacteria, fungi or parasite. The dithp collection minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence represents a dithp protein of the invention, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panazer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen BJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzei
                                                                                                                                                                                                                                                                                                                         gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                                                                                                                                                                                                                                                                                      Human diagnostic and therapeutic pprotein SEQ ID NO:3230.
                    Indels
                    ;
0
 red. No. 8.4;
Mismatches
   Pred.
                                                                                                                                                                              ABM82981 standard; protein; 539 AA.
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100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-SEP-2002; 2002US-0410259P.
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                                                                                                                                                                                                                                                   (first entry)
Best Local Similarity 100.
Matches 9; Conservative
                                                                                      69
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Kwong M,
Shi X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-329368/30
                                                                              61 LODNLVIAL
                                                   1 LODNLVIAL
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                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                 ABM82981
                                                                                                                                         RESULT 26
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 272 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnost a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine disorder, neurological disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp conclusions as also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ö,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                        gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reddy TP;
9, Gerstin EH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kirton ES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin E Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Ligadoce RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gle Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 41; DB 8; Length 539; 100.0%; Pred. No. 9; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                  Human diagnostic and therapeutic pprotein SEQ ID NO:3231
                                                                                                                                   ABM82982 standard; protein; 539 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; Page; 190pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-SEP-2003; 2003WO-US028227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-2002; 2002US-0410259P.
12-SEP-2002; 2002US-0410260P.
                                                                                                                                                                                                             18-NOV-2004 (first entry)
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Best Local Similarity lvv...
9, Conservative
                                  69
1 LODNLVIAL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INCY-) INCYTE CORP.
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                        N-PSDB; ACN41634.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene mapping.
                                                                                                                                                                                                                                                                                                                                                                       WO2004023973-A2
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2004.
                                                                                                                                                                         ABM82982;
                                                                                              RESULT 27
                                                                                                                 ABM82982
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Gietzen D;

RESULT 28 ABG2226

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ABG22264 standard; protein; 551 AA ABG22264;

(first entry) 18-FEB-2002

Novel human diagnostic protein #22255

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Homo sapiens

WO200175067-A2

11-OCT-2001.

30-MAR-2001; 2001WO-US008631

31-MAR-2000; 2000US-00540217 23-AUG-2000; 2000US-00649167

(HYSE-) HYSEQ INC.

Tang YT; Drmanac RT, Liu C,

WPI; 2001-639362/73. N-PSDB; AAS86451.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID NO 52623; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences

Sequence 551 AA;

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                              Gaps
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0
     DB 4; Length 551;
                            0; Indels
   100.0%; Score 41; DB 4 100.0%; Pred. No. 9.2;
                            Mismatches
                           ;
0
Query Match
Best Local Similarity 100.
Matches 9; Conservative
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plant; transgenic plant; crop improvement; abiotic stress tolerance; plant growth regulation.
                                                                                                                                                                                                                                                                      New isolated nucleic acid molecule modifying plant phenotypes and characteristics and the polypeptide it encodes, useful for making transgenic plants with improved characteristics.
                                                                                          Lead_CeresClone35742 protein homolog SEQ ID NO:2309.
                                                                                                                                                                                                                                          Mascia P, Feldmann K;
                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 2309; 612pp; English.
                                            AEF30109 standard; protein; 480 AA.
                                                                                                                                                                                          30-JUN-2004; 2004US-0583621P.
30-JUN-2004; 2004US-0584800P.
30-JUN-2004; 2004US-0584829P.
                                                                                                                                                                             30-JUN-2005; 2005WO-US023326.
                                                                           (first entry)
                                                                                                                                                                                                                                          Alexandrov N, Brover V,
Arabidopsis thaliana.
                                                                                                                                                                                                                                                        WPI; 2006-090599/09.
                                                                                                                                                                                                                          (CERE-) CERES INC.
                                                                                                                                               WO2006004955-A2
                                                                           23-MAR-2006
                                                                                                                                                              12-JAN-2006.
                                                           AEF30109;
                               RESULT 29
                                       AEF30109
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The inversion relates to an instance in the sequence listing or in the condess an amino acid sequence exhibiting at least 85% sequence that encodes an amino acid sequence exhibiting at least 85% sequence it that encodes an amino acid sequence in the sequence listing or in the ortholog alignments of Figure 1, a nucleic acid, which is the reverse of the nucleotide sequence in (a), a nucleic acid, which is the reverse of the nucleotide sequence order which is the reverse of the sequence order of (a) or a nucleic acid capable of the reverse of the sequence order of (a) or a nucleic acid capable of bybridizing (a-c), under conditions that permit formation of a nucleic acid duplex at a temperature of 40-48 degrees C below the melting temperature of the nucleic acid daying a regulatory sequence construct (comprising a first nucleic acid having a regulatory sequence construct (comprising a host cell comprising the isolated nucleic acid molecule that is flanked by except on a second nucleic acid having the sequence of the isolated nucleic acid having the sequence of the isolated of call or sequence exhibiting at least 85% sequence identity to those cited above, introducing an isolated polypeptide comprising an amino acid sequence exhibiting at least 85% sequence identity to those cited above, introducing an isolated nucleic acid in a seample, a host cell or organism comprising the nucleic acid molecule, a plant generated from the plant comprising the nucleic acid molecule (where the plant material or seed, a plant (plant call, plant material or seed) comprising the plant) improving plant characteristics as compared to a wild type plant), improving plant the nucleic acid sequence, and a transcaric plant a and a transgenic plant having a gene construct (comprising the nucleic encoding a component operably linked to a plant promoter so that the component is ectopically overexpressed in the transgenic plant). The transgenic plant exhibits faster rate of growth, greater fresh of dry weight of maturation, greater fruit or seed yield, higher tolerance to pH, higher tolerance to pH, higher tolerance to low purepurate concerning, which does not to low nitrogen concentration than a progenitor plant, which does not invention relates to an isolated nucleic acid molecule modifying

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contain the progenitor construct, when the transgenic plant and progenitor plant are cultivated under identical environmental conditions, where the component is any one of the polypeptides cited above. The nucleic acid molecules are useful for producing transgenic plants with improved characteristics. The present sequence is an ortholog of a protein encoded by a plant nucleic acid (CDNA) of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
                                                                                                                                                                                                                                                                                  82.9%; Score 34; DB 10; Length 480; 66.7%; Pred. No. 2.4e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice abiotic stress responsive polypeptide SEQ ID NO:4420.
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D, Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABM86174 standard; protein; 761 AA.
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N, Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-033227P
21-NOV-2001; 2001US-0332132P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUN-2002; 2002WO-US019668
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Moughamer T, Provart N,
                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                47 LSDNLIVAL 55
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                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                        Sequence 480 AA;
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The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotidee. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, osmotic stress and the inventions. The present sequence is used in the exemplification of their invention New stress-responsive nucleic acid, useful for altering the responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold stress, salt stress or osmotic stress. Claim 1; SEQ ID NO 4420; 89pp; English

Sequence 761 AA;

Katagiri F;

Goff SA,

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Gaps
                            ó;
 Length 761;
Score 33; DB 7; Length 761
Pred. No. 6.6e+02;
4; Mismatches 0; Indels
h 80.5%;
Similarity 55.6%;
5; Conservative '
  Query Match
Best Local S:
Matches 5
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Search completed: June 29, 2006, 09:13:18 Job time : 90.8313 secs

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Gaps

373.10 procein - S hypothetical prote sporzoite antigen hypothetical prote hypothetical prote hypothetical prote hypothetical 25.0K spore coat polysac hypothetical prote teraspan TSPAN-5 aspartate carbamoy coproporphyrinogen exsG protein (AJ22 transcription regute component sens ethanolamine opero hypothetical protesucal protesuca altronate hydrolas altronate hydrolas peroxisome prolife peroxisome prolife peroxisome prolife peroxisome prolife probable sugar ABC multidrug resistan probable signal re hypothetical prote hypochetical proce probable cell divi hypothetical prote hypothetical prote hypothetical prote hypothetical prote phospholipas A2 r apolipophorin prec hypothetical prote hypothetical prote UDP-N-acetylmuramy hypothetical prote conserved hypothet processing protein peroxisome prolife ABC transporter AT peroxisome prolife probable altronate hypothetical prote cell division cont hypothetical prote protein kinase hom conserved hypothet probable transcrip hypothetical prote hypothetical prote transcription regu hypothetical prote hypothetical prote hypothetical prote pepP protein - Sta probable immediate prote prote probable membrane potential phosphat conserved hypothet branched-chain ami transcription regu probable amino aci probable receptorypothetical hypothetical A49707 T18358 D83221 AI0141 T47611 AD3163 T06159 S58359 G84991 T10919 AG1990 S31498 AD1917 G91273 G91273 S56408 S39723 A75200 A75200 A75200 A75200 A75200 A75200 A75200 A75200 A75200 F98218 AD2130 AE3068 G71465 AI3054 D98231 AH3469 S77156 JE0279 JC4264 F96985 D69853 B83711 JE0280 JC5777 JC4859 T41301 T15168 F71424 T37944 F81361 S37886 T40354 AF2356 G87641 T42610 AD2434 T50141 AC0599 T03477 C75403 T40365 E69277 S66482 T20917 B69170 A64343 T36857 AC0813 969 1086 1105 1314 1458 3305 108

ALIGNMENTS

protein-tyrosine kinase (EC 2.7.1.112) lck, lymphocyte

A;Accession: 148845 A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA A; Residues: 1-509 < VOR1>

A; Accession: A23639

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A;Reference number: JQ0152; MUID:90108697; PMID:2558056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-86, P', 88-509 < PER>
A; Residues: 1-86, P', 88-509 < PER>
A; Cross. - references: UNIPARC: UPIO000163BD5; EMBL: X13529; NID: g34294; PIDN: CAA31884.1; PID
B; Koga, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.
Eur. J. Immunol. 16, 1643-1646, 1986
Eur. J. Immunol. 16, 1643-1646, 1986
A; Title: A human T cell-specific cDNA clone (YT16) encodes a protein with extensive homo
A; Reference number: S07200; MUID: 87133831; PMID: 3493153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-205, ASAITPI', 212-257, RCGW', 262, TTT', 266, T', 268-281, AGRLP', 287-503, ST.
A; Cross-references: UNIPARC:UP1000016B09E; EMBL:X05027; NID:g36807; PIDN:CAA28691.1; PID RK; Vaillette, A.; Foss, F.M.; Sausville, E.A.; Bolen, J.B.; Rosen, N.
Oncogene Res. 1, 357-374, 1987
A; Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other n A; Reference number: S01879; MUID:88217332; PMID:2835736
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A; Residues: 368-471, 'H', 473-509 < VEI>
A; Residues: 368-471, 'H', 473-509 < VEI>
A; Residues: 368-471, 'H', 473-509 < VEI>
A; Cross-references: UNIPARC:UPTO00016ABFC; EMBL:X06369; NID:g34288; PIDN:CAA29667.1; PID
R; Cross-references: Univ Y: Chen, S.J.; Phillips, C.A.; Canna, C.; Linna, T.J.
Biochim. Biophys. Acta 888, 286-295, 1986
A; Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56 (LSTRA).
A; Reference number: S07143; MUID:87000726; PMID:3489486
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A;Residues: A',376-509 <TRE>
A;Gross-references: UNIPARC:UP1000016AF39; EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PID
A;Cross-references: UNIPARC:UP1000016AF39; EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PID
R;Takadera, T.; Leung, S.; Gernone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W
Mol. Cell. Biol. 9, 2173-2180, 1989
A;Title: Structure of the two promoters of the human lck gene: differential accumulation
A;Reference number: A32797; MUID:89313764; PMID:2787474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UD100016ABFD; GB:M21510; NID:g187031; PIDN:AAA59501.1; PID:
C;Comment: Protein tyrosine kinases play important roles in the control of cell growth a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP C; Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C; Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho: F;2-509/Product: protein-tyrosine kinase lck #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID:
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Reference number: 157636; MUID:89096891; PMID:2850479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UD100016ABFF; GB:M26692; NID:g341523; PIDN:AAA59503.1; R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M. Mol. Cell. Biol. 8, 3058-3064, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 1p35-1p34.3
A;Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
                                                                                                                                                                                                                                                                                                                                                                                                                      C.B.
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F;43-501/Domain: protein kinase homology <KIN>
F;251-259/Region: protein kinase APP-binding motif
F;251-259/Region: protein kinase APP-binding motif
F;27/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3,5/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P06239; UNIPARC:UPI0000151F17; EMBL:X14053 R;Perlmutter, R.M.; Marth, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, J. Cell. Biochem. 38, 117-126, 1988 A;Titles: Structure and expression of lck transcripts in human lymphoid cells. A;Reference number: S07822; MUID:89123626; PMID:3265417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GDB:119360; OMIM:153390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-35,'VR' <RES>
                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-509 <ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-35 < TAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: S01879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: I57636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB: LCK
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A, Residues: 1-282, VP', 285-509 < MAR>
A, Crosidues: 1-282, VP', 285-509 < MAR>
A, Note: the sequence is revised in GenBank entry MUSLCK, release 116.0, (PIDN:AABS9674.1
R, Voronova, A.F.; Adler, H.T.; Sefton, B.M.
Mol. Cell. Biol. 7, 4407-4413, 1987
Mol. Cell. Biol. 7, 4407-4413, 1987
Mol. The limit and the containing different 5' untranslated regions are present in A, Reference number: 157629; MUID:88142832; PMID:3501824
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Residues: 1-11 < VOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promote
A,Reference number: 148845; MUID:86146842; PMID:3081813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Cross-references: UNIPROT:Q91X65; UNIPARC:UPI000000418D; EMBL:X03533; NID:g54813; PIDN Marth, Jo.D.; Peet, R.; Krebs, E.G.; Perimutter, R.M.
1933-404, 1985
11 43, 393-404, 1985
11 13. Alymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpres Reference number: A23639; MUID:86079521; PMID:2416464
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A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel A;Reference number: 157636; MUID:89096891; PMID:2850479
A;Accession: 177452
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Subperfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;
Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro
;68-116/Domain: SH3 homology <SH3>
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                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: p56; protein-tyrosine kinase tck C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 18-Peb-2000 #sequence revision 18-Peb-2000 #text_change 05-Oct-2004
C;Accession: 148845; A23639; Ī57629; 177452
R;Voronova, A.F.; Sefton, B.M.
Nature 319, 682-685, 1986
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Status: preliminary; translated from GB/EMBL/DDBJ

Molecule type: DNA Residues: 1-35,'VR' <GAR>

0; Mismatches

69

RESULT 2 OKHULK

LQDNLVIAL 61 LODNLVIAL

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Query Match 100. Best Local Similarity 100. Matches 9; Conservative

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protein-tyrosine kinase (EC 2.7.1.112) tkl [similarity] - chicken
N.Alternate names: kinase-related transforming protein (tkl); T-cell surface antigen ass
C;Species: Gallus gallus (chicken)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: A42126; A39939
R;Chow, L.M.; Ratcliffe, M.J.; Veillette, A.
Mol. Cell. Biol. 12, 1226-1233, 1992
A;Title: tkl is the avian homolog of the mammalian 1ck tyrosine protein kinase gene.
A;Reference number: A42126; MUID:92186654; PMID:1545804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBIP:88833)
R;Strebhardt, K.; Mullins, J.1.; Bruck, C.; Ruebsamen-Waigmann, H.
Proc. Natl. Acad. Sci. US.A. 84, 8778-8782, 1987
A;Title: Additional member of the protein-tyrosine kinase family: the src-and lck-relate A;Reference number: A39939; MUID:88097370; PMID:3321053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: mRNA
A,Residues: 52-507 cSTR>
A,Kestidues: 52-507 cSTR>
C,Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C,Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C,Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
E,66-114/Domain: SH3 homology <SH3>
F;125-222/Domain: SH2 homology <SH2>
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2499-257/Region: protein kinase ATP-binding motif
F;249-257/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (8Jy) (in mature form) #status predicted
F;392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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C;Genetics:
A;Gene: RC0716
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C'Jacesion: D9789
C'Jacession: D97789
R'Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A,Tille: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A,Reference number: A97700; MUID:21442074; PMID:11557893
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Pred. No. 18;
3; Mismatches 0; Indels
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A;Experimental source: thymus, spleen
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      225 LQDSLVIAI 233
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Local 6; Conserv?
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LQDKLVVAL
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A;Molecule type: DNA
A;Residues: 1-234 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-88 <CHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
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G72285
Hybrid cluster [4Fe-2S-30] protein TM1172 [similarity] - Thermotoga maritima (strain MSE N;Alternate names: prismane [6Fe-6S] protein [misnomer]
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: G72285
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sec
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: G72285
A;Molecule type: DNA
F;273/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: UNIPROT.09X004; UNIPARC:UPI000012C367; GB:AE001774; GB:AE000512; NID
A,Experimental source: strain MSB8
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A,Residues: 1-269 <AND>
A,Cross-references: UNIPROT:Q9ZD70; UNIPARC:UPI0000139866; GB:AJ235271; GB:AJ235269; NID
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hypothetical protein RP474 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: G71706
C;Accession: G71706
C;Accession: G71706
A;Anderesson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499; PMID:9823893
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A, Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                     Gaps
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                                                                                        Length 509;
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                                                                                                                                                  0; Indels
                                                                                  100.0%; Score 41; DB 1;
100.0%; Pred. No. 0.74;
iive 0; Mismatches 0,
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C, Genetics:
A, Gene: RP474
                                                                                                                 Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                 61 LQDNLVIAL 69
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Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 7; Conserv
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                                                                                     Query Match
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C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97092
R;Nolling, J.; Bareton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Closh, Reference number: A96900; MUID:21359325; PMID:21359325
A;Recession: G97092
A;Accession: G97092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 decovaribodipyrimidine photolyase [imported] - Salmonella enterica subsp. enterica serova decovar decis: Salmonella enterica subsp. enterica serovar Typhi C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: A10587 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connetton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova A;Reference number: AB0502; MUID:21534947; PMID:11677608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              decoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - Salmonella typhimurium N;Alternate names: DNA photolyase; photoreactivating enzyme C;Species: Salmonella typhimurium C;Species: Salmonella typhimurium C;Species: Jan.1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004 C;Accession: S22321; S78105
                                                                                                                                                                                                                                                                             endoglucanase (truncated) [imported] - Clostridium acetobutylicum
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Pred. No. 1e+02;
1; Mismatches
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Pred. No. 12;
3; Mismatches
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C; Superfamily: deoxyribodipyrimidine photo-lyase
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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94 LQDNLLFAI 102
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12 LKDNLIVVL 20
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1 LQDNLVIAL 9
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Best Local Similarity
5, Conserve
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14 LQDNLALA 21
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A;Molecule type: DNA
A;Residues: 1-473 <PAR>
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A;Residues: 1-67 <KUR>
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A; Residues: 'M',17-491 <MTH2>
A; Residues: 'M',17-491 <MTH2>
A; Cross-references: UNIPARC; UPI0000165BBA; GB: AE000906; GB: AE000666; NID: g2622557; PIDN: A; Experimental source: strain Delta H
A; Note: an incorrect initiation codon was used
C; Genetics:
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C; Keywords: 4Fe-2S-30; 4Fe-4S; electron transfer; iron; iron-sulfur protein; metalloprot
F; 2-40/Domain: rubredoxin homology «RUB»
F; 170-456/Domain: hybrid cluster [4Fe-2S-30] homology «HCL»
F; 5, 8, 38, 41/Binding site: iron (Cys) #status predicted
F; 77, 70, 79, 85/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F; 193, 217, 261, 347, 375, 400, 434, Binding site: 4Fe-2S-30 cluster (His, Glu, Cys, Cys, Cys, F; 347/Modified site: cysteine persulfide (Cys) #status predicted
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                                                                                                                                                                                         C; Accession: C90505
R; She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jobe, J.; Joffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: C90505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: UNIPROT: Q97U24; UNIPARC: UP10000649BC; GB: AE006641; NID: g1381636;
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                                 C90505

conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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hybrid cluster [4Fe-2S-30] protein MTH1453 [similarity]
N;Alternate names: prismane [6Fe-6S] protein [misnomer]
C;Species: Methanobacterium thermoautotrophicum
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text
C;Accession: A59199; E69060
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A,Gene: SSO3201
C,Superfamily: hypothetical protein AF0171
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55.6%;
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Best Local Similarity 55.vv.
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LKDNVIVAL 123
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A; Molecule type: DNA
A; Residues: 1-199 < KUR>
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A;Cross-references: UNIPROT:Q9LMN7; UNIPARC:UP100000A8092; GB:AE005172; NID:g8920637; P1
C;Genetics:
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Cispecies Nostoc sp. PCC 7120
A;Note: Nostoc sp. ptrain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AG3136
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21552285; PMID:11759840
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A;Experimental source: strain PCC 7120
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: genomic RNA
A;Residues: 1-2630 cVNA>
A;Cross-references: UNIPROT:055319; UNIPARC:UPI00000F73C5; EMBL:AF024514; NID:g2668619;
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C;Species: Acyrthosiphon pisum virus
C;Species: Acyrthosiphon pisum virus
C;Accession: 10-869-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: 108868
R;Van der Wilk, F.; Dullemans, A.M.; Verbeek, M.; van den Heuvel, J.F.J.M.
Virology 238, 353-352, 1997
A;Rtle: Nucleotide sequence and genomic organization of Acyrthosiphon pisum virus.
A;Reference number: 216501; MUID:98063255; PMID:9400608
               Southwick, A.M.; Sun,
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            A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; S. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Accession: E86545 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                A;Map position: 1
C;Superfamily: wall-associated protein kinase; protein kinase homology
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                                                                                                                                                                                                                                                                                                                                                                                                      75.6%; Score 31; DB 2; Length 733
55.6%; Pred. No. 1.7e+02;
iive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 2; Length 148
Pred. No. 3.6e+02;
0; Mismatches 1; Indels
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Best Local Similarity 66.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 3; Mismatches 0;
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87.5%;
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 55.0.
Fra 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427 LODNSIVAI 435
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A; Residues: 1-1488 < KUR>
                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-733 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                   A;Accession: 578105
A;Molecule type: DNA
A;Residues: 1-19,21-39,41-59,61-79,81-99,101-119,121-139,141-159,161-179,181-198,200-219
A;Cross-references: UNIPARC:UPI00001703BB; EMBL:X60662; NID:g48950; PIDN:CAA43069.1; PID
A;Gene: phr
C;Function:
                                                                         Sal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barcosine oxidase alpha chain truncated homolog PAB1842 [similarity] - Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q9V0K6; UNIPARC:UPI00006692E; GB:AJ248285; GB:AL096836; NIC
C;Genetics:
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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C;Accession: E86345
R;Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Anauchors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
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R;Li, Y.F.; Sancar, A.

Nucleic Acids Res. 19, 4885-4890, 1991

A;Title: Cloning, sequencing, expression and characterization of DNA photolyase from $4.7 itle: Cloning, sequencing, expression and characterization of DNA photolyase from $4.8 eference number: $22321; MUID:92020120; PMID:1840665

A;Reference number: $78105

A;Reference number: $78105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: DNA repair; catalyzes the light-dependent (300-600 nm) monomerization A strand, upon exposure to ultraviolet radiation C;Superfamily: deoxyribodipyrimidine photo-lyase C;Reywords: carbon-carbon lyase; DNA binding; DNA repair; flavoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C, Accession: H75122
R, anonymous, Genoscope submitted to the EMBL Data Library, July 1999
A, Description: Pyrococus abyssi genome sequence: insights into archaeal chromosome
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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Pred. No. 1.1e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.6%; Score 31; DB 2; Length 473; 75.0%; Pred. No. 1e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.6%;
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130 LQDDLTVAL 138
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Matches 6; Conserv
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A; Status: preliminary
A; Molecule type: DNA
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Gene: PAB1842
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C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97009
R;Molling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4833-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q97KN1; UNIPARC:UP10000C9FFC; GB:AE001437; PIDN:AAK78862.1; A;Experimental source: Clostridium acetobutylicum ATCC824 C;Genetics:
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A;Residues: 1-420 <DEV>
A;Residues: 1-420 <DEV>
A;Cross-references: UNIPROT:Q09873; UNIPARC:UPI000013A09E; EMBL:Z66568; NID:g1052518; PI
A;Devlin, K.; Odell, C.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
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A;Cross-references: UNIPARC:UPI000013A03E; EMBL:Z66568; PIDN:CAA91505.1; GSPDB:GN00066; 
A;Experimental source: strain 972h-; cosmid c12G12
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C.Species: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C.Accession: 862541; 137591
A.Devlin, K.; Odell, C.; Churcher, C.M.
submitted to the EMBL Data Library, November 1995
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                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                          A;Molecule type: DNA
A;Residues: 1-319 <BEV>
A;Cross-treferences: UNIPROT:P82715; UNIPARC:UPI00000ABB2A; EMBL:AL163815
A;Experimental source: cultivar Columbia; BAC clone F15N18
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C97009
hypothetical protein CAC0886 [imported] - Clostridium acetobutylicum
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Pred. No. 1.1e+02;
2; Mismatches 1;
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Pred. No. 1.3e+02;
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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271 VQDNIVISV 279
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Best Local Similarity
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A;Molecule type: DNA
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A;Status: preliminary
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A,Gene: SPAC12G12.10
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A; Introns: 35/2; 9
A; Note: F15N18.40
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A;Residues: 1-213 <KAN>
A;Residues: 1-213 <KAN>
A;Cross-references: UNIPROT:P74251; UNIPARC:UPI00000C0E3C; EMBL:D90913; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein s111089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4-hydroxybenzoate octaprenyltransferase related protein CAC0800 [imported] - Clostridium C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C;Accession: E96998 R;Nolling, J; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J; Ascersion: Squence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                          Cispecies: Synechocystis sp.
A; Variety: PCC 6803
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C; Accession: 875886
R; Kaneko, T.; Saro, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O; K.; Oyumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA, Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q97KW6; UNIPARC:UPI00000C9FAD; GB:AE001437; PIDN:AAK78776.1; A;Experimental source: Clostridium acetobutylicum ATCC824 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C'Accession: T48504
R'Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, A;Reference to the Protein Sequence Database, April 2000
A;Reference number: Z24490
A;Accession: T48504
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0
                                                                                                                                                                                          hypothetical protein sll1089 - Synechocystis sp. (strain PCC 6803)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.2%; Score 30; DB 2; Length 213; 85.7%; Pred. No. 72; 1: Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Accession: S75886
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T48504
hypothetical protein F15N18.40 - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30; DB 2;
Pred. No. 1e+02;
2; Mismatches
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Best Local Similarity 85.7 Matches 6, Conservative

Query Match

87 QDNVVIA 93

2 ODNLVIA 8

ò 임 73.2%; 66.7%;

Query Match Best Local Similarity 66., 6, Conservative

A; Gene: CAC0800

A Status: preliminary A Molecule type: DNA A;Residues: 1-297 <KUR>

138 IQPNLVLAL 146

1 LQDNLVIAL

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CjAccession: B64530
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne, Beterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne, Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.G. A;Reference number: A64520; MUID:97394467; PMID:9252185
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A;Cross-references: UNIPROT:024911; UNIPARC:UPI0000D3119; GB:AE000530; GB:AE000511; NID
C;Superfamily: probable methyl-accepting chemotaxis transducer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q9X814; UNIPARC:UPI00000DB081; EMBL:AL049841; PIDN:CAB42757
                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accesion: T36330
R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: ftsH2; SCOEDB:SCE9.11c
C;Superfamily: cell division protein ftsH; FtsH/SEC18/CDC48-type ATP-binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methyl-accepting chemotaxis transducer (tlpC) - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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                                                                            Gaps
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      Score 30; DB 2; Length 569;
Pred. No. 2.1e+02;
2; Mismatches 1; Indels
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Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                         RESULT 23
T36330
cell division protein ftsH2 - Streptomyces coelicolor
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Pred. No. 2.5e+02;
1; Mismatches 0
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   73.2%;
62.5%;
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85.7%;
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Best Local Similarity 85.7-
5.7-6; Conservative
                                                                        5; Conservative
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A;Accession: T36330
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186 LNDNLIVA 193
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                                                                                                                                    1 LQDNLVIA 8
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                                       Best Local Similarity
Matches 5; Conserv
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A; Residues: 1-668 <OLI>
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         Query Match
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69769
R;Kunst, F: Ogasawara, N:; Moszer, I:; Albertini, A.W.; Alloni, G.; Azevedo, V.; Berter
R;Kunst, F.; Ogasawara, N:; Moszer, C.V.; Caldwell, B.; Capuano, V.; Carter, N.W.; ChA
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kunano, M.; Kurita, K.; Lapidus, A.; Ladinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Mauuda, S.; Museel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Saconlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Schiguchi, J.; Sckowska, A.; Sacor,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Schiguchi, J.; Sckowska, A.; Sacor,
A;Authors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUDD:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                           Cippedies: Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. Strain PCC 7120
C;Accession: AH2468
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Accession: AH2468
A;Anolegule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q8YLJ4; UNIPARC:UPI00000CEE24; GB:BA000019; PIDN:BAB77003.1;
A;Experimental source: strain PCC 7120
C;Genetics:
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AH2468
hypothetical protein all5304 [imported] - Nostoc sp. (strain PCC 7120)
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                                                                        Length 420;
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C;Superfamily: Bacillus subtilis hypothetical protein ydaL
                                                                  73.2%; Score 30; DB 2; 1
87.5%; Pred. No. 1.5e+02;
                                                                                                                              0; Mismatches
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87.5%;
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                                                                                                                                 Conservative
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                             Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                1 LODNLVIA 8
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Best Local Similarity
Matches 7; Conserv
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A; Residues: 1-569 < KUN>
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A; Map position: 1L
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C; Superfamily: translation initiation factor IF-2; translation elongation factor Tu homo C; Keywords: GTP binding; nucleotide binding; P-loop F;395-512/Domain: translation elongation factor Tu homology <ETU>F;405-512/Region: nucleotide-binding motif A (P-loop) F;505-512/Region: GTP-binding MXXD motif F;515-512/Region: GTP-binding SAK/L motif F;411,412,432,509,510,512,545/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #
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C;Accession: T03094

R;Han, J.D.; Baker, N.E.; Rubin, C.S.
J. Biol. Chem. 272, 26611-26619, 1997

A;Title: Molecular characterization of a novel A kinase anchor protein from drosophila 1 A;Reference number: Z14835; MUID:97476266; PMID:9334242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
X;Residues: 1-2359 cHMN-
A;Cross-references: UNIPROT:Q9W4E2; UNIPARC:UPI000008370A; EMBL:AF003622; NID:g2393879;
A;Experimental source: strain Canton S
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42025
S;Harasyw, M.; Bernan, V.; Ally, D.; Piret, J.
submitted to the EMBL Data Library, August 1995
A;Reference number: 222032
A;Reference number: 222032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A-kinase anchor protein DAKAP550 - fruit fly (Drosophila melanogaster) (frac
C;Species: Drosophila melanogaster
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                            Score 30; DB 2; Length 900;
Pred. Nc. 3.5e+02;
3; Mismatches 0; Indels
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A;Molecule type: DNA
A;Residues: 1-71 cHAR>
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100.0%; Pred. No. 36;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: FlyBase: FBgn0021748
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative 3
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Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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843 LRDNIVVA 850
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: B70694
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, MA-; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference prominary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-900 <COL>
A;Cross-references: UNIPROT:P71613; UNIPARC:UP1000012D2E2; GB:Z81331; GB:AL123456; NID:96;Genetics:
A;Experimental source: strain H37RV
C;Genetics:
                                                                                         A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: A71978
A;Accession: A71978
A;Retatus: preliminary
A;Molecule type: DNA
A;Residues: 1-673 <ARN>
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A;Resperimental source: strain J99
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: probable methyl-accepting chemotaxis transducer
         R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
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A;Cross-references: UNIPROT:Q20357; UNIPARC:UPI00000759ED; EMBL:U40427; NID:g1065557; PI C;Genetics: C;Genetics: A;Genetics: A;Genetics: A;Introns: 34/3; 67/2; 101/1; 178/1; 227/1; 262/3; 307/2; 449/3; 476/1; 502/3; 595/3; 63
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C;Accession: T16356
R;Fulton, B.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F43C9.
A;Reference number: Z18499
A;Accession: T16356
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1;
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hypothetical protein [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Species: Buchnera sp.
C;Accession: G84991
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
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R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
R;Shigenobu, S.; Watanabe, H.; Hattori, Hattori, M.; Sakaki, Y.; Ishikawa, H.
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R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Mattanabe, M.; Hattori, M.; Hat
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Best Local Similarity 66.7
Matches 6; Conservative
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Search completed: June 29, 2006, 09:31:43 Job time: 15.3373 secs

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mannheimia bifidobacte clostridium

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homo sapien mus musculu

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08G7K1_BIFLO
0971S7_CLOAB
092NW9_RHIME
0379L5_9PERO
05HBL2_EHRRW
02NP95_9EURY
05US92_HALMA
06K9B5_0RYSA
0948H3_0RYSA
MUTS_COLE3
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07757M7_NEUCR
077577_ANGGA
0811R8_NEUCR
077577_ANGGA
0814H4_NOGA
070H44_ANGGA
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097U24 SULSO
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0349T4 RH0PA
037N36 RH0PA
021Z55 RH0PA
06N3M7 RH0PA
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Q6CU917
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Q35N10_
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

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InterPro; IPR008266; Tyr_pkinase_AS.
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LCK HUMAN

AC P0539

DT 01-578

DT 07-MA

DE PFOCO

DE SPECTION

DE SPECTION

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DE SPECTION

COC BUKAR

OC BUKAR

OC MAMMO

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RR MEDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine phosphate.

SUBUNIT: Binds to the cytoplasmic domain of cell surface receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also binds to effector molecules, such as P14K, VAV1, RASA1, FYB and to other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes through its SH3 domain and to the tyrosine phosphorylated form of KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.

Interacts with phosphorylated LIME1. Interacts with CBLB (By
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
                                                                                                                                                                                                         08-NOV-2005, sequence version 3.
07-MAR-2006, entry version 13.
Proto-oncogene tyrosine-protein kinase LCK (BC 2.7.1.112) (p56-LCK)
(Lymphocyte cell-specific protein-tyrosine kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULÂR LOCATION: Cytoplasmic and attached to the membrane. Present in lipid rafts in an unactive form (By similarity). DOWAIN: The SH2 domain mediates interaction with SQSTM1. Interaction is regulated by Ser-58 phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity). SIMILARITY: Belongs to the Tyr protein kinase family. SRC \ensuremath{\mathsf{SIMILARITY}}
                                                                                                    LCK AOTNA STANDARD; PRT; 508 AA.
Q5PXS1;
08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subfamily.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMR; QSPXSI; 64-508.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001454; Tyr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                               Aotus nancymaae (Ma's night monkey)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=37293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aotinae; Aotus
                                                                                                                                                                                                                                                                                                                                                              Name=LCK;
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RESULT 1

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Phosphotyrosine (negative regulation) (By similarity).
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDLINE-87133831; PubMed-3493153;
Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
Mak T.W.;
"A human T cell-specific cDNA clone (YT16) encodes a protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (By similarity).
Phosphotyrosine (by autocatalysis) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proto-oncogene tyrosine-protein kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-myristoyl glycine (By similarity).
S-palmitoyl cyteine (By similarity)
S-palmitoyl cysteine (By similarity)
8B61951BC192A3A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
INIT 0 0 Probable.
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein kinase.
ATP (By similarity).
Interactions with CD4 and CD8 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proton acceptor (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTId=PRO_0000088123
                                                                                                                                                                                                       ProDom; PD000093; SH2; 1.
ProDom; PD000066; SH3; 1.
SWART; SW00252; SH2; 1.
SWART; SW00219; TYTKC; 1.
SWART; SW0019; TYTKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS500109; PROTEIN KINASE TYR; 1.
PROSITE; PS500109; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity)
                                                         Pfam; PF00018; SH3 1; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD0000001; Proc. Kinase; 1.
ProDom; PD000001; SH2; 1.
ProDom; PD000066; SH3; 1.
Pfam; PF07714; Pkinase Tyr; 1.
Pfam; PF00017; SH2; 1.
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us-10-062-257a-11.rup

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REVIEW
   MEDLINE=2218825; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=2218825; PubMed=12477932; DOI=10.1073/pnas.242603899;

MI Klausner R.D., Collins F.S., Wargner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A platchen R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenco L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

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                                                                                                                                                                                                                                 gene: differences in genomic organisation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89096891; PubMed=2850479;
Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
"Structure of the murine lck gene and its rearrangement in a murine
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MEDLINE=90108697; PubMed=2558056; DOI=10.1016/0378-1119(89)90144-3;
Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
Benarous R.;
"Structure of the human lck gene: differences in genomic organisati.
within src-related genes affect only N-terminal exons.";
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MEDLINE=9608519; PubMed=7495859; DOI=10.1016/0167-4781(95)00162-A;
WOGEL I.B., Arthur R., Fujita D.J.;
"An aberrant lck mRNA in two human T-cell lines.";
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                                                                                                         "Structure and expression of lck transcripts in human lymphoid
                                                         MEDLINE=89123626; Pubmed=3265417;
Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F.
protein-tyrosine kinases.";
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MEDLINE=89313764; PubMed=2787474;
Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consortium;
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Human chromosome 1 international sequencing co
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Eur. J. Immunol, 16:1643-1646(1986)
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                                              NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse cDNA sequences.
                                                                                                                                                                                                                                                                 Gene 84:105-113(1989).
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down regulates its catalytic activity.";
EMBO J. 11:2919-2924(1992).
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MEDLINE=2046261; PubMed=11009097;
DOI=±0.1002/1521-4141(200009)30:9<2632::AID-IMMU2632>3.0.CO;2-C;
Boncristiano M., Majolini M.B., D'Elios M.M., Pacini S., Valensin S., Ulivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
Baldari C.T.;
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"Structure of the two promoters of the human lck gene: differential accumulation of two classes of lck transcripts in T cells.";
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MEDLINE=87000726; PubMed=3489486; DOI=10.1016/0167-4889(86)90228-4;
Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Greenway A.L., Azad A., Mills J., McPhee D.A.; "Human immunodeficiency virus type 1 Nef binds directly to LCK imitogen-activated protein kinase, inhibiting kinase activity."; J. Virol. 70:6701-6708(1996).
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"The SH3 domain of p561ck is involved in binding to phosphatidylinositol 3'-kinase from T lymphocytes.";
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J. Biol. Chem. 270:2506-2511(1995).
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Vogel L.B., Fujita D.J.;
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INTERACTION WITH PI3K.
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NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
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target for signal intervention by Herpesvirus saimiri and other
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J. Exp. Med. 198:1453-1462(2003).
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                      PubMed=14610046; DOI=10.1084/jem.20031484;
Brdickova N., Brdicka T., Angelisova P., Horvath O., Spicka J.,
Hilgert I., Paces J., Simeoni L., Kliche S., Merten C., Schraven B.,
Horejsi V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCK MOUSE STANDARD; PRT; 508 AA.
P06240; Q61794; Q61795; Q62320; Q91X65;
01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
25-OCT--2005, sequence version 3.
07-MAR-2006, entry version 74.
Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK) (Lymphocyte cell-apecific protein-tyrosine kinase) (LSK).
Mus musculus (Mouse).
                                                                                                                                                                   TISSUE=Mammary cancer;
MEDLINE=21829512; PubMed=11840567;
DOI=10.1002/1615-9861(200202)2:2<212::AID-PROT212>3.0.CO;2-H;
Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
Zvelebil M.J.;
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                                                                PubMed=12218089;
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Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
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J. Immunol. 169:2813-2817(2002).
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NUCLEOTIDE SEQUENCE [MRNA].

NUCLEOTIDE SEQUENCE [MRNA].

VORONOVA A.F., Sefton B.M.;

"Expression of a new tyrosine protein kinase is stimulated by retrovirus promoter insertion.";

Nature 319:682-685(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 41; DB
100.0%; Pred. No. 8.1
Live 0; Mismatches
             l gene products.";
J. Biochem. 267:3413-3421(2000)
                                                                                                                                                                                                                                                         protein expression map database.";
Proteomics 2:212-223(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100
Matches 9; Conservative
                                                                                                                                                                                                                                                                                            INTERACTION WITH LIME1.
                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION WITH LIMEL.
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                                               SUBCELLULAR LOCATION
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                                                                                                                                                            SPECTROMETRY.
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                                                            PubMed=12218089
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viral
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LCK_MOUSE
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki
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                                 PubMed=16141072; DOI=10.1126/science.1112014;
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STRAIN=NOD; TISSUE=Thymus;
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"Interaction of the unique N-terminal region of tyrosine kinase p561ck
with cytoplasmic domains of CD4 and CD8 is mediated by cysteine
                                                                                                                                                                                                                                                             INTERACTIONS WITH CD4 AND CD8, AND MUTAGENESIS OF 2-CYS--CYS-4; CYS-19
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"Palmitoylation of multiple Src-family kinases at a homologous N-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTAGENESIS OF TYR-504.
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-!- FUNCTION: Tyrosine kinase that plays an essential role for the selection and maturation of developing T-cell in the thymus and in mature T-cell function. Is constitutively associated with the cytoplasmic portions of the CD4 and CD8 surface receptors and plays a key role in T-cell antigen receptor(TCR)-linked signal transduction pathways. Association of the TCR with a peptide antigen-bound MHC complex facilitates the interaction of CD4 and CD8 with MHC class II and class I molecules, respectively, and thereby recruits the associated LCK to the vicinity of the TCR/CD3
                                                                                                                                                                                                                           the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saimiri sciureus (Common squirrel monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-NOV-2005, sequence version 2. 07-MAR-2006, entry version 26. Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK) (Lymphocyte cell-specific protein-tyrosine kinase).
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                                                                                                PubMed=10646608; DOI=10.1038/35003228;
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terminal motif.";
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nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                       INTERACTION WITH CBLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68
                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION. PubMed=12218089;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               natural host.";
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095KR7;
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LCK_SAISC
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PROTEIN_KINASE_TYR;

PS50011; PS00109;

PROSITE;

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tyrosine phosphate.

1. ENZYME REGULATION: Regulated by phosphatases.

2. -1- ENZYME REGULATION: Regulated by phosphatases.

3. SUBJUNIT: Binds to the cytoplasmic domain of cell surface receptors, such as CD2, CD4, CD5, CD8, CD4, CD5 and CD12. Also binds to effector molecules, such as F14K, VAV1, RASA1, FYB and to other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds to phosphatidylinositol 3' Kinase (P13K) from T lymphocytes through its SH3 domain and to the tyrosine phosphorylated form of KHDRES1/p70 through its SH2 domain. Interacts with CBLB (By similarity). Interacts with Saminine herpesvirus 2 TIP.

2. SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.

3. Present in lipid rafts in an unactive form (By similarity).

3. SUBJUNITELINIAR LOCATION: Cytoplasmic form (By similarity).

3. SUBJUNITELINIAR SECTICITY: Expressed specifically in lymphoid cells.

4. DEVELOPMENTAL STAGES: Levels remain relatively constant throughout
              immunoreceptor tyrosines besed activation motifs (ITAMs) in the cytoplasmic tails of the TCRgamma chains and CD3 subunits, initiating the TCRCP1 signaling pathway. In addition, contributes to signaling by other receptor molecules. Associates directly with the cytoplasmic tail of CD2, and upon engagement of the CD2 molecule, LCK undergoes hyperphosphorylation and activation. Also plays a role in the IL2 receptor-linked signaling pathway that controls T-cell proliferative response. Binding of IL2 to its receptor results in increased activity of LCK. Is expressed at all stages of thymocyte development and is required for the regulation of maturation events that are governed by both pre-TCR and mature alpha beta TCR (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphorylation downregulates catalytic activity. Phosphorylated on Tyr-393 either by itself or another kinase, leading to increased enzymatic activity.

-!- SIMILARITY: Belongs to the Tyr protein kinase family.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
-!- GAUTION: LCK seems to be active in all vertebrates, except in squirrel monkey T-cells, in which it is inactivated. The reason seems to be that squirrel monkey are the natural host for Saimirine herpesvirus 2, which is able to efficiently transform T-cells through a mecanism involving viral Tip/ host LCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Distributed under the Creative Commons Attribution-NoDerivs License
LCK then phosphorylates tyrosines residues within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interaction. Its inactivation may a mecanism that specificaly counteracts the transformation effects of viral Tip.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T-cell ontogeny.

DOMAIN: The SH2 domain mediates interaction with SQSTM1.
Interaction is regulated by Ser-58 phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: Phosphorylated on Tyr-504 presumably by CSK. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P06239; 1LKK.
SMR; Q95KR7; 64-508.
InterPro; IPR000719; Prot kinase.
InterPro; IPR0007290; Ser_thr_pkinase.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PP07714; Pkinase_Tyr; 1.
Pfam; PP07017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ277921; CAC38871.1; -; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
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SMART; SM00252; SH2; 1. SMART; SM00326; SH3; 1. SMST; SM00319; TYKC; 1. PROSITE; PS00107; PROTEIN KINASE ATP; 1.

ProDom; PD000001; Prot_kinase; 1. ProDom; PD000093; SH2; 1. ProDom; PD000066; SH3; 1.

Pfam; PF00018; SH3 1; 1.
PRINTS; PR00401; SH2DOWAIN.
PRINTS; PR00452; SH3DOWAIN.
PRINTS; PR00109; TYRKINASE. PF00018; SH3

Pfam;

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                                                                                                                                                                                                                                                                             Phosphctyrosine (negative regulation) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMR; QYRTZ3; 65-509.
Ensembl; ENSG0000182866; Homo sapiens.
GO; GO:0042121; C:11pid raft; ISS.
GO; GO:0000242; C:pericentriolar material; ISS.
GO; GO:00004722; F:protein serine/threonine phosphatase activity; ISS.
GO; GO:0004723; F:protein-tyrosine kinase activity; ISS.
                                                                                                   Proto-oncogene tyrosine-protein kinase
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                                                                                                                                                                                                                                                    Phosphotyrosine (by autocatalysis) (By similarity).
                                                                                                                                                                                                                                                                                                       N-myristoyi glycine (By similarity).
S-palmitoyl cysteine (By similarity)
S-palmitoyl cysteine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "No association between lck gene polymorphisms and protein level
                                    ATP-binding; Kinase; Lipoprotein; Membrane; Myristate; Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene; SH2 domain; Transferase; Tyrosine-protein kinase. INIT MET 0 Probable. CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                     Protein kinase.
ATP (By similarity).
Interactions with CD4 and CD8 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -I- MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.
                                                                                                                                                                                                                           Proton acceptor (By similarity).
                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 41; DB 1; Length 508; 100.0%; Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                5088C64061853819 CRC64;
                                                                                                                 LCK.
/FT1d=PRO_0000088127.
                                                                                                                                                                                                                                      ATP (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-2003, integrated into UniProtKB/TrEMBL.
15-DEC-2003, sequence version 1.
07-FEB-2006, entry version 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        509 AA
                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                            similarity)
                                                                                                                                                                                                                 similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                          SH2.
                                                                                                                                                                                                                                                                                                                                                508 AA; 58122 MW;
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                                                                                                                                                                                                                                                                                                                                                                                      100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type 1 diabetes.";
Diabetes 51:3326-3330(2002).
                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein tyrosine kinase.
                                                                                                                                             120
223
497
258
71
                                                                                                                                                                                                                            363
272
393
                                                                                                                                                                                                                                                                                                                                                                                                                                             60 LQDNLVIAL 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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NUCLEOTIDE SEQUENCE.
                          PS50001;
PS50002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                             60
126
244
250
                                                                                                                                                                                                                            363
                                                                                                                                                                                                                                                       393
                                                                                                                                                                                                                                                                                504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O7RTZ3 HUMAN
ID Q7RTZ3 HUMAN
AC Q7RTZ3;
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BINDING
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                          PROSITE;
                                                                                                                                                                                   NP BIND
REGION
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                                                                                                                                                                                                                                                                              MOD RES
                                                                                                                                             DOMAIN
                                                                                                                                                                        DOMAIN
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GO, GO:0004712; F:protein raft; ISS.
GO; GO:0004712; F:protein serine/threonine phosphatase activity; ISS.
GO; GO:0004712; F:protein serine/threonine phosphatase activity; ISS.
GO; GO:0004712; F:protein-tyrosine kinase activity; ISS.
GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
GO; GO:0006919; P:sargadea activation; ISS.
GO; GO:0006919; P:mempotesis; ISS.
GO; GO:0006919; P:mempotesis; ISS.
GO; GO:0007242; P:mempotesis; ISS.
GO; GO:0007242; P:protein amino acid phosphorylation; ISS.
R GO; GO:0005080; P:protein amino acid phosphorylation; ISS.
R GO; GO:0007265; P:protein signal transduction; ISS.
R GO; GO:0007265; P:regulation of progression through cell cycle; ISS.
R GO; GO:000074; P:regulation of progression through cell cycle; ISS.
R GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
R GO; GO:0000074; P:response to drug; ISS.
R GO; GO:00000719; Protein ser.
R GO; GO:0000074; P:response to drug; ISS.
R GO; GO:000007714; P:response to drug; ISS.
R GO; GO:000007714; P:response to drug; ISS.
R GO; GO:000007714; P:response to drug; ISS.
R GO; GO:0000000000; Ser_thr_pkinase.
R InterPro; IPR000456; Tyr_pkinase.
R R Fam; PF00017; SH2; 1.
                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                   Thesis (2001), Department of Experimental Oncology laboratory, U.
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PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR000452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD0000061; Proc. Kinase; 1.
ProDom; PD0000065; SH3; 1.
SWART; SW00252; SH2; 1.
SWART; SW00219; TYRKC; 1.
SWART; SW00219; TYRKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                     EMBL; AJ320182; CAC44027.1; -; mRNA.
HSSP; P06239; 1LCK.
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Q3ZCMO BOVIN
ID Q3ZCMO_BOVIN PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
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SEQUENCE 509 AA; 57
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Matches
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MEDLINE=22031236; PubMed=12033791; DOI=10.1006/viro.2002.1381;
Picard C., Greenway A., Holloway G., Olive D., Collette Y.;
Interaction with simian HCk tyrosine kinase reveals convergent evolution of the Nef protein from simian and human immunodeficiency viruses despite differential molecular surface usage.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hylobatidae, Hylobates.
NCBI_TaxID=9581;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           509 AA; 58001 MW; 44BFF0D43FFB420D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.0%; Score 41; DB 2; Local Similarity 100.0%; Pred. No. 8.2; les 9; Conservative 0; Mismatcher ^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001, integrated into UniProtKB/TrEMBL. 01-DEC-2001, sequence version 1. 07-FBB-2006, entry version 18.
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095M32 9P
10 095M
AC 095M
AC 095M
DT 01-D
DT 01-D
DT 01-D
DT 01-D
DT 01-D
DC 07-B
DC Name
CO Hylo
OC Hylo
OC Hylo
OC Hylo
COC Hylo
RN NUCL
RX MEDICA
RT "IDT
RT evol
RT viru
RT viru
RT viru
RT Viro
RR Viro
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Debugger 15496914; DOI=10.1038/nature03025;

A Jailon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
Andrell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Androud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Anthouad V., Jubin C., Gastelli V., Katinka M., Vacherie B.,
Anthouad V., Jubin C., Gastelli V., Katinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Arra G., Lardier G., Chapple C., McXernan K.J., McEwan P., Bosak S.,
Kellis M., Volff J.-M., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Schachter V., Guigo R., Sauthi W., Scarpelli C.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                             19-JUL-2005, sequence version 1.
Chr-EBB-2006, entry Version 4.
Chromosome 15 SCAF1452, whole genome shotgun sequence. (Fragment)
ORFNames=GSTENG00014985001;
                                                                                                                                                                                                           Tetraodon nigroviridis (Green puffer).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleosteai,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 663;
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GO; GO:0003676; F:nucleuc acid binding; IEA.
GO; GO:0005515; F:nucleic acid binding; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
InterPro; IPR000210; BTB.
InterPro; IPR007087; Znf_C2H2.
Pfam; PF00096; zf_C2H2; 4.
SMART; SM00225; BTB; 1.
SMART; SM00355; Znf_C2H2; 4.
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Q3YSG0 EHRCJ
ID Q3YSG0. EHRCJ
AC Q3YSG0.
DT 27-SEP-2005, integrated into UniprotKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
                                        19-JUL-2005, integrated into UniProtKB/TrEMBL
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the early vertebrate proto-karyotype."; Nature 431:946-957(2004).
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Best Local Similarity 77.8
Matches 7; Conservative
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EMBL. BC102046; AA102047.1.

GO; GO:004512; C:lpid raft; ISS.

GO; GO:000421; C:pericentriolar material; ISS.

GO; GO:0004712; F:protein-tyrosine kinase activity; ISS.

GO; GO:0004712; F:protein-tyrosine kinase activity; ISS.

GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.

GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.

GO; GO:00042169; F:SH2 domain binding; ISS.

GO; GO:00042169; F:SH2 domain binding; ISS.

GO; GO:00042169; F:SH2 domain binding; ISS.

GO; GO:0007247; P:promein-amplied; ISS.

R GO; GO:0007247; P:promein-amplied; ISS.

R GO; GO:0006466; P:protein-amplied; ISS.

R GO; GO:0006466; P:protein-amplied; ISS.

R GO; GO:000047; P:resplation of progression through cell cycle; ISS.

R GO; GO:000047; P:resplation of progression through cell cycle; ISS.

R GO; GO:000047; P:resplation of progression through cell cycle; ISS.

R GO; GO:000047; P:resplation of progression through cell cycle; ISS.

R GO; GO:000047; P:resplation of progression through cell cycle; ISS.

R GO; GO:000047; P:resplation of progression through cell cycle; ISS.

R GO; GO:000047; P:resplation of progression through cell cycle; ISS.

R GO; GO:000047; P:resplation of progression through cell cycle; ISS.

R GO; GO:000044; P:resplation of progression through cell cycle; ISS.

R GO; GO:0000980; SH2.

DR HINESPEN: IRRO01452; SH2.

DR FEAN; PRO0017; SH2: 1.

DR FEAN; PRO0017; SH2: 1.

DR PENNTS; PRO0041; SH2: 1.

DR PENNTS; PRO0041; SH2: 1.

DR PRODM: PRO0099; SH3: 1.

DR PRODM: PRO0099; SH3: 1.

DR PRODM: PRO0099; SH3: 1.

DR PROMETE; PRO00109; PROFEIN KINASE ATP; 1.

DR PROSITE; PRO00109; PROFEIN KINASE TYR; 1.

DR PROSITE; PRO00109; PROFEIN KINASE TYR; 1.

DR PROSITE; PRO00109; PROFEIN KINASE TYR; 1.
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                                                                                                                                            STRAIN=Crossbred X Angus; TISSUE=11eum; Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y., Tanaguchi M., Wang Z., Yu', Prange C., Schreiber K., Shenmen C., Wagner L., Bala M., Barbaruk S., Barber S., Babakaiff R., Beland J. Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J., Marsuo C., Mayo M., Santos R.R., Stott U., Tsai M., Wong D., Siddiqui A., Holt R., Jones S.J., Marra M.A.; Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS50002; SH3; 1.
Hypothetical protein.
SEQUENCE 509 AA; 58116 MW; CE0E80DCD6D0F2F8 CRC64;
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MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;

MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;

Haft D.H., Hickey E.K., Gill S.R., Gwinn M.L., Dodenn K.J.,

McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,

Heidelberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";

Nature 399:233-329(1999).

-1- FUNCTION: Catalyzes the reduction of hydroxylamine to form NH(3)
                                                                                                                                         Glavina T.,
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                                                                                                                                                                                                                                                                    Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999, sequence version 1.
07-MAR-2006, entry version 38.
Hydroxylamine reductase (EC 1.7.-.) (Hybrid-cluster protein) (HCP)
Name=hcp; OrderediocusManes=TM1172;
                                                                                                                       US DOE JOINT Genome langitude;
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M., Vergez L., Schmutz J., Larimer F., Land M., Mavrommatis K., Richardson P.,
                                                                                                                                                                                                                                                                                                      GO; GO:0005737; Creytoplasm; i. Creytoplasm; i. Go; GO:0005737; Creytoplasm; i. Go; GO:000576; F:nucleic acid binding; IEA.

GO; GO:0005412; F:translation elongation factor activity; IEA.

GO; GO:0006414; P:translational elongation; IEA.

R GO; GO:0006414; P:translational elongation; IEA.

R InterPro; IPR011766; EF-P.

R InterPro; IPR0113185; EF-P.

R InterPro; IPR01132; EFP; 2.

R Pfam; PF01132; EFP; 2.

R TIGRRAMS; TIGR00038; efp; 1.

Complete proteome; Elongation factor.

V Complete proteome; Elongation factor.
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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                                                Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.4%; Score 35; DB 2; Length 189; 77.8%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                          "Complete sequence of Ehrlichia canis str. Jake.";
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and H(2)O (By similarity).
-!- COFACTOR: Binds 1 4Fe-4S cluster (By similarity)
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                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                                                                                                                                                                                           EMBL; CP000107; AAZ68345.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
21-FEB-2006, entry version 7. Elongation factor P (EF-P). OrderedLocusNames=Ecaj 0301;
                            OrderedLocusNames=Ecaj_0301;
Ehrlichia canis (strain Jake)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 77.8
Matches 7; Conservative
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LQDNIVITL 114
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PubMed=15995209; DOI=10.1128/JB.187.14.4935-4944.2005;
Mongodin B.F., Hance I.R., Deboy R.T., Gill S.R., Daugherty S.,
Huber R., Fraser C.M., Stetter K., Nelson K.E.;
"Gene transfer and genome plasticity in Thermotoga maritima, a model
J. Bacteriol. 187:4935-4944(2005).
                                                                                                                                                                                                                                                                                                                                                                        similarity).
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similarity).
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Thermotoga sp. RQ2.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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-!- COFACTOR: Binds 1 hybrid 4Fe-20-2S cluster (By similarity) -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity) . -!- SIMILARITY: Belongs to the HCP family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (By
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Pred. No. 1.4e+02;
1; Mismatches 1; Indels
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similarity).
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Iron-sulfur (4Fe-4S) (By sin
Iron-sulfur (4Fe-4S) (By sin
Iron-sulfur (4Fe-4S) (By sin
Iron-oxo-sulfur (4Fe-2O-2S)
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similarity)
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                                                                                                                                                                                                                                                                                                                                         Hydroxylamine reductase.
                                                                                                                                                                                                                                                                                                                                                     /FTId=PRO 0000151684.
Iron-sulfur (4Pe-4S)
Iron-sulfur (4Fe-4S)
Iron-sulfur (4Fe-4S)
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                                                                                                                 EMBL; AE000512; AAD36247.1; -; Genomic_DNA PIR; G72285; G72285.
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                                                                                                                                                                                   TIGR; TM1172; -.
BioCyc; TMAR2336:TM1172-MONOMER; -.
                                                                                                                                                                   GenomeReviews; AE000512_GR; TM1172.
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                                                                                                                                                                                                                  HAMAP; MF_00069; -; 1.
InterPro; IPR010048; Hybrid clust.
InterPro; IPR04137; Prismane.
Pfan; PP03063; Prismane; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           431 AA; 47958 MW;
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77.8%;
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Q4FF10;
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4atches 7; Conservative
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                                                                                                                                                  HSSP; Q01770; 1GNI
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"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S., Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T., Davis R.W., Scherer S., "The diploid genome sequence of Candida albicans."; Proc. Natl. Acad. Sci. U.S., 101:7329-7331(2004).

-! - CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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STRALN-MA, 4680 / ATCC 31267 / NCTMB 12694 / NREL 8165;
MEDLINE-21477403; Pubbed=11572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00228; TUBULIN B AUTOREG; UNKNOWN 1.
SEQUENCE 463 AA; 50480 MW; 21F5E66B04F73DAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=MA-4680 / ATCC 31267 / NCIME 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.4%; Score 35; DB 2; 177.8%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AACC01000002; EAL04615.1; -; Genomic_DNA.
EMBL; AACC01000001; EAL04811.1; -; Genomic_DNA.
InterPro; IPR002453; Beta_tubulin.
InterPro; IPR005152; LIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-UN-2003, integrated into UniProtKB/TrEMBL. 01-UUN-2003, sequence version 1. 21-FRB-2006, entry version 23. 1-FRB-2006, entry version 23. OrderedLocusNames=SAV5959;
                                                                                             26-APR-2005, integrated into UniProtKB/TrEMBL 26-APR-2005, sequence version 1. 07-FEB-2006, entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=15123810; DOI=10.1073/pnas.0401648101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA)
                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                          C. albicans secretory lipase 6.
Name=LIP6; ORFNames=CaO19.12286, CaO19.4823;
                                               463 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1045 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 77.8
                                                                                                                                                                                                                             Candida albicans SC5314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 LEDNLLIAL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF03583; LIP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LQDNLVIAL 9
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=237561;
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                                             QSAPE2_CANAL
QSAPE2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Q82AU6 STRAW
ID Q82AU6 S'
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                                                                                                                             IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINES-2014758; PubMed=11131027; DOI=10.1007/s002030000218;
Mubbe B., Stehr F., Bossenz M., Mazur A., Kretschmar M., Schaefer W.;
"Secreted lipases of Candida albicans: cloning, characterisation and
expression analysis of a new gene family with at least ten members.";
Arch. Microbiol. 174:362-374(2000).
-!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                               Gaps
Distributed under the Creative Commons Attribution-NoDerivs License
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Charge relay system (By similarity).
N-linked (GlCNAc. . ) (Potential).
N-linked (GlCNAc. . ) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carboxylate.
-!- SUBCELLULAR LOCATION: Secreted protein.
-!- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
                                                                                                                             ni.
                                                                                                                                                                                                                                                                                                                                                               ;
0
                          EMBL, D0073436; AAZ04353.1; -; Genomic_DNA.
GO; GO:0005737; C:cytoplaem; IEA.
GO; GO:000556; F:iron ion binding; IEA.
GO; GO:000518; F:iron ion binding; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR010048; Hybrid_clust.
Ffan, PP0363; Prismane; 1.
SEQUENCE 431 AA; 47929 MW; D7C7B2C4E309E7FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.4%; Score 35; DB 1; Length 463; 77.8%; Pred. No. 1.5e+02; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                       Length 431;
                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21F5E66B04F73DAF CRC64;
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InterPro; IPR005152; LIP.
Pfam; PF03583; LIP; 1.
Glycoprotein; Hydrolase; Lipid degradation; Signal.
SIGNAL 1 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipase 6. /FTId=PRO_0000017825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-NOV-2003, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                    85.4%; Score 35; DB 2; I 77.8%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000, sequence version 1. 07-FEB-2006, entry version 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lipase 6 precursor (EC 3.1.1.3).
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                            7; Conservative
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322 LEDNLLIAL 330
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Best Local Similarity
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CARBOHYD
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Q9P4E8;
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Length 463; 0; Indels

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Transferase
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BioCyc; SAVE227882:SAV5959-MONOMER; -.

RO; GO: 0004176; F.ATP-dependent peptidase activity; IEA.

RO; GO: 0004367; F.Dinding; IEA.

RO; GO: 0004252; F: Serine-type endopeptidase activity; IEA.

RO; GO: 0004252; F: Serine-type endopeptidase regulator activity; IEA.

RO; GO: 0006508; P: Proteclysis; IEA.

RO; GO: 0006555; P: regulation of transcription, DNA-dependent; IEA.

RO; GO: 0006555; P: regulation of transcription, DNA-dependent; IEA.

RO; GO: 0006508; P: Proteclysis; IEA.

RO; GO: 0006509; P: Procenponent signal transduction system (p. . .; IEA.)

RO; GO: 0006509; P: Two-component signal transduction system (p. . .; IEA.)

RO; GO: 0000460; P: TRANSPOSTISE.

RITEEPTO; IPRO01984; Peptidase S16.

RITEEPTO; IPRO01984; Peptidase S16.

RITEEPTO; IPRO01984; Peptidase S16.

RITEEPTO; IPRO01984; Peptidase ROG.

RITEEPTO; IPRO01984; Peptidase ROG.

RITEEPTO; IPRO01984; PERDISASERSIST.

RROSTIE; PRO0364; DISEASERSIST.

RROSTIE; PRO0364; DISEASERSIST.

RROSTIE; PRO0311; ABC_TRANSPORTER_1; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Ehrlichia chaffeengis str. Sapulpa.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Ehrlichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.4%; Score 35; DB 2; Length 1045; 87.5%; Pred. No. 3.5e+02; ive 1; Mismatches 0; Indels
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Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2005, integrated into UniProtKB/TrEMBL. 27-SBP-2005, sequence version 1. FFB-2006, entry version 5. Elongation factor P (EP-P).
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US DOE Joint Genome Institute (JGI-ORNL);
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les 7; Conserv
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0401E4 EHR
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Distributed under the Creative Commons Attribution-NoDerivs License
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Distributed under the Creative Commons Attribution-NoDerivs License
"Annotation of the draft genome assembly of Ehrlichia chaffeensis str.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Wolinella.
                                                                                                                                                                                                                                                                                                                                                        EMBL, AAIF01000095; EAAM95378.1; -; Genomic_DNA.
R GO; GO:0005737; C:cytoplasm; IEA.
R GO; GO:0003676; F:nucleic acid binding; IEA.
R GO; GO:000346; F:nucleic acid binding; IEA.
R GO; GO:0006412; P:protein biosynthesis; IEA.
R GO; GO:0006414; P:translation elongation; IEA.
R GO; GO:0006414; P:translational elongation; IEA.
R InterPro; IPR011768; EF-P.
R InterPro; IPR01059; EF-P.
R InterPro; IPR01135; EFP-P.
R PERSP; PIRSP05901; EFP-P.
R PIRSP; PIRSP05901; EFP-P.
R TIGRFAM9; TIGR00038; efp; 1.
                                         Sapulpa.";
submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, BX571659; CAE10003.1, -; Genomic_DNA.
BioCyc, WSUC844:WS0898-MONOMER; -.
GO; GO:0016757; F:transferas ectivity, transferring glycosyl.
GO; GO:0009116; P:nucleoside metabolism; IEA.
InterPro; IPR000836; PRtransferase.
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Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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                                                                                                                                                                  preliminary data.
-!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-2003, integrated into UniProtKB/TrEMBL.
15-DEC-2003, sequence version 1.
07-FBB-2006, entry version 17.
07-PBD-thetical protein.
OrderedLocusNames=WSO898;
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SEQUENCE 189 AA;
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Length 230;

DB 2;

82.9%; Score 34;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                 STRAIN=Wilmington;
PubMed=15317790; DOI=10.1128/JB.186.17.5842-5855.2004;
PubMed=15317790; DOI=10.1128/JB.186.17.5842-5855.2004;
McLeod M.P., Qin X., Karpathy S.E., Gioia J., Highlander S.K., Fox G.E., McNeill T.Z., Jiang H., Muzny D., Jacob L.S., Hawes A.C., Sodergren E., Gill R., Hume J., Morgan M., Fan G., Amin A.G., Gibbs R.A., Hong C., Yu X.-J., Walker D.H., Weinstock G.M.;
"Complete genome sequence of Rickettsia typhi and comparison with sequences of other Rickettsiae.";
J. Bacceriol. 186:5842-5855(2004).
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GO; GO:0004852; F:uroporphyrinogen-III synthase activity; IEA.
GO; GO:0006783; P:heme biosynthesis; IEA.
InterPro; IPR003784; HEM4 synth.
InterPro; IPR003728; Rickett_RPE.
PANTHER; PTHR12049; DUF185; 1.
TIGRFAM9; TIGR01045; RPE; 1.
Complete protecome; Hypothetical protein.
SEQUENCE 271 AA; 31679 MW; 5502F890BFFP8CA0 CRC64;
                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia; typhus group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.9%; Score 34; DB 2; Length 271
77.8%; Pred. No. 1.4e+02;
tive 2; Mismatches 0; Indels
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PubMed=15994558; DOI=10.1126/science.1110439;
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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07-FEB-2006, entry version
Hypothetical protein.
OrderedLocusNames=RT0461;
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Matches 7; Conservative
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STRAIN=Muguga;
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                                                                                                      Rickettsia typhi
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ID Q4NZAG THEPA
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ID 02-AUG-2005, int
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DT 07-FEB-2006, ent
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KN AJIEN J., Lynn
KN SALD H. J., Lynn
KN SALD H. S. SILVAU
KN JIEN J., NINETH
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Distributed under the Creative Commons Attribution-NoDerive License
                                    Gaps
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MEDLINE=20485642; PubMed=11030655; DOI=10.1126/science.290.5490.347; Ogata H., Audic S., Barbe V., Artiguenave F., Fournier P.-E., Raoult D., Claverie J.-M.; "Selfish DNA in protein-coding genes of Rickettsia."; Science 290:347-350(2000).
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Rickettsiaceae; Rickettsieae; Rickettsia; typhus group.
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      Pred. No. 1.2e+02;
2; Mismatches 0; Indels
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/FTId=PRO_0000101380.
RPE1 insert.
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                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
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Q68WQ6 RICTY
ID Q68WQ6 RICTY
AC Q68WQ6;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
br 11-OCT-2004, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                        269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ235271; CAA14929.1; -; Genomic_DNA. PIR; G71706; G71706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome, Hypothetical protein.
CHAIN 1 269 Hypothetica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenomeReviews; AJ235269_GR; RP474.
BioCyc; RPR0782:RP474-MOMOMER; -.
InterPro; IPR003784; HEM4_Synth.
InterPro; IPR003754; HEM4_Synth.
InterPro; IPR005758; Rickett RPE.
PANTHER; PTHR12049; DUF185; I
                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999, sequence version 1.
OT-MAR-2006, entry version 25.
Hypothetical protein RP474.
OrderedLocusNames=RP474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31209 MW;
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Best Local Similarity 7/...
7; Conservative
   Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 396:133-140(1998).
                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQDNLVIAL 9
                                                                                                                                      30 QDNLVVAI 37
                                                                                               2 QDNLVIAL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Madrid E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                     Y474 RICPR
Q9ZD70;
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                                                                                                                                                                                                                                                                             Y474 RICCRR
JD 79474 RICCRR
JD 70-MAY
DT 10-MAY
DT 10-MAY
DT 10-MAY
DT 10-MAY
DE HYDORGE
OC BACKET
OC RICKET
OC COPYT
RA RADULI
RA RADUL
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Gaps

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Length 271;

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Best Local Similarity
                                            Q9M5G4_EUPES
Q9M5G4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Gardner M., Bishop R., Shah T., de Villiers B., Carlton J.M., Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L., Lynn J., Weaver B., Shoaibi A., Waswoo D., Crabtree J., Wortman J.R., Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C., Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L., Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.; Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-: CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=KCTC 2396;
PubMed=1632867; DOI=10.1093/nar/gki1016;
Adeng H., Yim J.H., Lee C., Choi S.-H., Park Y.K., Yoon S.H.,
Hur C.-G., Kang H.-Y., Kim D., Lee H.H., Park K.H., Park S.-H.,
Park H.-S., Lee H.K., Oh T.K., Kim J.P.;
"Genomic blueprint of Hahella chejuensis, a marine microbe producing an algicidal agent.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
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                                                                                                                                                                                                                                                                                                                                    Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.9%; Score 34; DB 2; Length 322; 75.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                        301 AA; 34174 MW; B2EC5E9D0BD7592C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 AA; 35693 MW; 9B9FF4C6AD3635E2 CRC64;
                                                                                                                                                                                                                                                                                                                                 82.9%; Score 34; DB 2; I
87.5%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                       EMBL; AAGKO1000004; EAN31796.1; -; Genomic_DNA.
InterPro; IPR003639; Mov34-1.
InterPro; IPR000555; Mov34_MPN_PAD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JAN-2006, integrated into UniProtKB/TrEMBL. 24-JAN-2006, sequence version 1. 07-FBB-2006, entry version 2. Transaldolase (BC 2.2.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; CP000155; ABC29279.1; -; Genomic DNA. GO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 33:7066-7073(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=tal2; ORFNames=HCH 02473;
Hahella chejuensis KCTC 2396.
                                                                                                                                                                                                                                                              Pfam, PF01398; Mov34; 1.
ProDom; PD363422; Mov34-1; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QZSJ95_9GAMM PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              Local Similarity 87.5
ses 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                         preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                      |||||:||
274 LQDNLMIA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hahellaceae, Hahella
NCBI_TaxID=349521,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                        1 LQDNLVIA 8
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                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                   Query Match
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||||||:|: 75 QDNLVVAM 82

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF230740; AAF34804.1; -; mRNA.

HSSP; P24941; 1010.

R G0; G0:0005524; F:nucleotide binding; IEA.

G0; G0:000166; F:nucleotide binding; IEA.

G0; G0:0004674; F:protein serine/threonine kinase activity; IEA.

G0; G0:0006468; P:protein amino acid phosphorylation; IEA.

R G0; G0:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR000719; Prote kinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002245; TYP_pkinase.

R Pfam; PF00069; Pkinase; 1.

R Prom; PD0000001; Prot kinase; 2.

R SMART: SM00220: S TKC: 1.
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P42683; Q53WS8;
01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
01-NOV-1995, sequence version 1.
07-MAR-2006, entry version 47.
Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (Protein-tyrosine kinase C-TKL) (p56tk1).
                                                                                                                                                                                                                                                                                                      Euphorbia esula (Leafy spurge).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicotyledons; cosids; eurosids I; Malpighiales; Euphorbiaceae; Euphorbioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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Anderson J.V., Horvath D.P.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 480;
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SEQUENCE 480 AA: 54187 WW; 6E3924F21BD9AF45 CRC64;
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                                                                                          01-OCT-2000, integrated into UniProtKB/TrEMBL.
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PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nucleotide-binding;
                                                                                                                                           01-OCT-2000, sequence version 1. 07-PEB-2006, entry version 27.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euphorbieae; Euphorbia.
NCBI_TaxID=3993;
                                                                                                                                                                                                                                                     CDK-activating kinase.
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47 LSDNLIVAL 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] —NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE (MRNA) OF 46-507.

NUCLEOTIDE SEQUENCE (MRNA) OF 46-507.

NUCLEOTIDE SEQUENCE (MRNA) OF 46-507.

NUBLINE-88097370; PubMed=321053;

NEDLINE-88097370; PubMed=321053;

AMULINE J., Bruck C., Ruebsamen-Waigmann H.;

LA CARLACTE C., Mullina J. I., Bruck C., Ruebsamen-Waigmann H.;

T. Additional member of the protein-tyrosine kinase family: the src- and recent protein Course.

I. CARLACTION Tyrosine kinase that plays an essential role for the selection and maturation of developing T-cell in the thymus and in mature T-cell function. Is constitutively associated with the cytoplasmic portions of the CD4 and CD8 surface receptors and plays a key role in T-cell antigen receptor (TCR)-linked signal transduction pathways (By similarity).

C. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.

C. CATALYTIC Binds to the cytoplasmic domain of cell surface receptors, such as CD4, CD8 (By similarity).

C. SUBGELLULAR LOCATION: Bound to the cytoplasmic domain of either receptors.

C. SUBCELLULAR LOCATION: Bound to the cytoplasmic domain of mature in the cytoplasmic domain of mature in the cytoplasmic domain of either receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                        MEDLINE=92186854; PubMed=1545804;
Chow L., Ratcliffe M., Veillette A.;
"tkl is the avian homolog of the mammalian lck tyrosine protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PTM: Phosphorylated on Tyr-503. This phosphorylation downregulates catalytic activity. Phosphorylated on Tyr-392 either by itself or another kinase, leading to increased enzymatic activity.
-!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proto-oncogene tyrosine-protein kinase LCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
SH2 domain; Al3 domain; Transferase; Tyrosine-protein kinase.
INIT_MET 0 Probable.
Gaertner T., Khnel H., Strebhardt K., Ruebsamen-Waigmann H., Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00018; SH3 1; 1.

PRINTS; PR00401; SH3DOMAIN.

PRINTS; PR00402; SH3DOMAIN.

PRINTS; PR004019; TYRKINASE.

ProDom; PD0000039; TYRKINASE.

ProDom; PD0000039; SH2; 1.

PRODOM; PD000056; SH3; 1.

SMART; SM00212; SH3; 1.

SMART; SM00219; TYRKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.
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EMBL, M85043; AAA49003.1; -; mRNA.
EMBL, J03579; AAA49081.1; ALT_INIT; mRNA.
HSSP, P06229; 3LCK.
SMR; P42683; 63-507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMR; P42683; 63-507.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase_AS.
Pfam; PF07714; Pkinase_Tyr; 1.
Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subfamily.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                              Mol. Cell. Biol. 12:1226-1233(1992).
                                                                                                                          NUCLEOTIDE SEQUENCE [MRNA] OF 1-88.
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                        Phosphotyrosine (negative regulation) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P., "Sequencing of the draft genome and assembly of Syntrophobacter
                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Deltaproteobacteria; Syntrophobacterales;
                                                                                            Phosphotyrosine (by autocatalysis) (By similarity).
                                                                                                                                                  N-myristoyl glycine (By similarity).
S-palmitoyl cysteine (By similarity).
S-palmitoyl cysteine (By similarity).
BC83C4FA891B6170 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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0
                                     Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity).
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US DOE Joint Genome Institute (JGI_ORNL);
Larimer F., Land M.;
Annotation of the draft genome assembly of Syntrophobacter fumaroxidans MPOB.";
                                                                                                                                                                                                                      82.9%; Score 34; DB 1; Length 507; 77.8%; Pred. No. 2.7e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.9%; Score 34; DB 2; Length 731; 77.8%; Pred. No. 3.9e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 731 AA; 81207 MW; DCF63286081FAB29 CRC64;
                                                                                 ATP (By similarity).
FTId=PRO_0000088128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AAJF01000065; EA019434.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2005, integrated into UniProtKB/TrEMBL.
25-OCT-2005, sequence version 1.
07-FBB-2006, entry version 3.
Hypothetical protein.
97-FKB-anes=SfumDRAFT 0052,
Syntrophobacter fumaroxidans MPOB.
                                                                                                                                                                                                                                                                                                                                                                               731 AA
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US DOB Joint Genome Institute (JGI-PGF);
                                                                                                                                      similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Syntrophobacteraceae; Syntrophobacter
                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                             507 AA; 58009 MW;
                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                       Query Match 82.9
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.9
Best Local Similarity 77.8
Matches 7; Conservative
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587 LRDNLLIAL 595
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59 LQDKLVVAL 67
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=335543;
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               59
125
243
249
362
271
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Q3MWW8;
                                                     NP BIND
ACT SITE
BINDING
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                                                                                              MOD_RES
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ProDom; PD000001; Prot_kinase; 1.
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                                                                                                                                                                                     HSSP;
SMR; Q
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                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
STRAIN=BisA53;
US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
Sequencing of the draft genome and assembly of Rhodopseudomonas palustris BisA53.";
Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
MEDLINE=21107677; PubMed=11158601; DOI=10.1073/pnas.98.3.1101;
MRDLINE=21107677; PubMed=11158601; Dolman G., Webb G.C., Bottema C.D.,
Gooley A.A., Goodman M., Holland R.A.;
"An orphaned mammalian beta-globin gene of ancient evolutionary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Macropodidae, Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nitted (OCT-2005) to the EMBL/GenBank/DDBJ databases. CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         origin.";
Proc. Natl. Acad. Sci. U.S.A. 98:1101-1106(2001).
-!- FUNCTION: Involved in oxygen transport from the lung to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Larimer F., Land M.; "Annotation of the draft genome of Rhodopseudomonas palustris
                                                                                                                                                                                     OKFNames=RPDRAFT 1953;
Rhodopseudomonas palustris BisA53.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 2; Length 94;
Pred. No. 78;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 94 AA; 10700 MW; 1853E2990023DE2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AALA01000011; EAO89920.1; -; Genomic_DNA.
                                                                                                                06-DEC-2005, integrated into UniProtKB/TrEMBL.
06-DEC-2005, sequence version 1.
07-FBB-2006, entry version 3.
Hypothetical protein.
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                                                                               94 AA
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US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                               PRELIMINARY; PRT;
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07-FEB-2006, entry version 20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BE12_MACEU PRELIMINARY;
Q9BE12;
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary data.
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                                                                             Q371F3 RHOPA
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AC 0371F
AC 0371F
DT 06-DE

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Q9BEIZ MAC
Q9BEIZ MAC
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DT 07-FE
DE OMEGA
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OC MAMMAC
OC MAMMAC
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Bukaryocta; Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzaa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
various peripheral tissues (By similarity).
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GO; GO:0004574; F.protein serine/threonine kinase activity; IEA.
GO; GO:000413; F.protein amino acid phosphorylation; IEA.
InterPro; IPR0000119; Prot kinase.
InterPro; IPR0000119; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR001245; Tyr_pkinase.
PF0055; Pkinase.
PF00714; Pkinase_Tyr; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 2; Length 14.7.
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0814; BETAHAEM.
PROSTITE; PSO1033; GLOBIN; 1.
Heme; Iron; Metal-binding; Oxygen transport; Transport.
SEQUENCE 147 AA; 16109 MW; 54AD783F0B5BF488 CRC64;
                                                                                                                                                                                                                                                isSP; PO2112; IHBR.

30R; Q9BEI2; 2-147.

30; G0:0005833; C:hemcglobin complex; IEA.

30; G0:0005037; F:hemc binding; IEA.

30; G0:0046872; F:metal ion binding; IEA.

30; G0:0019825; F:oxygen binding; IEA.

30; G0:0019825; F:oxygen binding; IEA.

30; G0:0015671; F:oxygen transporter activity; IEA.

30; G0:0015671; P:oxygen transport; IEA.
                                                   (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002, integrated into UniProtKB/TrEMBL.
01-OCT-2002, sequence version 1.
01-FEB-2006, entry version 17.
Serine/threonine protein kinase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 AA.
                                                                                                                                                                                                                         EMBL; AY014769; AAK11484.1; -; Genomic_DNA.HSSP; P02112; 1HBR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002337; Beta haem.
InterPro; IPR000971; Globin.
InterPro; IPR012292; Globin_related.
Pfam; PF00042; Globin; 1.
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Best Local Similarity 77.0.
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RA Carvalho MO. Pinto P.M., Almeida D.F., Almeida LG.F., Almeida R.,

RA Carvalho MO., Pinto P.M., Almeida D.F., Almeida LG.F., Almeida R.,

RA Alves-Junior L., Assuncao B.N., Azevedo V.A.C., Bogo M.R.,

RA Erigido M.M., Brocchi M., Burity H.A., Camargo A.A., Camargo S.S.,

RA Cavalcanti G., Chemale G., Collevatti R.G., Cunha C.W.,

RA Cavalcanti G., Chemale G., Collevatti R.G., Cunha C.W.,

RA Fantinatti-Garboggini F., Felipe M.S.S., Fiorentin L., Franco G.R.,

RA Freitas N.S.A., Frisa D., Garageiro T.B., Garisard E.C.,

RA Maranhao A.G., Martinkovics C.T., Madeira H.M.F., Manfio G.P.,

RA Maranhao A.G., Martinkovics C.T., Madeira M.A.,

RA Pereita Parrait L., Pintolas M.F., Oliveira M.A.M.,

RA Pereita P.R., Schmitt R., Schneider M.P., Pereira M., Schrank B.A., Souza K.E., Schrank A., Souza K.E., Schrank A., Souza K.E., Schrank A., Souza K.E., Schrank A., Souza K.E., Schaeler Perrait C., Steffens M.B.R.,

R. Santos F.R., Schmitt R., Schneider M.P.C., Schrank A., Souza K.E., Schael K.B., Sonza K.C., Steffens M.B.R.,

R. Sontos C.M.A., Souza K.E.L., Souza R.C., Steats C.C., Steffens M.B.R.,

R. Sontos A.J. Schneider M.B., Succheratto L.W.,

R. Simpson A.J.G., Zaha A.,

R. Tswin and poultry pathogens: the complete genome sequences of two preserved and a strain of Moronlasma Proprosumonia proprosumonia proprosumonia proprosumonia proprosumonia proprosumonia proprosumonia proprosumon
                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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Distributed under the Creative Commons Attribution-NoDerivs License
                           Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                  evolution in Rickettsia conorii and R. prowazekii.";
MEDLINE=21442074; PubMed=11557893; DOI=10.1126/science.1061471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma synoviae (strain 53). ¯
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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                                                                                                                                                                                                                                                                                     EMBL; AE008629; AAL03254.1; -; Genomic_DNA.
PIR; D97789; D97789.
BioCyc, RCON781:RC0716-MONOMER; -.
GO; GO:0004852; F:urcporphyrinogen-III synthase activity; IEA.
GO; GO:0006783; P:heme biosynthesis; IEA.
InterPro; IRR003784; HEMA_synth.
COMDIète protecome; Hypotherical protein.
SEQUENCE 234 AA; 27272 MW; 59822E33674E014F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.5%; Score 33; DB 2; 66.7%; Pred. Nc. 2e+02;
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GO; GO:0050897; F:cobalt ion binding; IEA.
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Name=map, OrderedLocusNames=MS53_0579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Bacteriol. 187:5568-5577(2005).
                                                                                                                                             Science 293:2093-2098(2001).
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189 LODSLVVAI 197
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Best Local Similarity
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Malek J.A., Eremeeva M.E., Dasch G.A.;
Submitted (FEBL-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AABW01000001; EAA26484.1; -; Genomic_DNA.
GO; GO:0004852; F:uroporphyrinogen-III synthase activity; IEA.
GO; GO:0006783; P:heme biosynthesis; IEA.
InterPro; IPR003764; HEM4_synth.
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                                                                                                                                                                                                    Score 33; DB 2; Length 172;
Pred. No. 1.5e+02;
4; Mismatches 0; Indels
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                                                                                                                                                    D51E19848444428A CRC64;
   ; PS50011; PROTEIN KINASE DOM; 1.
; PS00108; PROTEIN KINASE ST; UNKNOWN 1.
Serine/threonine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-2003, integrated into UniProtKB/TrEMBL. 15-DEC-2003, sequence version 1.
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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Q92HQ5;
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55.6%;
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9 LEDNMVVAI 17
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Rickettsia_sibirica.
                                                                                                                                                172 AA;
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Q7P8Q9;
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092405 RIC
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GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0004239; F:methionyl aminopeptidase activity; IEA.
GO; GO:000523; F:methionyl aminopeptidase activity; IEA.
GO; GO:0005508; P:proteolysis; IEA.
InterPro; IPR001714; Pept M24 MAP.
InterPro; IPR002467; Pept M24 MAP.
InterPro; IPR002467; Pept M24 MAP.
FFAM: PF00557; Peptidase M24; I.
FRINTS; PR00599; MAPEPTIDASE.
TIGRRAMS; TIGR00500; met pdase I; 1.
Aminopeptidase; Cobalt; Complete proteome; Hydrolase; Metal-binding;
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DNA Res. 9:189-197 (2002).
-!- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22484998; PubMed=12597275; DOI=10.1093/dnares/9.6.189; Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K., Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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Q89UG67

Q1-3UN-2003, integrated into UniProtKB/TrEMBL.

Q1-JUN-2003, sequence version 1.

Q7-FEB-2006, entry version 22.

ABC transporter ATP-binding protein.

OrderedLocusNames=bli1451,

Bacteria, proteobacteria; Alphaproteobacteria; Rhizobiales;

Bradyzhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                              80.5%; Score 33; DB 2; Length 248; 66.7%; Pred. No. 2.1e+02; ive 2; Mismatches 1; Indels
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ATP-binding; Complete proteome; Inner membrane; Membrane; Nucleotide-binding; Transport.
SEQUENCE 253 AA; 27939 MW; 5C953BC4B0E8CDE8 CRC64;
                                                                                                                                                                                                                                                                                                                                         248 AA; 27397 MW; 189E63EF9DE86F5B CRC64;
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HSSP, Q5863; 169X.
BioCyc; BJAP224911.BLR1451-MONOMER; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0015866; C:organelle inner membrane; IEA.
GO; GO:0015824; F:ATP binding; IEA.
GO; GO:0016887; F:ATP binding; IEA.
GO; GO:0001666; F:nucleotide binding; IEA.
GO; GO:000166; F:ransport; IEA.
InterPro; IPR003439; AAA_ATPase.
InterPro; IPR003439; ABC_transport
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Prop. PR00005; ABC_transport
PR00005; ABC_transport
PR0005; ABC_Transport
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Best Local Similarity 66.70,
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80.5%; Score 33; DB 2; Length 253; 66.7%; Pred. No. 2.2e+02;

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ADY552574
AEA35920
 \begin{array}{c} 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\ 0.00\\
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Abr84354 Human lck
Ads87126 Human gen
                                                                                      June 29, 2006, 08:59:14; Search time 87.8313 Seconds (without alignments) 46.851 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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The invention relates to a method for the detection of antigen specific recells in a blood sample involving the use of a plurality of antigenic peptides. The method comprises sampling of peripheral blood monocytes; stimulation of the collected peripheral blood monocytes with antigens without direct use of antigen presenting cells; and detection of T-cells specific to the antigen in the stimulated monocytes. The method is particularly used for the detection of cancer specific tan be used in semi-quantitative determination of cancer specific T-cells. It can also be used for cancer vaccine therapy for patients with cervical or prostate cancer. The method can additionally be used to monitor of cellular immunity and cancer immune therapy by detection of specific T-cell frequencies. Sequences ABR84165 represent HLA-A2 (human leukocyte antigen) peptides of human origin used in an example from the
                                                                                                                                                                                                                     A detection method of antigen specific T-cells, comprises the use of plural antigenic peptides, useful in semi-quantitative determination of cancer specific T-cell frequencies and for monitoring cellular immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; ubiquitin; Ub; T-cell target; melanoma; sarcoma; Hodgkins lymphoma; non-Hodgkins; leukaemia; neuroblastcoma; myeloma; lung cancer; stomach; skin; thyroid; ovary; prostate; womb; pancreas; colon; bladder; breast; oesophagus; kidney; brain; human; epitope; Lck.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genetic vaccine/ubiquitin (Ub)/Lck-related epitope peptide 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 41; DB 6; Length 9; 100.0%; Pred. No. 2.1e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                     Example 7; Page 8; 18pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADS87126 standard; peptide; 9 AA.
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                                                                                            18-SEP-2001; 2001JP-00283413
                                                                                                                           13-NOV-2000; 2000JP-00345094
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Matches 9; Conserv
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                                JP2002365286-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9 AA;
                                                                                                                                                          (ITOY/) ITO Y.
    Homo sapiens.
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 Ady14846 PRO polyp
Abm92571 M. xanthu
Ady10869 Plant ful
Abu20456 Protein e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and polynucleotides encoding them for treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to peptides which are partial sequences of stor/lok family proteins. The present sequence is one such peptide. The peptides are useful for producing vaccines for the treatment of cancer, including colon cancer and small-cell lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen specific T-cell; detection; diagnosis; cancer specific T-cell; cancer; tumour; cervical cancer; prostate cancer; cellular immunity; immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide; human; human leukcyte antigen; HLA-A2 epitope.
                                                                                                                                                                                                                                                                                                   Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
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                                                                                              ALIGNMENTS
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ADY14846
ABM92571
ADY10869
ABU20456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 69; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABR84354 standard; peptide; 9 AA.
                                                                                                                                                                         AAB73128 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000; 2000WO-JP005220
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-00222101
                                                                                                                                                                                                                                                                      Tumour antigen peptide #12
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                                                                                                                                                                                                                                                                                                                                                                WO200111044-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9 AA;
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represents the amino acid sequence of a lck peptide cancer antigen.
                                        Sequence 9 AA;
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                                                                                                                                                                    The invention relates to a novel genetic vaccine containing the ubiquitin gene together with a gene encoding an antigenic protein containing a T-cell target sequence. The vaccine of the invention may be useful for prevention and treatment cencers including melanoma, sarcoma, lymphoma (Hodgkins or non-Hodgkins), leukaemia, neuroblastoma, myeloma and cancer of the lung, stomach, skin, thyroid, ovary, prostate, womb, pancreas, colon, bladder, breast, oesophagus, kidney or brain. The current sequence is that of a human genetic vaccine/ubiquitin (Ub)-related epitope peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of treating a cancer patient by administering cancer antigens to patient, involves evaluating presence or absence of specific cytotoxic T-lymphocyte precursors for individual peptides contained in set of cancer antigen peptides, in patient, removing peptide being non-specific to precursors, from cancer antigen peptide set to prepare set for administration, and administering cancer antigen peptide set to patient. The method is useful for treating cancer patient by administering cancer natigens to patient. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating cancer by evaluating specific cytotoxic T-lymphocyte precursors for each peptide of cancer antigen peptide set, in patient, administering peptide set obtained after removing peptide being non-specific to
                                                                             Gene vaccine containing cancer antigen genes ligated to ubiquitin genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                               or cytokine genes for prevention and treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 8; I
Pred. No. 2.1e+06;
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                                                                                                                                   Disclosure; SEQ ID NO 142; 266pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer antigen 1ck peptide SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 7; 36pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEE99217 standard; peptide; 9 AA.
Maehara Y;
                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
100.0%;
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KLVERLGAA 9
Furue M,
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                                    WPI; 2004-357144/33
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Himeno K,
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The invention provides a novel method of altering the activity of the protein kinase A (PKA) signaling pathway in a cell that comprises altering the extent of phosphorylation of one or more PKA aubstrates, or kinase substrates downstream in the PKA signaling pathway. Pharmaceutical compositions containing a nucleic acid molecule that encodes a PKA substrate, or fragment, precurers or functionally equivalent variant, where the sequence is modified to alter its susceptibility to phosphorylation by PKA can be used for treating a disorder exhibiting abnormal PKA signaling activity, immunosuppressive disorders or proliferative diseases. They can be used for treating e.g. HIV infection, ALDS, common variable immunodeficiency or cancers. Conditions in which upregulation of the PKA pathway is required, such as autoimmune disease, e.g. systemic lupus erythematosus, may also be treated. The present sequence represents a PKA substrate, wherein the substrate is in the Srcfamily, preferrably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk, c-tkl,
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Altering the activity of protein kinase signaling pathways, used for treating immunosuppressive disorders, e.g. AIDS, proliferative disorders, e.g. cancers or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                         Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer; kinase substrate; immunosuppressive disorder; proliferative disease; HIV infection; AIDS; immunodeficiency; autoimmune disease; systemic lupus erythematosus; Src-family.
                                   Gaps
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100.0%; Score 41; DB 10; 100.0%; Pred. No. 2.1e+06;
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Altman A, Munshi A;
                                 0; Mismatches
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                                                                                                                                                                                        AAY49420 standard; protein; 509 AA
                                                                                                                                                                                                                                                                                             PKA substrate, Src-family protein.
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                                                                   1 KLVERLGAA 9
                                                                                                   KLVERLGAA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hansson V, Levy FO,
Tasken K, Vang T, 1
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                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JONE/) JONES E L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AS.
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                                                                                                                                                                                                                                                           13-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAY-1999;
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30-DEC-1998;
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 Query Match
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disorders.
                                                                                                    ADP48374;
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                           ADP48374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method of identifying a candidate p21 or p53 pathway modulating agent. This comprises providing an assay system comprising a modulator of p21 or p53 (MP2153) polypeptide or nucleic acid, contacting the assay system with a test agent, where in its presence the system provides a reference activity, and detecting a test agent-biased activity of the assay system, wherein a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p21 or p53 pathway modulating agent. The methods and compositions of the present invention are useful for the dispansis and/or treatment of diseases or conditions associated with aberrant expression or activity of the p21 or p53 pathway, such as cancer, preferably colon or head and neck cancer. The present sequence is a human MP2153 protein sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a candidate p21 or p53 pathway modulating agent using an assay system having a modulator of p21 or p53 (MP2153) polypeptide or nucleic acid, useful for diagnosing or treating cancer, such as colon or
                                                    Gaps
                                                    ó;
Query Match 100.0%; Score 41; DB 3; Length 509; Best Local Similarity 100.0%; Pred. No. 18; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Friedman L, Kidd T, Roche S,
kteig K, Zhang H, Amundsen CD;
                                                                                                                                                                                                                                                                                                                                                                                                                     Human MP2153 polypeptide sequence SEQ ID NO: 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 94-96; 110pp; English.
                                                                                                                                                                                                                                                                     ADL22907 standard; protein; 509 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; MP2153; p21; p53; cancer.
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16-SEP-2002; 2002US-0411017P.
30-DEC-2002; 2002US-0437107P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-2003; 2003WO-US024505
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Plowman GD, Lickteig K,
                                                                                                                                  KLVERLGAA 254
                                                                                                    1 KLVERLGAA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-180653/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      breast cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense oligonucleotide compounds, useful for diagnosing, preventing and/or treating diseases or conditions associated with aberrant expression or activity of Lck, such as hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                 Human lymphocyte specific tyrosine kinase (Lck) polypeptide #1
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                                                                                                                                                                                                                   Human; lymphocyte specific tyrosine kinase; Lck;
antisense oligonucleotide; phosphorothioate linkage;
2'-0-methoxyethyl augar moiety; 5-methylcytosine;
hyperproliferative disorder; cancer; cytostatic; enzyme.
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100.0%; Pred. No. 18;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 4; 40pp; English.
ADP48374 standard; protein; 509 AA.
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                                                                                                            (first entry)
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N-PSDB; ADP48301.
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nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                         09-SEP-2004
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Local Similarity

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Sequences AAY43902-Y44015 represent proteins used in a novel method of predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure, active sites, and parsing segments. Secondary structural units are assigned by identifying periodicity in the assignments, and assembled into globular form using distance constraints imposed by disulfide bridges, active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein molecule, as interaction of a protein with other molecules
                                                                                   Predicting the folded structure of proteins.
                                                                                                                 Disclosure; Col 253-256; 113pp; English
                                                   WPI; 1999-570766/48
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                     Benner SA;
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Prediction; secondary structure, alignment; evolutionary conservation; homology; periodicity; co-variation analysis; antigenic site; site directed mutagenesis; interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prediction; secondary structure; alignment; evolutionary conservation; homology; periodicity; co-variation analysis; antigenic site; site directed mutagenesis; interaction.
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                                                                                                                                                                                                                                                                                                                           Predicting the folded structure of proteins.
                                                                                                                                                                                                                                                                                                                                                           Disclosure, Col 255-258; 113pp; English.
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100.0%; Pic
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                                                                                                                                                                                                                           (BENN/) BENNER S A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 259 AA;
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                                                                                                                                                                                               25-MAR-1992;
                                                                                                                                                               25-MAR-1992;
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                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular scaffold; nuclear hormone receptor; TNF receptor; G-protein coupled receptor; methyl transferase; ligase; LCK tyrosine kinase; enzyme.
                                                                        Score 37; DB 2; Length 259;
Pred. No. 59;
0; Mismatches 0; Indels
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                                                                        % Match 90.2%; Sci
Local Similarity 100.0%; P. P. 165 8; Conservative 0;
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16-SEP-2002; 2002US-0411398P.
20-SEP-2002; 2002US-0412341P.
02-JAN-2003; 2003US-0437929P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCK tyrosine kinase protein.
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                                                                                                                                                                                                                                                   KLVERLGA
Sequence 259 AA;
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The present sequence is a mutated fragment of the human Lck sequence, which approximately comprises the catalytic domain

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The present invention relates to a method of designing a ligand binding scaffolds compounds binding to members of a molecular family, detecting or instance compounds binding to members of a molecular family, detecting orientation of scaffolds at binding site of target, and synthesising ligand. The invention is useful for designing drug products and for designing ligand binding to target molecules such as nuclear hormone receptors, TNF receptors, G-protein coupled receptors, methyl transferases, ligases, etc. The present sequence is the LCK tyrosine kinase protein. This sequence is used to illustrate the method of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Src-family protein tyrosine kinase; T-cell; immune response; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New crystalline polypeptide comprising ligand binding domain or cat domain of Lck protein, for determining three-dimensional structure catalytic domain of Lck, has predetermined unit cell parameters.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant Lymphocyte Cell Kinase, Lck, fragment (237-501, D364N).
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
59;
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                                                                                                                                                                                                                                                                                                                                                                                                       90.2%; Score 37; DB 100.0%; Pred. No. 59; ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR56203 standard; protein; 265 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-AUG-2002; 2002WO-US024546.
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Best Local Similarity 100
Matches 8; Conservative
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KLVERLGA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-300872/29
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                                                                                                                                                                                                                                                                                                                                        Sequence 263 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                   invention.
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The present invention relates to a crystalline polypeptide (I), comprising the catalytic domain of human Lymphocyte Cell Kinsse (Lck) protein. Lck is a Src-family protein tyrosine kinsse expressed primarily in T-cells and plays an essential roll in immune response. (I) is useful for identifying a compound which is an inhibitor of human Lck protein.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New crystalline polypeptide comprising ligand binding domain or catalytic domain of Lck protein, for determining three-dimensional structure of catalytic domain of Lck, has predetermined unit cell parameters.
                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Wild-type D substituted with N. This position is 364 in the full-length sequence (see ABR56202 for the wild-type full length sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a crystalline polypeptide (I), comprising the caralytic domain of human Lymphocyte Cell Kinase (Lck) procein. Lck is a Sro-family protein tyrosine kinase expressed primarily in T-cells and plays an essential role in immune response. (I) is useful for identifying a compound which is an inhibitor of human Lck protein. The present sequence is a mutated fragment of the human Lck sequence, which approximately comprises the catalytic domain
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                                                                                        Gaps
                                                                                                                                                                                                                                                                                                           Human, protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme
Src-family protein tyrosine kinase; T-cell; immune response; mutein;
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                                                                                                                                                                                                                                                                                   Lck, fragment (231-501, D364N)
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                                                             Length 265
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                                                     90.2%; Sco...
100.0%; Pred. No. co...
... 0; Mismatches
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100.0%; Pred. No. er,
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                          ABR56204 standard; protein; 271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 3; 994pp; English
                                                                                                                                                                                                                                                                                    Mutant Lymphocyte Cell Kinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-2002; 2002WO-US024546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2001; 2001US-0310051P.
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                                                                                       8; Conservative
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                                                                                                               1 KLVERLGA 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                            Sest Local Similarity
                                                                                                                                      KLVERLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 271 AA;
                                      Sequence 265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003020880-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
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Synthetic.
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                                                                Query Match
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a kinase binding site), attaching a kinase binding

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Kinase; protein co-ordinate data; protein structure; cancer; cytostatic; neoplasm; inflammation; antiinflammatory.
                                                                                                                                                                                                                                                                       New scaffold library used for identifying and developing ligands for protein kinases and treating kinase associated disorders e.g. cancer, comprises set of compounds comprising N-heterocyclic compounds.
                                                                                                                                                                                                                                   Gillette SJ, Hurt CR, Ibrahim PL;
                                                                                                 Catalytic domain of PIM kinase-like protein LCK
                                                                                                                                                                                                                                                                                                       Disclosure; Page 170-174; 236pp; English.
                                                     ADY85449 standard; protein; 279 AA.
                                                                                                                                                                                     15-SEP-2004; 2004WO-US030360.
                                                                                                                                                                                                    15-SEP-2003; 2003US-0503277P.
                                                                                  (first entry)
                                                                                                                                                                                                                                   Artis DR, Bremer RE,
Zuckerman RL;
                                                                                                                                                                                                                   (PLEX-) PLEXXIKON INC
            KLVERLGA 23
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                                                                                                                                                       WO2005028624-A2
                                                                                                                                       Unidentified.
                                                                                  16-JUN-2005
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                                                                    ADY85449;
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               16
                                     RESULT 13
                                             ADY85449
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cattachment component (which comprises identifying energetically allowed stress for attachment of the component on a kinase binding compound (I)—

(VII) and attachment of the component on a kinase binding compound (I)—

(VII) and attachment of the component on a kinase binding compound (I)—

(VII) and attachment of the allowed site), modified compounds (Comprising (I)—(VIII)

with an attached linker grup, and developing a ligand for a kinase

CC comprising conserved residues matching at least on of Pim-1 residues 49,

CC comprising conserved residues matching at least on of Pim-1 residues 49,

CC comprising conserved residues matching at least on of Pim-1 residues 49,

CC to the kinase. The kinases comprise Pim-1, Pyk2, c.Abi, Her2, cMet,

Vascular endothelial growth factor receptor, endothelial growth factor

CC vascular endothelial growth factor receptor, endothelial growth factor

CC receptor, cKit. Rkbeter, p88, Cdk2, Akt or Gskbeta. The kinase scaffold

CIIDTATY is used for identifying and developing ligands binding to

CIIDTATY is used for identifying and developing ligands binding to

CIIDTATY is used for identifying and for treating disease

CC condition associated with abnormal kinase activity e.g. cancer,

Inflammatory disease. The method identifies improved ligands binding to a

CK kinase resulting in ligands having high affinity and specificity towards

CC sufficient size and quality to allow structural determination of at least

CC Angstroms. The present sequence is a catalytic domain from a PIM-like

CK kinase. NOTE: It is not clear whether the sequence as presented

CC represents a continuous amino acid sequence. Identifying a compound that modulates T lymphocyte activation, useful for monitoring changes in cell surface marker expression, comprises contacting a T cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with Human; T lymphocyte activation; T-cell; A-raf-1; TCPTP/PTPN2; asthma; immunosuppressive; antiasthmatic; antiallergic; antiniflammatory; hymphocyte activation; lymphocyte migration; cytokine production; cell surface markation; antibody production; apoptosis; allergy; antibody proliferation; antibody differentiation; hypersensitivity; graft versus host disease; inflammation; p561ck. DB 9; Length 279; 63; 0; Indels Zhao Pardo J, Score 37; DB 9; Pred. No. 63; 0; Mismatches Disclosure; Page 64; 126pp; English ABR59690 standard; protein; 363 AA. Masuda E, 90.2%; bcc 100.0%; Pre 02-OCT-2002; 2002WO-US031618. 03-OCT-2001; 2001US-0327212P (first entry) 8; Conservative (RIGE-) RIGEL PHARM INC. Liao XC, 16 KLVERLGA 23 œ WPI; 2003-363276/34. Local Similarity 1 KLVERLGA N-PSDB; ACC81082 Sequence 279 AA; WO2003029277-A2. Li C, Human p561ck. Homo sapiens. 25-JUL-2003 10-APR-2003. ABR59690; Query Match Chu P, Matches RESULT 14 ABR59690 ò 원 SX THE STATE OF STATE The invention relates to a new kinase scaffold library comprises at least 1 set of compounds, each set comprising at least 1 N-heterocyclic compound of formulae (1)-(VII) given in the specification. Also included are a system for fitting compounds in binding sites of protein kinases (comprising an electronic kinase scaffold, and a scaffold library computer is computer device and (VII), where the scaffold library is embedded in a computer device and the electronic representations of the compounds can be selectively controlly connected with computer software adapted to fit electronic representations of two mounts in an electronic adopted to fit electronic representations of a kinase, obtaining improved ligands binding to a protein kinase (which comprises determining if a derivative of (1)-(VII) binds to the kinase with greater affinity and/or specificity than (1)-(VII)), developing ligands specific for a particular kinase than (1)-(VII), developing ligands specific for a particular kinase (which comprises has greater for specificity for the particular kinase than (1)-(VII), developing ligands binding to a kinase (which comprises of the kinase, identifying chemical structures of the capticular kinase (which at least 1 chemical structures of the scaffold change the binding affinity and/or specificity between the scaffold change the binding affinity and ligand in an least 1 chemical structure of the scaffold change the binding a position of the scaffold change the binding a position of the scaffold change the binding a binding a ligand in all least 1 chemical structures of the scaffold change the binding a position of the scaffold change the binding a ligand in all least 1 chemical structure of the scaffold change the binding a ligand in all least 1 change the binding a ligand in all least 1 change the binding a ligand in all least 1 change the binding a ligand in all least 1 change the scaffold change and synthesizing a ligand in all least 1 change the light of the scaffold change and synthesizing a ligand in all c developing ligands with increased specificity on a kinase (which comprises testing a derivative of a kinase binding compound (I)-(VII) for increased specificity on the kinase), identifying a ligand binding to a kinase (which comprises determining if a derivative compound including a core structure (I)-(VII) binds to the kinase with changed binding a fifthity and/or specificity), a co-crystals of a kinase and a binding a compound (I)-(VII), preparation of co-crystals of pim-1 with (I)-(VII), identifying potential kinase binding compounds (which comprises fitting electronic representations of (I)-(VII) in an electronic representation

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Gaps

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modulates T lymphocyte activation. The method comprises contacting a T cell comprising an A-raf-1 or TCPPP/PTPNZ polypeptide with a compound, where the A-raf-1 or TCPPP/PTPNZ polypeptide with a compound, the A-raf-1 or TCPPP/PTPNZ polypeptide is encoded by a nucleic acid that hybridises to a nucleic acid encoding a polypeptide having a sequence selected from two 606-amino acid sequence and a 415-amino acid sequence given in the specification. The method of the invention has immunosuppressive, antiasthmatic, antiallargic, and antiinflammatory activity. The method is useful for identifying compounds that modulate lymphocyte activation and migration, and for monitoring changes in cell surface marker expression, cytckine production, antibody production, proliferation and differentiation, and apoptosis, using either cell lines or primary cells. The A-raf-1 or TCPTP/PTPNZ proteins may be used as drug tragets for compounds that suppress or activate lymphocyte activation and migration, e.g. for the treatment of diseases in which modulation of the immune response is desired such as delayed type activation and acute and chronic inflammation. Modulators of lymphocyte activation and migration are useful for treating disorders related T and B cell activation and inspration and migration in the exemplification of the immune is used in the exemplification of the immune immune is used in the exemplication of the immune im
                           invention relates to a novel method for identifying a compound that
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antisense oligonucleotide; phosphorothicate linkage;
2'-0-methoxyethyl augar moiety; 5-methylcytosine;
hyperproliferative disorder; cancer; cyrostatic; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 363 AA;
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New antisense oligonucleotide compounds, useful for diagnosing, preventing and/or treating diseases or conditions associated with aberrant expression or activity of Lck, such as hyperproliferative
Human lymphocyte specific tyrosine kinase (Lck) polypeptide #2
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Example 17; SEQ ID NO 75; 40pp; English.

disorders

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The invention relates to a compound targeted to a nucleic acid molecule encoding the human lymphocyte specific tyrosine kinase (Lck) polypeptide. The compound is an antisense oligomucleotide that specifically hybridises with the nucleic acid and inhibits expression of the polypeptide. The antisense oligomucleotide comprises at least one modified internucleoside linkage i.e. a phosphorothioate linkage, at least one modified sugar moiety, preferably a 2'-0-methoxyethyl sugar moiety, or at least one modified nucleobase comprising a 5-methyloyrosine. The antisense compounds are useful for modulating the expression of the human Lck polypeptide and in preparation of a composition for treating hyperproliferative disorders, e.g. cancer. This sequence represents a human Lck polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fused polypeptide - has amino acid sequence of beta-galactosidase with a LCK gene conjugated to the N-terminal via DNA having multi-cloning site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         galactosidase gene fused with the ick gene. It is produced by B.coli transformed with a recombinant vector (see AAQ13983). It is useful for producing an antibody specifically immunoreactive with only a lck genederived polypeptide in T cells. The antibody may recognise lck genederived polypeptides in human cells
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence consists of the N-terminal amino acids of the beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Beta-galactosidase N-terminal)-(lck gene prod.) fusion protein.
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0
                                                                                                                                                                                                                                                          8; Length 363;
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                                                                                                                                                                                                                                                                                           0; Indels

    .26
    /note= "beta-galactosidase fragment"

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                                                                                                                                                                                                                                                        90.2%; Score 37; DB E 100.0%; Pred. No. 80; ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89JP-00338268
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nes 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                          246 KLVERLGA 253
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                            1 KLVERLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ14201.
                                                                                                                                                                                                                         Sequence 363 AA;
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The invention discloses isolated human nucleic acid alternative splicing variants that are all tumour-involved genes (TIGS). The nucleic acids and polypeptides are useful for determining the level of a nucleic acid or polypeptide in a biological sample, for determining the level of polypeptide sequence in a biological sample, for determining the level of variant sequence in a biological sample and for polypeptide sequences in a biological sample and for polypeptide sequence in a biological sample and for polypeptide sequence in a biological sample and for polypeptide sequence from which the variant has been varied by alternative splicing in a second the variant ample and for raising antibodies. A pharmaceutical composition comprising a carrier and the nucleic acid, is useful for treating diseases (e.g. cancer) that can be ameliorated or cured by increasing or decreasing the level of the encoded protein. The nucleic cacids are also useful for diagnostic purposes, especially for detecting cancer or a predisposition to cancer, for evaluating the state or aggressiveness of cancer disease, in basic research, for understanding the print of the priginal Tide (in targeting or health).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   developing pharmaceuticals, for distinguishing various stages in the life cycle of the same type of cells which may be helpful for the development of pharmaceuticals for various cancer stages in which cell cycle is nonnormal, for determining mutations in tumour-involved genes and in gene therapy. The polypeptides are useful for identifying compounds capable of binding to the variant product and modulating its activity and for
                                                                                                                                                                                                                                                                                                                            Human; splice variant; tumour-involved gene; TIG;
pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
endothelial cell; cell differentiation; cell proliferation; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid sequence, which is an alternative splicing variant tumor involved genes, useful for detecting cancer, predisposition to cancer, for evaluating cancer state and in gene therapy for treating
 Gaps
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 Indels
                                                                                                                                                                                                                                                                                         Tumour involved gene (TIG) splice variant protein, NV-3.
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Mismatches
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                                                                                                                                                                       ABG79672 standard; protein; 437 AA.
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16-MAY-2000; 2000IL-00136154.
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                                                                                                                                                                                                                                                   (first entry)
8; Conservative
                                                           ||||||||
154 KLVERLGA 161
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ROMANO C.
BERNSTEIN J.
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                                     KLVERLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEVINE Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABS65202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002086384-A1
                                                                                                                                                                                                                                                                                                                                                                                            gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                   15-NOV-2002
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                                                                                                                                                                                                             ABG79672;
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(BERN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Levine
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Matches
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              modulate apoptosis either ex vivo or in vivo. The sequences presented in ABG796700-ABG79705 are the new variants (NV) 1-36 proteins of the TIGs
modulating endothelial differentiation and proliferation, as well as to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crystal of a protein-ligand complex for identifying kinase inhibitors, comprises a truncated lymphocyte kinase and a ligand, and diffracts X-rays to determine atomic coordinates at a resolution greater than 5
                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     Human; lymphocyte kinase; protein co-ordinate data; lck; crystal.
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                                                                                                             Length 437;
                                                                                                                                            Indels
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                                                                                                           DB 5;
95;
                                                                                                                            100.0%; Pred. No. 95; ive 0; Mismatches
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                                                                                                             Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 434-5; 438pp; English.
                                                                                                                                                                                                                                                                                        AAB37700 standard; protein; 508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enzymes involved in their pathology
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100.0%; Pr.
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                                                                                                             . 90.2%;
                                                                                                                                                                                                                                                                                                                                                        02-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KINE-) KINETIX PHARM INC
                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        Human lymphocyte kinase.
                                                                                                                                                                                                        KLVERLGA 253
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                                                                                                                          Local Similarity
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                                                                                                                                                                          1 KLVERLGA
                                                                             Sequence 437 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200070030-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-NOV-2000.
                                                 disclosed
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Matches
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                                                                                                                                                                                                                                                          RESULT 18
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KLVERLGA

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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                              Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                           Costigan M;
                                                                                Human Protein P06239, SEQ ID NO 4689.
                                    ADE58802 standard; protein; 508 AA.
                                                                                                                                                                                                                                           Befort K,
                                                                                                                                                                                                                                                                                                     Claim 1; Page; 1017pp; English.
                                                                                                                                                                                      14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                       14-AUG-2002; 2002WO-US025765.
                                                                 (first entry)
                                                                                                                                                                                                                    (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
245 KLVERLGA 252
                                                                                                                                                                                                                                          Woolf C, D'urso D,
                                                                                                                                                                                                                                                         WPI; 2003-268312/26.
                                                                                                                                                                                                                                                                  GENBANK; P06239.
                                                                                                                                          WO2003016475-A2.
                                                                                                                              Homo sapiens
                                                                 29-JAN-2004
                                                                                                                                                         27-FEB-2003.
                                                   ADE58802;
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a method for producing a pharmaceutical composition, a conjucty in an animal of one or more of the polypeptides or their antibodies. The polynucleotide or the compound that sequence presented for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polymetises its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene compound the specification) which is differentially expressed during pain. Note: The specification) but was obtained in electronic form directly from WIPO at the printed the contract of the con frp.wipo.int/pub/published_pct_sequences.

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Sequence 508 AA;
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Query Match

90.2%; Score 37; DB 7; Length 508;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymicleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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                    Indels
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 8; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Befort K, Costigan M;
                                                                                                                                                                                                                                                                                                                                            Human Protein P06239, SEQ ID NO 4686.
                                                                                                                                                                                                               ADE58799 standard; protein; 508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-2001; 2001US-0312147P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-2002; 2002WO-US025765.
                                                                                                                                                                                                                                                                                                    29-JAN-2004 (first entry)
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245 KLVERLGA 252
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                                                              1 KLVERLGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENBANK; P06239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-FEB-2003.
                                                                                                                                                                                                                                                          ADE58799;
                                                                                                                                                                     RESULT 20
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antiinflammatory; antibacterial; virucide;

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fungicide; nootropic; neuroprotective; kinase inhibitor; crystal; protein-ligand complex; lymphocyte kinase; Lck; Lck ligand; kinase inhibitor; therapeutic; kinase-mediated physiological event; cancer; autoimmunological; metabolic; inflammatory; infection; central nervous system degenerative disease; transplant rejection; human; globular core; protein co-ordinate data.
                                                                                                                                                                                                                                                                                                                                                                                                       protein-ligand complex useful for identifying an inhibitor of kinase (Lck), comprises truncated Lck and a ligand.
                                                                Human lymphocyte kinase (Lck) globular core.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1; 295pp; English.
                                                                                                                                                                                                                                                                         21-MAY-2001; 2001US-00862154.
                                                                                                                                                                                                                                                                                                  19-MAY-2000; 2000US-0205510P.
                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-810380/76
                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC
                                       20-MAY-2004
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                       US6589758-B1
                                                                                                                                                                                                                                                08-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                      lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                        Crystal of
              ADL34479;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method for identifying a ligand (L), which binds to an inactive conformation of target protein kinase (T). The method involves contacting inactive conformation of (T), which contains or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bonding to the reactive group thus forming a kinase-(L) conjugate (C). The method is useful for identifying protein kinase inhibitors that preferentially bind to inactive conformation of a target protein kinase. The present sequence is a protein kinase which may be modified via an amino acid substitution, for use in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying ligand binding to inactive conformation of target protein Kinase (T) comprises contacting the conformation modified (T) which contains reactive group at binding site, with ligands and detecting kinase-ligand conjugate formation.
                                                                            Gaps
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                                                   Length 508;
                                                                           0; Indels
                                                                1.1e+02;
                                                 90.2%; Score 37; DB 7;
100.0%; Pred. No. 1.1e+0:
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                  Human; protein kinase; enzyme; inhibitor; LCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 41; 260pp; English.
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                            ADF45072 standard; protein; 508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                       20-MAR-2003; 2003WO-US008725.
                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2002; 2002US-0366892P.
                                                                                                                                                                                                                                              (first entry)
                                     Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SUNE-) SUNESIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prescott JC, Braisted A;
                                                                                                                           KLVERLGA 252
                                                                                                   1 KLVERLGA 8
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                                                                                                                                                                                                                                                                         Human kinase LCK
                         Sequence 508 AA;
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                                                                                                                                                                                                                                                                                                                                                     WO2003081210-A2
                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                               12-FEB-2004
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                                                                                                                                                                                                                     ADF45072;
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                                                                                                                                                                 RESULT 21
ADF45072
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The invention describes a crystal (I) of a protein-ligand complex (C) comprising a truncated lymphocyte kinase (Lck) and a ligand, where (I) effectively diffracts X-rays for determination of atomic coordinates of (C) to a resolution of greater than 5.0 angstroms, and truncated Lck (C) to a resolution of greater than 5.0 angstroms, and truncated Lck (C) to a resolution of greater than 5.0 angstroms, and truncated Lck (C) to a resolution of greater than 5.0 angstroms, and truncated Lck (C) is useful in an inhibitor screening assay and to length Lck. (I) is useful in an inhibitor screening assay and to identify, design, select, and evaluate potential inhibitors of kinases (C) that are associated with kinase-mediated physiological events. The inhibitors identified by the methods may also be useful for inhibition of kinase activity of one or more enzymes. The inhibitors are also useful for inhibiting the biological activity of any enzyme comprising greater than 90%, alternatively greater than 85%, or alternatively greater than 50% alternatively greater than 85% or alternatively greater than 50% sequence homology with a kinase sequence. The inhibitors are useful for treating disease or disease symptoms mediated by any enzyme that binds ATP. The inhibitors are useful in inhibiting kinase activity and communal, particularly a human e.g., cancer, autoimmunological, metabolic, inflammatory, infection, (bacterial, viral, yeast, fungal, etc.), central nervous system degenerative disease etc. The inhibitors are useful in traating or preventing disease including, transplant rejection etc. This is the amino acid sequence of a human lymphocyte kinase (Lck) comprising the Lck globular core.
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Matches

Best Local Similarity

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ADL34479 standard; peptide; 508 AA.

RESULT 22 ADL34479 ID ADL3 RESULT 24

ABR58699

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This invention relates to novel protein complexes of the tumour necrosis factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to methods for preparing these complexes comprising at least two component proteins, as well as screening methods to identify modulators of the pathway, which include antibodies, agonists and antagonists thereof. The present invention describes a protein complex and kit that are useful for diagnosing, prognosing or treating chronic inflammatory diseases such as septic shock and bacterial infections; neurological diseases such as setroke-induced inflammation in neurons; neurological diseases such as stroke-induced inflammation in neurons; neurological diseases such as stroke-induced inflammation in neurons; neurological diseases and cancer. Accordingly, these complexes can be used for the development of pharmaceutical compositions that exhibit antiinflammatory, antiarthritic, antirheumatic, cytostatic and antibacterial activities and can be used for gene therapy purposes. In particular, the invention further provides is IRNA-oligomucleotides useful for inhibiting protein expression for in vitro or cell culture assays. This polypeptide is a human protein that can be used in combination with other proteins provided in the specification, to form novel complexes of the TNF-alpha signalling pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New protein complex comprising at least one first and second protein of
the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
diagnosing or treating inflammation, neurological diseases, infectious
                                                                                                                                                                                                                                                                         Human protein of a TNF-alpha signalling pathway protein complex SeqID 3.
                                                                                                                                                                                                                                                                                                                                              protein complex; tumour necrosis factor-alpha signalling pathway; TNF-alpha; chronic inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; infectious disease; septic shock; bacterial infection; neurological disease; stroke-induced inflammation; neurodegenerative disease; cancer; antiinflammatory; antiarthritic; antirheumatic; cytostatic; antibacterial; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bauch A, Ruffner H, Bauer A, Kuester B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.2%; Score 37; DB 8; Length 508; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
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                                    ADS88148 standard; protein; 508 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CELL-) CELLZOME AG
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Best Local Similarity
Matches 8; Conserv
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Superti-Furga G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 508 AA;
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                                                                                                                  ADS88148;
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The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-comprises the sequence of any of the genes that are up-regulated in apecific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer cacter lymphocytic leukemia). ACC72641 to ACC72860 represent cancer cacter absence of a pathological cell in a patient; (2) an expression vector absence of a pathological cell in a patient; (2) an expression vector comprising the vector; (4) an isolated polypeptide, which is encoded by the netting a nucleic acid, (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a comprising a pathology, e.g. cancer (e.g. cancer of the bone marrow, chargeness, pressing a pathology, e.g. cancer (e.g. cancer of the bone marrow, collader, brain, breast, cervix, colon/rectum, kidney, lung, ovary, collader, brain, breast, cervix, colon/rectum, kidney, lung, ovary, contracters, prain, breast, cervix, colon/rectum, kidney, lung, ovary, atherosclerosis and endometriosis. The nucleic acid is also useful in the content of drug screening, particularly for identifying agents for treating these contents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New genes that are up-regulated or down-regulated in cancers, useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                                       Human, cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
heart disease; atherosclerosis; endometriosis.
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Pred. No. 1.1e+02;
0; Mismatches 0;
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                                                                                                       Human cancer related protein SEQ ID NO:356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 762; 767pp; English.
ABR58699 standard; protein; 509 AA
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100.0%; Pre-
0;
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; 2002US-0355145P.
; 2002US-0355257P.
; 2002US-0372246P.
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                                                                                                                                                                                                                                                                     27-MAR-2003
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                                 ABR58699;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a crystalline polypeptide (1), comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck) protein. Lck is a Src-family protein tyrosine kinase expressed primarily in T-cells and plays an essential role in immune response. The present sequence is the full-length sequence of human Lck (1-509). (1) is useful for identifying a compound which is an inhibitor of human Lck protein
                                                                                                                                                                                                                                                 Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme; Src-family protein tyrosine kinase; T-cell; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Loew A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 7; Length 509;
Pred. No. 1.1e+02;
0; Mismatches 0; Indels
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                                                             ABR56202 standard; protein; 509 AA
                                                                                                                                                                                                    Human Lymphocyte Cell Kinase, Lck.
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100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Fig 1; 994pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-2002; 2002WO-US024546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2001; 2001US-0310051P
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                                                                                                                                                       (first entry)
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                                                                                                        ABR56202;
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ID ABRES 6202

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Identifying a compound capable of diagnosing, preventing or treating AIDS or an HIV-related disorder comprises assaying the ability of the compound to modulate e.g. 1414, 1481 or 1553 nucleic acid expression or polypeptide activity.

25-JUN-2002; 2002US-0391306P. 27-AUG-2002; 2002US-0406297P. 19-SEP-2002; 2002US-0412007P. 10-OCT-2002; 2002US-0417508P.

13-MAY-2002;

10-DEC-2002; 2002US-0432318P (MILL-) MILLENNIUM PHARM INC

Weich NS

Powell DM,

WPI; 2003-671808/63. N-PSDB; ADE40448.

13-FEB-2003; 2003WO-US004246

WO2003070883-A2

28-AUG-2003

Claim 1; SEQ ID NO 28; 167pp; English.

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The invention relates to a method of identifying a compound useful in the treatment of AIDS (acquired immunodeficiency syndrome) or an HIV (human immunodeficiency virus) related disorder. The invention involves assaying the ability of a test compound to modulate the activity or expression of 26 human proteins. These proteins and nucleic acids encoding them (ADE4022-ADE40473) are differentially expressed in tissues relating to AIDS or an HIV-related disorder compared to their expression in normal tissues. The invention also relates to the use of the compounds candentified to modulate viral replication in a cell and to treat a patient with AIDS or an HIV-related disorder. The invention further discloses methods for the diagnostic evaluation and prognosis of various HIV-clated disorder. The invention further discloses method disorders, and for the identification of individuals exhibiting a predisposition to such modulatory compounds identified using the method of the invention may be small organic molecules. The methods of peptides, antibodies or antisense nucleic acid molecules. The methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the invention are useful in diagnosing, preventing or treating AIDS or HIV-related disorders. The present sequence represents a human protein which is differentially expressed in AIDS or HIV-related disorders.
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AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus; HIV-related disorder; differential expression; drug screening; viral replication modulation; diagnosis; prognosis; predisposition; anti-HIV; gene therapy; antiesense therapy; human; proto-oncogene Tyr protein kinase LCK; enzyme.

Homo sapiens

Human proto-oncogene Tyr protein kinase LCK (gene ID 1611) protein.

(first entry)

29-JAN-2004

ADE40449
XX
AC ADE4
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DT 29-J
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KW AIDS
KW HIVKW VIRS
KW ANTS

ADE40449;

ADE40449 standard; protein; 509 AA

RESULT 26

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AEA35921 standard; protein; 509 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Src family kinase, Lck kinase.
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                       WPI; 2005-315455/32.
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                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                            1 KLVERLGA
                                                                                                                                                                                                                                                                  Sequence 509 AA;
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AEA35921
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                                                                                                                                                                                                    Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
                                                                                                                                                                                                                                                                                                     rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, pancreas individual. The method is also useful in assessing the immune status of an individual. The method see also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple solerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
                                                                                                                                                                                                                  pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein kinase inhibitor; inactive conformation; Tethering; Tyr kinase;
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                                                                                                                                                                                                                                                                                           present invention relates to diagnosing or monitoring transplant
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Pred. No. 1.1e+02;
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100.0%; Pred
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                                               24-APR-2003; 2003WO-US012946.
                                                                       24-APR-2002; 2002US-00131831
20-DEC-2002; 2002US-00325899
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WO2004042346-A2
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                                                                                                                                   Wohlgemuth J,
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                       21-MAY-2004
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                                                                                                                                                                                                                                            the genes.
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Identifying ligand binding to inactive conformation of target protein kinase, by contacting inactive conformation of target with ligand candidates specific to target, detecting formation of kinase-ligand conjugate and identifying ligand.
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                                                                                                                                                                                                                  Example 1; SEQ ID NO 9; 101pp; English.
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The invention relates to a method (M1) for identifying, selecting and/or characterizing a compound which modulates Src family kinase (SFK)

cativity, by expressing nucleic acids encoding SFK or mutated SFK in cells, contacting cells with test compound and determining whether phenotype of cells is changed as compared with phenotype of cells not expressed with above nucleic acids, where difference in phenotype indicates that test compound and/or characterized by (M1); and (2) a compound (1) identified, selected and/or characterized by (M1); and (2) a pharmaceutical composition (PCI) containing (I), and a carrier, adjuvant or vehicle. (I) is useful as a medicament, particularly for the treatment of diseases, which are at least in part caused by a Src family kinase. (I) and PCI are useful for producing a medicament for the treatment of diseases, which are at least in part caused by a Src family kinase, particularly by a dysfunction of a Src family kinase, in particular cancer, hypercalcemia, restenosis, osteoporosis, osteoarthritis, inflammatory bowel disease, multiple Src family kinase, in particular caused by a Src family kinase, in family and sease, results of the sease, rell mediated hypersensitivity disease, inflammatory bowel disease, multiple solerosis, sociacid arthritis, restenosis, solerosis, sociacid arthritis, versus host disease, reall mediated hypersensitivity disease, submaniant of bone metastasis, sociacid arthritis, respectively contact demartitis, paget's disease, asthma, isochemic or reperfusion injury, allergic disease, atopic dermatitis, transplant rejection or allergic rhinitis. The present sequence represents invention. The present invention.
Disclosure; SEQ ID NO 8; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 509 AA;
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Best Local Similarity 100. Matches 8; Conservative Query Match

90.2%; Score 37; DB 9; Length 509; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels

|||||||| 246 KLVERLGA 253 1 KLVERLGA 8 셤 ð

ABM82981 standard; protein; 539 AA. 18-NOV-2004 ABM82981; RESULT 30

Human diagnostic and therapeutic pprotein SEQ ID NO:3230. (first entry)

gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

Homo sapiens

WO2004023973-A2

25-MAR-2004.

12-SEP-2003; 2003WO-US028227

12-SEP-2002; 2002US-0410259P. 12-SEP-2002; 2002US-0410260P.

(INCY-) INCYTE CORP.

Gietzen D; Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; Money EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Liagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Vu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzer Pattry S, Shi X, Suarez CJ;

WPI; 2004-329368/30. N-PSDB; ACN41633.

The invention relates to novel diagnostic and therapeutic polymucleotides selected from one of the 2722 sequences defined in the specification. A polymucleotide of the invention may have a use in gene therapy. The human ciagnostic and therapeutic polymucleotides (dithp) or polymeptides may be used to diagnost a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorder, neurological disorders, developmental disorders, or disorder, neurological disorders, dastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence represents a dithp protein of the invention, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or Claim 27; Page; 190pp; English in gene mapping.

Sequence 539 AA;

Gaps ö Length 539; 0; Indels 1.2e+02; Score 37; DB 8; 100.0%; Pred. No. 1.2 ive 0; Mismatches 90.2%; 8; Conservative Best Local Similarity Matches 8; Conserv Query Match

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Search completed: June 29, 2006, 09:13:06 Job time : 90.8313 secs

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5.1.9 Biocceleration Ltd.	earch time 105.831 Seconds 3	updates/sec	• • • •	s rs: 2849598		n un un vo		s predicted by chance to have a score of the result being printed, total score distribution.	•••	otion	Q288x6 hahella che Q4k6w6 pseudomonas P72012 methanobact	mus musculu rattus norv	aotus nancy homo sapien mus musculu	saimiri sci homo sapien	hylobates s bos taurus	jannaschia pseudomonas	pseudomonas pseudomonas pseudomonas	chlamydia m chromohalob	trypanosoma trypanosoma	trypanosoma arthrobacte	arthrobacte alcaligenes	mus musculu pseudomonas	QSfvqO rattus norv Q8btq3 mus musculu
GenCore version Copyright (c) 1993 - 2006	OM protein - protein search, using sw model Run on: June 29, 2006, 08:59:39 ; Searcl	78.6 Title: US-10-062-257A-12 Perfect score: 41 Sequence: 1 KLVERLGAA 9	coring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 2849598 segs, 925015592 residue: Total number of hits satisfying chosen paramete:	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries	<pre>Database : UniProt_7.2:* 1: uniprot_sprot:* 2: uniprot_trembl:*</pre>	Pred. No. is the number of results predict score greater than or equal to the score and is derived by analysis of the total se	* Query	Score Match Length DB	1 38 92.7 559 2 Q2S8X6_9GAMM 2 37 90.2 173 2 Q4KGW6_PSEP5 3 37 90.2 226 I RPIA METTH	37 90.2 368 2 37 90.2 368 2 37 90.2 379 2	37 90.2 508 1 37 90.2 508 1 37 90.2 508 1	37 90.2 508 1 37 90.2 509 2	2 37 90.2 509 2 3 37 90.2 509 2	4 36 87.8 179 2 5 36 87.8 399 2	5 36 87.8 399 2 7 36 87.8 399 2 8 36 87.8 400 2	9 36 87.8 419 1 0 36 87.8 467 2	1 36 87.8 508 2 2 36 87.8 597 2	3 36 87.8 791 2 1 35 85.4 160 2	35 85.4 252 2 35 85.4 322 2 35 85.4 336 2	35 85.4 341 2 35 85.4 393 2	35 85.4 462 2 1 35 85.4 462 2

pseudomonas synechococo gallus gall clostridium syntrophoba nitrobacter dechloromon burkholderi rhodobacter silicibacter silicibacter ricicum ae hordeum vul nitrobacter thiobacillu bordetella bordetella bordetella sus scrofa sus scrofa sus scrofa sus scrofa

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PubMed=15980861; DOI=10.1038/nbt1110;
Paulsen I.T., Press C.M., Ravel J., Kobayashi D.Y., Myers G.S.A.,
Mavrodi D.V., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
Durkin A.S., Brinkac L.M., Daugherty S.C., Sullivan S.A.,
Rosovitz M.J., Gwinn M.L., Zhou L., Schneider D.J., Cartinhour S.W.,
Nelson W.C., Weidman J., Wackins K., Tran K., Khouri H., Pierson E.A.,
"Complete genome sequence of the plant commensal Pseudomonas
fluorescens Pf-5.";
                                                                                                                                                                                                                                                                                                                                    STRAIN=KCTC 2396;
PubMed=16352867; DOI=10.1093/nar/gki1016;
Jeong H., Yim J.H., Lee C., Choi S.-H., Park Y.K., Yoon S.H.,
Hur C.-G., Kang H.-Y., Kim D., Lee H.H., Park K.H., Park S.-H.,
Park H.-S., Lee H.K., Oh T.K., Kim J.F.;
"Genomic blueprint of Hahella chejuensis, a marine microbe producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Hahellaceae, Hahella.
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Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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Complete proteome; Hypothetical protein.
SEQUENCE 173 AA; 18500 MW; 010C421E02BD8E28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; CP000155; ABC32898.1; -; Genomic DNA.
SEQUENCE 559 AA; 64117 MW; 25D965C3322DF02F CRC64;
                                                                                     24-JAN-2006, integrated into UniProtKB/TrEMBL. 24-JAN-2006, sequence version 1. 07-FEB-2006, entry version 2. Whoharacterized protein conserved in bacteria. ORFNames=HCH 0621; Hahella chejuensis KCTC 2396.
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                                                  559 AA.
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Nucleic Acids Res. 33:7066-7073(2005)
                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-FEB-2006, entry version 5. Hypothetical protein.
                                             PRELIMINARY;
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nes 8; Conservative
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Q2S8X6;
24-JAN-2006, in
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RESULT 1

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WEDLINE-98037514; PubMed=9371463;
WEDLINE-98037514; PubMed=9371463;
WEDLINE-98037514; PubMed=9371463;
MAdredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
Spadafora R., Wicare R., Wang Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
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Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
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deltaH: functional analysis and comparative genomics.",
J. Bacteriol. 179:7135-7155(1997).
                                                                   Gaps
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Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanobacterium thermoautotrophicum.
Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
   Length 173;
                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000, integrated into UniProtKB/Swiss-Prot
   Score 37; DB 2;
Pred. No. 90;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                            226 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koga Y., Kyuragi T., Nishihara M., Sone N.;
J. Mol. Evol. 47:631-631(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=rpiA; OrderedLocusNames=MTH608;
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HSSP: G60083; 1LK5.
GenomeReviews; AE000666_GR; MTH608.
BioCyc; MTHE187420:MTH608-MONOMER;
LinkHub; P72012;
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InterPro; IPR004788; RpiA.
PANTHER; PTHR11934; RpiA; 1.
Pfam; PF06026; Rib 5-P isom A; 1.
Prodom; PD005813; RpiA; 1.
TIGRFAMS; TIGR00021; rpiA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         , sequence version 1.
90.2%;
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      Query Match 90.2
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                               STANDARD;
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20 OLVERLGAA 28
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                                                                                                                               1 KLVERLGAA
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07-MAR-2006,
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninol P., Hayashizaki Y.;
Hidd-efficiency fill-length CDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                07-FEB-2006, entry version 7.
Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched
library, clone:G830026006 product:lymphocyte protein tyrosine kinase,
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.
Hayashizaki Y.,
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RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005).
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                                    11-OCT-2005, integrated into UniProtKB/TrEMBL. 11-OCT-2005, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Mammary gland;
PubMed=16141072; DOI=10.1126/science.1112014;
                                                                                                                                                               library, clone:G830025000 productul insert sequence. (Fragment)
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PubMed=16141073; DOI=
                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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      DOT TO DO TO THE SERVICE OF THE SERV
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                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Larimer F., Land M.;
"Annotation of the draft genome assembly of Solibacter usitatus.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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   Ribose-5-phosphate isomerase A.
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GO; GO:0008959; F:phosphate acetyltransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:001512; F:metabolism; IEA.
InterPro; IPR012147; P. Ac Bu trans.
InterPro; IPR004614; PhpActrans.
                                                                                                                              Score 37; DB 1; Length 226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                             /FTId=PRO 0000158513.
F5EE6E929C08792B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Solibacter usitatus Ellin6076.
Bacteria, Acidobacteria, Solibacteres, Solibacterales, Solibacteraceae, Solibacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACYLLTANSferase, Transferase.
SEQUENCE 331 AA; 34576 MW; 4BF1DA6049A448E3 CRC64;
                                                                                                             90.2%; Score 37; LD 1, 100.0%; Pred. No. 1.16+02; rive 0; Mismatches 0;
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88.9%; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 AA.
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US DOE Joint Genome Institute (JGI-ORNL);
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TIGRFAMS; TIGR00651; pta; 1.
                                                           226 AA; 23785 MW;
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PIRSF; PIRSF000428; P Ac_t:
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نمر 8; Conservative
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226
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Q43YL3;
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           TISSUE-Mammary gland;

MEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;

MEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;

MARAWA T., Binnagawa A., Shibata K., Yoshino M., Ishih Y.,

Arawawa T., Hara A., Fukunishi Y., Komono H., Adachi J., Fukuda S.,

A izawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Caswant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Caswant T.,

Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fuljita M., Gariboldi M.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nymbaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nymbay-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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TISSUE=Mammary gland;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mormalization and subbraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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MEDLINE_2053013; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE_20530913; PubMed=and K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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Bukaryota; Metazoa; (Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                    EMBL; AK166263; BAE38668.1; -; mRNA. MGI: 96756; Lck. GO; GO:0004674; F:protein serine/threonine kinase activity; RCA. InterPro; IPR002290; SPC Ltr_pkinase. InterPro; IPR002290; Sec_thr_pkinase. InterPro; IPR00148; Tyr pkinase. InterPro; IPR00148; Tyr pkinase. InterPro; IPR001866; Tyr pkinase. InterPro; IPR008266; Tyr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kaw
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 AA; 42018 MW; 7AB6AE53AF1A5059 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Kinase; Nucleotide-binding; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 2; Lo
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-AUG-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.2%; Scor.
100.0%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS500119; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00109; TYRKINASB.
PRODOM; PD000001; Proct kinase; 1.
ProDom; PD000093; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-AUG-2005, sequence version 1. 07-FEB-2006, entry version 7. LCk_mapped protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF07714; Pkinase Tyr; 1.
Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 KLVERLGA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω
                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KLVERLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Lck mapped;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q4FZR6 RAT
Q4FZR6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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04 F2R6 RAT
10 G0 F2R6
AC 04 F2R6
DT 30 - AUG
DT 07 - FEB
DE LCk mai
GN Rattus
CO Bukary
CO Bukary
CO Muroid
CO Muroid
CO Muroid
CO NE RATTUS
CO MUROID
CO MUROID
CO MUROID
CO NE CO MUROID
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LCK (EC 2.7.1.112) (p56-LCK)

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Aotus nancymaae (Ma's night monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Platyrrhini, Cebidae,
                                                             (Lymphocyte cell-specific protein-tyrosine kinase).
     08-NOV-2005, integrated into UniProtKB/Swiss-Prot
                    08-NOV-2005, sequence version 3.
07-MAR-2006, entry version 13.
Proto-oncogene tyrosine-protein kinase
     Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K.F. Farmer A.A., Rubin G.M., Hong L.,
A Brahecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren B.J., Iu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schuutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                    NIH MGC Project;
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Surviy, Vartano; Argarb binding; IEA.

GO; GO:00015524; F:ATP binding; IEA.

GO; GO:0000166; F:nuclectide binding; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0017242; P:intracellular signaling cascade; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR00199; Prot kinase.

R InterPro; IPR00199; Ser Ehr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Pfam; PF00171; SH2; 1.

R PRINTS; PR00109; SH2DOMAIN.

R PRINTS; RR00109; TYRKINASE.

R PRODOM; PD000001; Prot kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.2%; Score 37; DB 2; Length 379; 100.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 AA; 43336 MW; 7CDEB573BAFB53AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding; Kinase; Nucleotide-binding; Transferase;
                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00252; SH2; 1.
SMART; SM00219; TYPKC; 1.
PROSITE; PS00010; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS500109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC099218; AAH99218.1; -; mRNA.
SMR; Q4FZR6; 2-379.
                                                                                                                                                                                                                                                and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tyrosine-protein kinase.
NON TER 1 1
SEQUENCE 379 AA; 43336
                                                                                                                                                                                                                                                                                                                                                                tyrosine phosphate.
                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLVERLGA 8
                                                                                                                                                                                                                                                                                                        rissue=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
SUBCELIOLAR LOCATION: Cytoplasmic and attached to the membrane.
Present in lipid rafts in an unactive form (By similarity)
DOMAIN: The SH2 domain mediates interaction with SQSTM1.
Interaction is regulated by Ser-58 phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interacts with phosphorylated LIME1. Interacts with CBLB (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
-!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AY821852; AAV70114.2; -; mRNA. SNR; Q5PXS1; 64-508.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000230; Ser_thr_pkinase.
InterPro; IPR001452; SH3.
InterPro; IPR001452; SH3.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase_AS. Pfam; PF07714; Pkinase_Tyr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subfamily.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00401; SH2DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam: PF00018; SH3
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508 AA.

PRT;

STANDARD;

LCK AOTNA QSPXS1;

RESULT 7
LCK AOTNA
ID LCK AC
AC QSPXS:

116 KLVERLGA 123

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9

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Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F.,
                          Wilson C.B.;
      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphotyrosine (negative regulation) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] —
NUCLEOTIDE SEQUENCE [WRNA].
MEDLINE=87133831; PubMed=3493153;
Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
Mak T.W.,
                                                                                                                                                                                                                                                                                                                                                                   Proto-oncogene tyrosine-protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphotyrosine (by autocatalysis) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK) (Lymphocyte cell-specific protein-tyrosine kinase) (LSK) (T cell-specific protein-tyrosine kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A human T cell-specific cDNA clone (YT16) encodes a protein with extensive homology to a family of protein-tyrosine kinases."; Eur. J. Immunol. 16:1643-1646(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-myristoyl glycine (By similarity).
S-palmitoyl cysteine (By similarity)
S-palmitoyl cysteine (By similarity)
                                                                                                                                                                                                                                                                          ATP-binding, Kinase, Lipoprotein, Membrane, Myristate,
Nucleotide-binding, Palmitate, Phosphorylation, Proto-oncogene,
SH2 domain, SH3 domain, Transferase, Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LCK HUMAN STANDARD, PRT; 508 AA.
P06239; P07100; Q12850; Q13152; Q5TDH8; Q5TDH9; Q96DW4; Q9NYT8; Q1-JAN-1988, integrated into UniProtKB/Swiss-Prot. 01-FBB-1994, sequence version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (By similarity).
Interactions with CD4 and CD8 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proton acceptor (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.2%; Score 37; DB 1; Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8B61951BC192A3A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             'FTId=PRO_0000088123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein kinase.
                            Probom; PD000001; Prot Kinase; 1.
Probom; PD0000093; SH2; 1.
Probom; PD0000065; SH3; 1.
SMART; SM00252; SH3; 1.
SMART; SM00219; TYKC; 1.
SMART; SM00129; TYKC; 1.
PROSITE; PS00109; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS50010; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity)
                                                                                                                                                                                                                                                                                                                                                 Probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89123626; PubMed=3265417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        508 AA; 58041 MW;
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 120
223
497
258
71
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Ricausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Ricausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Ricausperg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Schnerth A., Schein J.E., Jones S.J.M., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM SHORT), AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Leukemic T-cell;
MEDLIAE=9668510; PubMed=7495859; DOI=10.1016/0167-4781(95)00162-A;
MEDLIAE=9668510; Publita D.J.;
WOGGI L.B., Arthur R., Fujita D.J.;
"An aberrant lck mRNA in two human T-cell lines.";
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Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
Miyamoto N.G., Mak T.W.;
"Structure of the two promoters of the human lck gene: differential
accumulation of two classes of lck transcripts in T cells.";
Mol. Cell. Biol. 9:2173-2180(1989).
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MEDLINE=90108697; PubMed=2558056; DOI=10.1016/0378-1119(89)90144-3;
Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
Benarous R.;
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"Structure and expression of lck transcripts in human lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Lymph;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human chromosome 1 international sequencing consortium;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
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PubMed=12218089;
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Bergman M., Mustelln T., Oetken C., Partanen J., Flint N.A.,
Amrein K.E., Autero M., Burn P., Alitalo K.;
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MEDLINE-88217332; PubMed=2835736;
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"Expression of the lck tyrosine kinase gene in human colon carcinoma and other non-lymphoid human tumor cell lines.";
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MEDLINE-87000726; PubMed=3489486; DOI=10.1016/0167-4889(86)90228-4;
Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
                                                                                                                  ZAP-70 in common variable
NUCLEOTIDE SEQUENCE [MRNA] OF 13-508.

125SURE-Peripheral blood lymphocyte;

MEDLINE=20462621; Pubmde=11009097;

DOI=10.1002/1521-4141(200009)30:9<2632::AID-IMMU2632>3.0.CO;2-C;

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Baldari C.T.;
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"p70 phosphorylation and binding to p561ck is an early event in
interleukin-2-induced onset of cell cycle progression in T-
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MEDLINE=95155308; PubMed=7852312; DOI=10.1074/jbc.270.6.2506;
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INTERACTION WITH PI3K.
MEDLINE=94067101; PubMed=7504174;
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                                                                                                                                                                                                                                                                  Oncogene Res. 1:357-374(1987).
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SUBCELLULAR LOCATION

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STRAIN=NOD; TISSUE=Thymus;
PubMed=16141072; DOI=10.1126/science.1112014;
Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=86079521; PubMed=2416464; DOI=10.1016/0092-8674(85)90169-2; Marth J.D., Peet R., Krebs B.G., Perlmutter R.M.; "A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpressed in the murine T cell lymphoma LSTRA."; Cell 43:393-404(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a new membrane raft-associated adaptor protein involved in CD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                                                                                            TISSUE-Mammary cancer;
MEDLINE-21829512; PubMed=11840567;
DOI=10.1002/1615-9861(200202)2:24212::AID-PROT212>3.0.CO;2-H;
Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
Zvelebil M.J.;
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Brdickova N., Brdicka T., Angellsova P., Horvath O., Spicka J., Algerligert I., Paces J., Simeoni L., Kliche S., Merten C., Schraven Horejsi V.;
Horejsi V.;
"LIME: a new membrane raft-associated adaptor protein involved in
                                                                                                                                                                                                                                                                                                                                                 "Cluster analysis of an extensive human breast cancer cell line
            Yamada T.,
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Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T. Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.; "Fyn is essential for tyrosine phosphorylation of Csk-binding protein/phosphoprotein associated with glycolipid-enriched microdomains in lipid rafts in resting T cells."; Immunol. 169:2813-2817(2002).
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"Expression of a new tyrosine protein kinase is stimulated retrovirus promoter insertion.";
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Q1-JAN-1988, integrated into UniProtKB/Swiss-Prot.
25-OCT-2005, sequence version 3.
07-MAR-2006, entry version 74.
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                                                                                                                                                                                                                                                                                                                                                                            protein expression map database.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and CD8 coreceptor signaling.";
J. Exp. Med. 198:1453-1462(2003)
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Mus musculus (Mouse).
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TUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

STRAIN=FVB/N; TISSUB=Salivary gland;

MEDLINE=2338257; PubbMed=12477932; Oronse L.H., Derge J.G.,

MEDLINE=2338257; PubbMed=12477932; Derege J.G.,

MEDLINE=2338257; PubbMed=12477932; Derege J.G.,

MISSUBSERS R.L., Felingold E.A., Grouse L.H., Derge J.G.,

MISSUBSERS R.L., Buctow K.H., Scheefer C.F., Bhat N.K.,

MISSUBSERS R.P., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MISSUBSERS R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tobhiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Worden W.S., Carninci P., Prange C.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Mitting W., Addan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Mitting W., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Muterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Monsech A., Schein J.E., Jones S.J.M., Marra M.A.,

Monsech A., Schein J.E., Jones B.J.M., Marra M.A.,

Monsech A., Schein J.E., J., Marra M.A.,

Monsech A., Schein J.E., J., Marra M.A.,

Monsech A., Schein J., J., Marra M.A.,

Monsech A., Schein J. A Bajic V.B., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Ra Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J. Wilming L.G., Aidinis V., Allen J.E.,
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Al Bernardo D., Down T., Engstrom P., Fagololin M., Futalkins T., Green R.E.,
Action C.F., Fukushima T., Furuno M., Futaki S., Garibbidi M.,
Rad Georgil-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
Alll D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
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Kitano H., Kollias G. Krishnan S.P., Kruger A., Kummerfeld S.K.,
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Matsuda H., Matsusawa S., Maidan Babu M., Madera M., Marchonn L.,
Matsuda H., Matsusawa S., Maidan Babu M., Nadera M., Marchonn L.,
Matsuda H., Matsusawa S., Naiki H., Mignone F., Miyake S., Morris K.,
Matsuda H., Matsusawa S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
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Shimada H., Shimada K., Silva D., Sinclair B.,
Schonbach C., Sekiguchi K., Semple C.A., Seno S., Seesa L.,
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1. Virol. 75:925-9261(2001).

2. Virol. 75:925-9261(2001).

3. Virol. 75:925-9261(2001).

5. FUNCTION: Tyrosine kinase that plays an essential role for the selection and maturation of developing T-cell in the thymus and in mature T-cell function. Is constitutively associated with the cytoplasmic portions of the CD4 and CD8 surface receptors and transduction pathways. Association of the TCR with a peptide antigen-bound MHC complex facilitates the interaction of CD4 and CD8 with MHC class II and class I molecules, respectively, and thereby recruits the associated LCK to the vicinity of the TCR/CD3 complex. LCK then phosphorylates tyrosines residues within the immunoreceptor tyrosines-based activation motifs (ITAMS) in the cytoplasmic tails of the TCR/GD3 subunits, initiating the TCR/CD3 signaling pathway. In addition, contributes to signaling by other receptor molecules. Associates directly with
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MEDLINE=21424508; PubMed=11533187;
MEDLINE=21424508; PubMed=11533187;
MEDLINE=0.1128/UVI.75.19.9552-9261.2001;
Gree T., Tamgueney G., Fleischer B., Fickenscher H., Broeker B.M.;
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                                                                              "Negative regulation of lymphocyte activation and autoimmunity by the molecular adaptor Cbl-b.", Nature 403:211-216(2000).
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PubMed=1552455; DOI=10.1038/nbt1046;
Rush J., Moritz A., Lee K.A., Goo A., Goss V.L., Spek E.J., Zhang H.,
Zha X.-M., Polakiewicz R.D., Comb M.J.;
"Immunoaffinity profiling of tyrosine phosphorylation in cancer
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Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-NOV-2005, sequence version 2.
07-MAR-2006, entry version 26.
Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK) (Lymphocyte cell-specific protein-tyrosine kinase).
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Bachmaier K., Krawczyk C., Kozieradzki I., Kong Y.-Y., Sasaki T., Oliveira-dos-Santos A., Mariathasan S., Bouchard D., Wakeham A., Itie A., Le J., Ohashi P.S., Sarosi I., Nishina H., Lipkowitz S.,
                                                                                                                                                                                                        Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T., Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.; Fyn is essential for tyrosine phosphorylation of Csk-binding protein/phosphoprotein associated with glycolipid-enriched microdomains in lipid rafts in resting T cells.";
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Pred. No. 2.2e+02;
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100.0%; Pre
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Q95KR7;
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the Ortcolfamilate tail of CDD, and upon engagement of the CD2

molecule, LCK undergoes hyperphosphorylation and activation, also
plays a rotal in the LLZ receptor. Taked signaling pathway that
controls T-cell in the LLZ receptor. Taked signaling pathway that
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GO; GO:0050870; P:positive regulation of T cell activation; ISS.

GO; GO:0050862; P:positive regulation of T cell receptor sign. .; ISS.

GO; GO:0005265; P:Ras protein anino acid phosphorylation; ISS.

GO; GO:00051249; P:Ras protein anino acid phosphorylation; ISS.

GO; GO:00051249; P:Ras protein anino acid phosphorylation; ISS.

GO; GO:00042403; P:Ras protein of progression through cell cycle; ISS.

DR GO; GO:00042403; P:Regulation of progression through cell cycle; ISS.

DR GO; GO:00042403; P:Regulation of progression through cell cycle; ISS.

DR GO; GO:00042403; P:Response to drug; ISS.

DR GO; GO:00042403; P:Response to drug; ISS.

DR GO; GO:0004827; P:Rinase.

DR InterPro; IPR000290; SRT_th_pkinase.

DR InterPro; IPR000300; SRT_th_pkinase.

DR InterPro; IPR001245; Tyr_pkinase.

DR InterPro; IPR001245; Tyr_pkinase.

DR Ffam; PP00115; SH2; 1.

DR Ffam; PP00118; SH3; 1.

PRINTS; PR00109; TYRKINASE.

PRODOM; PD000001; Prot Linase; 1.

DR SWART; SW00225; SH3; 1.

BR PROSITE; PS00101; PROTEIN KINASE ATP; 1.

PR PROSITE; PS00101; PROTEIN KINASE TYR; 1.
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246 KLVERLGA 253
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                  Phosphotyrosine (negative regulation) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22289034; PubMed=12401726; Nervi S., Nicodeme S., Gartioux C., Atlan C., Lathrop M., Reviron D., Naquet P., Matsuda F., Imbert J., Vialettes B.; Nosociation between 1ck gene polymorphisms and protein level in type 1 diabetes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ensembl; ENSG0000112866; Homo sapiens.

GO; GO:00045121; C:11pid raft; ISS.

GO; GO:00004722; C:pericentriolar material; ISS.

GO; GO:0004712; F:protein serine/threonine phosphatase activity; ISS.

GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.

GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.

GO; GO:0006919; P:caspase activation; ISS.

GO; GO:0006919; P:nemopoiesis; ISS.

GO; GO:0006917; P:induction of apoptosis; ISS.

GO; GO:0007242; P:indracellular signaling cascade; ISS.
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                                                   Proto-oncogene tyrosine-protein kinase
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S-palmitoyl cysteine (By similarity).
S-palmitoyl cysteine (By similarity).
5088C64061853819 CRC64;
          Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
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                                                                                                                                                Interactions with CD4 and CD8 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type 1 diabetes..;
Diabetes 51:3326-3330(2002).
-!- MISCELLANBOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.
                                                                                                                                                                           Proton acceptor (By similarity).
          SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.

INIT_MET 0 0 Drahala
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les 8; Conser
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hylobatidae; Hylobates.
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Thesis (2001), Department of Experimental Oncology laboratory, U.
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Indels
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EMBL; BC102046; AAI02047.1; -; mRNA.

R GO; GO:0045121; C:lipid raft; ISS.

R GO; GO:0044212; C:pericentriolar material; ISS.

R GO; GO:0004713; F:protein serine/threonine phosphatase activity; ISS.

R GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.

R GO; GO:0006519; P:caspase activation; ISS.

R GO; GO:0006519; P:manapolesis; ISS.

R GO; GO:0006517; P:intracellular signaling cascade; ISS.

R GO; GO:0006468; P:protein amino acid phosphorylation; ISS.

R GO; GO:0006468; P:protein amino acid phosphorylation; ISS.

R GO; GO:000419; P:regulation of lymphocyte activation; ISS.

R GO; GO:000419; P:regulation of lymphocyte activation; ISS.

R GO; GO:000418; P:regulation of lymphocyte activation; ISS.

R GO; GO:000418; P:regulation of progression through cell cycle; ISS.

R GO; GO:0006812; P:response to duy; ISS.

R GO; GO:0008017; P:response to line homeostasis; ISS.
                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
   Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y., Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C., Wagner L., Bala M., Barbaruk S., Barber S., Babkaiff R., Beland J Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J., Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D., Siddiqui A., Holt R., Jones S.J., Marra M.A.; Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.2%; Score 37; DB 2; Length 509; 100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              il protein.
509 AA; 58116 MW; CEOE80DCD6D0F2F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q40AH8 9RHOB PRELIMINARY; PRT; 179 AA. Q40AH8; 27-SEP-2005, integrated into UniProtKB/TrEMBL. 27-FEB-2006, entry version 1. 21-FEB-2006, entry version 6. Adenine phosphoribosyl transferase (EC 2.4.2.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; JPR000719; Prot kinase.
InterPro; IPR000719; Prot kinase.
InterPro; IPR001990; Ser_thr_pkinase.
InterPro; IPR00145; SH3.
InterPro; IPR00145; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00117; SH2; 1.
Pfam; PF00117; SH2; 1.
Pfam; PF00018; SH2; 1.
PRINTS; PR00140; SH2DOMAIN.
PRINTS; PR00195; SH3DOMAIN.
PRINTS; PR00195; TYRKIMASE.
ProDom; PD000001; Prot kinase; 1.
ProDom; PD000001; Prot kinase; 1.
ProDom; PD000001; Prot kinase; 1.
SWART; SM01219; TYRKIASE.
PRODOM; PM00195; SH3; 1.
SWART; SM01216; SH3; 1.
SWART; SM01216; SH3; 1.
PROSITE; PS00110; PROTEIN KINASE ATP; 1.
PROSITE; PS00110; PROTEIN KINASE ATP; 1.
PROSITE; PS00110; PROTEIN KINASE TYR; 1.
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PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
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246 KLVERLGA 253
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SEQUENCE 50
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040AH8 9RH0B
1D 040AH8 9AC
040AH8;
DT 27-SEP-20
DT 27-SEP-20
DT 21-ESB-20
DE Adenine 2
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                                                                                             SMR; 1958/13; 56-509.

SMR; 1958/13; 56-509.

SMR; 1958/13; 56-509.

SMR; 1958/13; 56-509.

SMR; 1958/14; 15S.

GO; GO:0004712; F:protein serine/Inreonine phosphatase activity; 15S.

GO; GO:0004712; F:protein serine/Inreonine phosphatase activity; 15S.

SMR; 0958/14; F:SMR; 40main binding; 15S.

GO; GO:0004169; F:SMR; 40main binding; 15S.

GO; GO:0005919; P:caspase activation; 15S.

GO; GO:0005917; P:hemopoiesis; 15S.

GO; GO:0005917; P:hemopoiesis; 15S.

GO; GO:0005917; P:hemopoiesis; 15S.

GO; GO:0005917; P:protein amino acid phosphorylation; 15S.

GO; GO:0005686; P:Pras protein amino acid phosphorylation; 15S.

GO; GO:0005686; P:prastive regulation of T cell activation; 15S.

GO; GO:000766; P:prastive regulation of Typhocyte activation; 15S.

GO; GO:000766; P:prastive regulation of Jymphocyte activation; 15S.

GO; GO:000786; P:regulation of Jymphocyte activation; 15S.

GO; GO:000787; P:regulation of Jymphocyte activation; 15S.

GO; GO:000786; P:regulation of Jymphocyte activation; 15S.

GO; GO:000786; P:regulation of Jymphocyte activation; 15S.

GO; GO:000787; P:regulation of Jymphocyte activation; 15S.

GO; GO:000789; P:regulation of Jymphocyte activation; 15S.

B:rerPro; PR00109; P:regulation of Jymphocyte activation; 15S.

B:RIMTS; RR001018; SH2; 1.

B:RMRT; SM00129; TYRINASE TYR; 1.

B:RMRT; SM00129; TYRINASE DOM; 1.

B:RMRT; SM00129; PROTEIN KINASE DOM; 1.

B:RMRT; SM00129; PROTEIN KINASE DOM; 1.

B:RMRT; SM00129; SH3; 1.

B:RMRT;
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27-SED-2005, integrated into UniProtKB/TrEMBL.

27-SEP-2005, sequence version 1.

07-MAR-2006, entry version 6.

Hypothetical protein MGC126900.

Name=MGG126900;

Bos taurus (Bovine).

Bos taurus (Bovine).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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STRAIN=Crossbred x Angus; TISSUE=Ileum;
                        EMBL; AJ320182; CAC44027.1; -; mRNA.
HSSP; P06239; 1LCK.
SMR; Q95M32; 65-509.
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Q3ZCMO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 8; Conservative
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032CM0 BOV
10 030CM
AC 032CM
DT 27-SE
DT 27-SE
DT 07-MB
DE HYPOT
GN BOST
OC BUKST
OC BUKST
OC PECOT
OC MST
OC PECOT
OC NOST
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Distributed under the Creative Commons Attribution-NoDerivs License
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Kyrpides N.C., Ivanova N., Lindow S.E.;
"Comparison of the complete genome sepences of Pseudomonas syringae
pv. syringae B728a and pv. tomato D63000.";
Proc. Natl. Acad. Sci. U.S.A. 102:11064-11069(2005).
-! SIMILARITY: Belongs to the thiolase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=16043691; DOI=10.1073/pnas.0504930102;
Feil H., Feil W.S., Chain P., Larimer F., Dibartolo G., Copeland A.,
Lykidis A., Trong S., Nolan M., Goltsman E., Thiel J., Malfatti S.,
Loper J.E., Lapidus A., Detter J.C., Land M., Richardson P.M.,
                                                                                      PubMed=16199782; DOI=10.1128/JBL.897.18 :6488-6498.2005;
Joardar V., Lindeberg M., Jackson R., Selengut J., Dodson R.,
Jernkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
Gwinn Giglio M., Madupu R., Nelson W.C., Rosovitz M.J., Sullivan S.Crabtree J., Creasy T., Davidsen T.M., Haft D.H., Zafar N., Zhou I Halpin R., Holley T., Khouri H.M.; Feldblyum T.V., White O.,
Mansfield J., Collmer A., Buell R.;
"Whole-genome sequence analysis of Pseudomonas syringae pv.
phaseolicola 1448A reveals divergence among pathovars in genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=Psyr_4011;
Pseudomonas syringae pv. syringae (strain B728a).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 399;
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Pred. No. 2.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, CP000058, AAZ33439.1; -; Genomic_DNA.
GO; GO:0008415; F:acyltransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR012793; PcaF.
InterPro; IPR02155; Thiolase.
Pfam; PF02108; Thiolase.
Pfam; PF00108; Thiolase.
TIGREAMS; TIGR02430; AcCoA-C-Actrans; 1.
TIGREAMS; TIGR02430; DcaF; 1.
PROSITE; PS00099; THIOLASE.2; 1.
PROSITE; PS00099; THIOLASE.2; 1.
PROSITE; PS00099; THIOLASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome; Transferase. A; 41771 MW; 7F275F72A9B1DE25
                                                                                                                                                                                                                                                                                                                                                                                                                                involved in virulence and transposition.";
J. Bacteriol. 187:6488-6498(2005).
-!- SIMILARITY: Belongs to the thiolase family.
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                                                                 NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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21-FEB-2006, entry version 8.
Thiolase (EC 2.3.1.16).
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NCBI_TaxID=264730;
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Q4ZP81;
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GO; GO:000399; F:adenine phosphoribosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0005168; P:adenine salvage; IEA.
GO; GO:0005168; P:nucleoside metabolism; IEA.
GO; GO:0006166; P:purine ribonucleoside salvage; IEA.
InterPro; IPR005754; Ade_phspho_trans.
InterPro; IPR00375; Pr/py rp_transferase.
                                                                                                                                                                                                                       STRAIN=CCS1;
US DOE Joint Genome Institute (JGI-PGF);
US DOE Joint Genome Institute (JGI-PGF);
US DOE Joint Genome Institute (JGI-PGF);
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Jannaschia sp. CCS1.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary data. FUNCTION: Catalyzes a salvage reaction resulting in the formation of AMP, that is energically less costly than de novo synthesis (By

    -!- CATALYTIC ACTIVITY: AMP + diphosphate = adenine + 5-phospho-alpha-
D-ribose 1-diphosphate.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Larimer F., Land M.;
"Annotation of the draft genome assembly of Jannaschia sp. CCS1.";
"Annotation of the draft genome absembly of Jannaschia sp. CCS1.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
ORFNames=JannDRAFT 1465;
Jannaschia sp. CCSI.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005, integrated into UniProtKB/TrEMBL.
13-SEP-2005, sequence version 1.
21-FEB-2006, entry version 6.
Beta-ketoadipyl CoA thiolase (EC 2.3.1.-).
Name-epcaF; OrderedLocusNames-ESPPH 4017;
Pseudomonas syringae pv. phaseolicla (strain 1448A / Race 6).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00156; rill.
TIGRFAMS; TIGR01090; apt; 1.
PROSITE; PS00103; PUR PYR PR TRANSFER; 1.
TIGRFAMS; Tigrologe; Purine galvage; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: Purine salvage.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
-!- SIMILARITY: Belongs to the purine/pyrimidine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CCS1;
US DOE Joint Genome Institute (JGI-ORNL);
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                                                                                                    Rhodobacteraceae; Jannaschia
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Matches 7; Conservative
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                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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                                                                                                                                NCBI_TaxID=290400;
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PSE14
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RESULT 1 10 Q48EPO E 10 Q4EPO E 10 Q4EPO E 10 Q4EPO E 10 D1 13-10 E 13 DDT 13-10 E 13 DDT 13-10 E 13 DDT 13-10 E 14 DDT 13-10 E 16 DDT 13-10 E 17 DDT 13-10 E 18 D

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Q4KH35;
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ID Y906 CHLMU
AC Q9PJC5;
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A Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
A Madupu R., Daugherty S.C., Erhkac L.M., Beanan M.J., Haft D.H.,
A Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
A Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
A Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
A Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
A Bender C.L., White O., Fraser C.M., Collmer A.;
The complete genome sequence of the Arabidopsis and tomato pathogen
Pseudomonas syringae pv. Comato D23000.1;
Fproc. Natl. Acad. Sci. U.S.A. 100:10181-1018.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas syringae pv. tomato.
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
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GO; GO:0003988; F:acetyl-CoA C-acyltransferase activity; IEA.
GO; GO:0008415; F:acyltransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
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                                                                                                               InterPro; IPRO12793; Praf.
InterPro; IPRO12793; Praf.
InterPro; IPRO12793; Praf.
InterPro; IPRO2155; Thiolase.
IPRO3008; Thiolase C: 1.
Ffam; PF02008; Thiolase C: 1.
ITGREAMS; TIGRO130; AcCoA-C. Actrans; 1.
ITGREAMS; TIGRO130; AcCoA-C. Actrans; 1.
ITGREAMS; TIGRO130; Praf.
IPROSITE; PS00098; THIOLASE 1; 1.
IPROSITE; PS00099; THIOLASE 2; 1.
IPRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.8%; Score 36; DB 2; I
88.9%; Pred. No. 2.8e+02;
iive 0; Mismatches 1;
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InterPro; IPR02155; Thiolase.
PANTHER; PFHR18919; Thiolase; 1. Pfam; PF02803; Thiolase.
Pfam; PF02803; Thiolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003, integrated into UniProtKB/TrEMBL
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TIGRFAMS; TIGR02430; pcaF; 1.
PROSITE; PS00098; THIOLASE 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QB7X81 PSESM PRELIMINARY; PRT; Q87X81;
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21-FEB-2006, entry version 16.
3-oxoadipyl-CoA thiolase.
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Best Local Similarity
8; Conserve
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087X81 PSE
10 087X81 PSE
10 01-JU
DT 01-JU
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OX PSEUD
RA BEDIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

PubMed=15980861; DOI=10.1038/nbt1110;

Paulsen I.T., Press C.M., Ravel J., Kobayashi D.Y., Myers G.S.A.,

Mavrodi D.V., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,

Durkin A.S., Brinkac L.M., Daugherty S.C., Sullivan S.A.,

Rosovitz M.J., Gwinn M.L., Zhou L., Schneider D.J., Cartinhour S.W.,

Nelson W.C., Weidman J., Watkins K., Tran K., Khouri H., Pierson E.A.,

Pierson L.S. III, Thomashow L.S., Loper J.B.;

Complete genome sequence of the plant commensal Pseudomonas
                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=220664;
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0
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                                                                                                                      Score 36; DB 2; Length 397.
Pred. No. 2.8e+02;
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PROSITE; PS00737; THIOLASE 2; 1.
PROSITE; PS00099; THIOLASE 3; 1.
Acyltransferase; Complete proteome; Transferase.
SEQUENCE 399 AA; 41798 MW; 348D9656362D4129 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGR01930; AcCoA-c-Actrans; 1.
TIGRPAMS; TIGR01930; AcCoA-c-Actrans; 1.
TIGRPAMS; TIGR02430; Ders; 1.
PROSITE; PS00093; THIOLASE_2; 1.
PROSITE; PS00099; THIOLASE_2; 1.
Acyltransferase; Complete proteome; Transferase.
SEQUENCE 400 AA; 41641 MW; 97167PB14DC2639D CRC64;
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GO; GO:0008415; F:acyltransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR012793; PcaF.
InterPro; IPR02155; Thiolase.
PANTHER; PTHR18919; Thiolase; 1.
Pfam; PF02803; Thiolase 2; 1.
Pfam; PF02009; Thiolase 2; 1.
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77.8%; Pred. No. 2.8e+02;
tive 1; Mismatches 1;
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-!- SIMILARITY: Belongs to the thiolase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-2005, integrated into UniProtKB/TrEMBL
                                                                                                                         87.8%; Scor.
88.9%; Pred. No. 4...
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Beta-Ketoadipyl Coh thiolisae (EC 2.3.1.-).
Name-pcaf; Mame-eprl 1319;
Pseudomonas fluorescens (strain Pf-5 / ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-AUG-2005, sequence version 1.
                                                                                                                                                                                                        8; Conservative
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nes 7; Conserv
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'Annotation of the draft genome assembly of Chromohalobacter
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Q4CPA3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isomerase.
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Q4CPA3_TR
       KAYA MARAHATAN M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397; Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J., Bass S., Linher K.D., Weidman J.E., Khouri H.M., Craven B., Bowman C., Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F., McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.; Glonay J.F., Genomiae AR39."; Pharmoniae AR39."; Nucleic Acids Res. 28:1397-1406(2000).
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US DOE Joint Genome Institute (JGI-PGF);
US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Chromohalobacter
salexigens DSM 3043.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical UPF0242 protein TC0906.
/FT1d=PRO_0000216821.
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06-JUN-2003, integrated into UniProtKB/Swiss-Prot...
01-0CT-2000, sequence version 1.
07-MAR-2006, entry version 20.
Hypothetical UPF0242 protein TC0906.
OrderedLocusNames=TC0906;
Chlamydia muridarus, Chlamydiaceee; Chlamydia.
Bacteria; Chlamydiae; Chlamydiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.8%; Score 36; DB 1; Length 419;
88.9%; Pred. No. 2.9e+02;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0B813066FEAC1E06 CRC64;
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13-5EP-2005, sequence version 1.
07-FBB-2006, entry version 2.
Phosphomannownes (EC 5.4.2.8).
Chromohalobacter salexigens DSM 3043.
Chromohalobacter salexigens Gammaproteobacteria;
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NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE002357; AAF39699.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US DOE Joint Genome Institute (JGI-ORNL);
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InterPro; IPR009623; UPF0242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR, A81651, A81651.
GenomeReviews; AE002160_GR; TC0906.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 AA; 48901 MW;
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Best Local Similarity 85...
8; Conservative
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125 KLVERLGQA 133
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NUCLEOTIDE SEQUENCE.
STRAIN=DSM 3043;
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                   STRAIN=MoPn / Nigg;
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                                                                                                                                                                                                                                                    NCBI_TaxID=83560;
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044GN AC
044GN AC
044GN AC
044GN 13-SE
DT 13-SE
DT 07-FE
DE Phosp
GS Chrom
OC Bacte
OC Bacte
OC Bacte
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El-Sayed N.M.A., Myler P.J., Bartholomeu D.C., Nilsson D.,
Bladdin G., Westenberger S.J., Caler E., Delcher A.L.,
Blandin G., Westenberger S.J., Caler E., Cerqueira G.C., Branche C.,
Haas B., Anapuma A., Arner E., Aslund L., Attipoe P., Bontempi B.,
Bringaud F., Burton P., Cadag E., Campbell D.A., Carrington M.,
Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,
Brill K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,
Gull K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,
Naloge S., Koo H., Lacerda D., Levin M.J., Lorenzi H., Louie T.,
Nelson S., Ochaya S., Osoegawa K., Pai G., Parsons M., Pentony M.,
Pettersson U., Pop M., Ramirez J.L., Rinta J., Robertson L.,
Salzberg S.L., Sanchez D.O., Seyler A., Sharma R., Shetty J.,
Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
Charlet S., Ward P.N., Wickstead B., Wortman J., White O.,
                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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"The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J., Aggarwal G., Caler E., Renauld H., Worthey E.A., Hertz-Fowler C.,
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                                              -i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
salexigens DSM 3043.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467 AA; 50576 MW; 7E4AE5CF0C52B4CA CRC64;
                                                                                                                                                                                                                                 GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0004615; P:phosphomannomutase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.8%; Score 36; DB 2; Les
87.5%; Pred. No. 3.2e+02;
ive 1; Mismatches 0;
                                                                                                                                                                                                           EMBL; AAHZ01000008; EAM23978.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                         InterPro; IPR005841; PG/PMM mutase. Pfam; PF02878; PGM PMM 1: 1. Pfam; PF02879; PGM PMM II: 1. Pfam; PF02880; PGM PMM III: 1. Pfam; PF02880; PGM PMM III: 1. PR1NTS; PF0509; PGM PMM IV; 1. PR1NTS; PF0509; PGM PMM IV; 1.
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O-FEB-2006, entry version 2.
Hypothetical protein (Fragment).
ORFNames=TC00.1047053510721.10;
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Matches 7; Conservative
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189 KLIERLGA 196
                                                                                               preliminary data.
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B1-Sayed N.M.A., Myler P.J., Bartholomeu D.C., Nilsson D.,
Aggarval G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,
B1andin G., Westenberger S.J., Caler E., Cerqueira G.C., Branche C.,
B Blandin G., Westenberger S.J., Caler E., Cerqueira G.C., Branche C.,
B Haas B., Anapuma A., Arner E., Aslund L., Attipoe P., Bontempi E.,
B Tingaud F., Burton P., Cadag E., Campbell D.A., Carrington M.,
Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,
B mglund P.T., Fazelina G., Feldblyum T., Ferella M., Frasch A.C.,
A Chall K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,
Machado C.R., McCulloch R., McKenna A., Mizuno Y., Mottram J.C.,
Machado C.R., McCulloch R., McKenna A., Mizuno Y., Mottram J.C.,
Nelson S., Ochaya S., Osoegawa K., Pai G., Parsons M., Pentcony M.,
Pettersson U., Pop M., Ramirez J.L., Rinta J., Robertson L.,
Salzberg S.L., Sanchez D.O., Salver A., Sharma R., Shetty J.,
Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
Von Aken S., Vogt C., Ward P.N., Wickstead B., Wortman J., White O.,
Fraser C.M., Stuart K.D., Andersson B.,
Fraser C.M., Stuart K.D., Andersson B.,
Fraser C.M., Stuart K.D., Andersson B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Ghedin E., Peacock C., Bartholomeu D.C., Haas B.J., Tran A.-N., Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Badger J., Bringaud F., Cadag B., Carlton J.M., Cerqueira G.C., Creasy T., Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivens A.C., Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J., Salzberg S.L., Shallom J., Silva J.C., Sundaram J., Westenberger (White O., Melville S.E., Donelson J.E., Andersson B., Stuart K.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
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                                                                                                                                                                                                                                                                                          "Comparative Genomics of Trypanosomatid Parasitic Protozoa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.8%; Score 36; DB 2; Length 508;
88.9%; Pred. No. 3.4e+02;
live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CL Brener;
El-Sayed N., Bartholomeu D., Haas B.;
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      508 AA; 57226 MW; 8DCCBF424722CFC4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY; PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                            Science 0:0-0(2005).
                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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Q4D4X4;
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                                                                                                                                                                                                                                                             Hall N.;
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040434 TRY
10 404043
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Aggarwal G., Tran A.-1, Myler P.J., Bartholomeu D.C., Nilsson D.,
Aggarwal G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,
Blandin G., Westenberger S.J., Caller E., Cerqueira G.C., Branche C.,
Haas B., Anapuma A., Arrare E., Aslund L., Attipoe P., Bontempi E.,
Arrarer E., Aslund L., Attipoe P., Bontempi E.,
Bringaud F., Burton P., Cadag E., Campbell D.A., Carrington M.,
Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,
Benglund P.T., Fazelina G., Feldblyum T., Ferella M., Frasch A.C.,
A. Kluge S., Koo H., Lacerde D., Levin M.J., Lorenzi H., Louie T.,
A. Kluge S., Koo H., Lacerde D., Levin M.J., Lorenzi H., Louie T.,
Anchado C.R., McCulloch R., McKenna M., Mizuno Y., Mottram J.C.,
Anchor S., Ochaya S., Osoegawa K., Pai G., Parsons M., Pentony M.,
Pettersson U., Pop M., Ramirez J.L., Rinta J., Robertson L.,
Salzberg S.L., Sanchez D.O., Seyler A., Sharma R., Shetty J.,
Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
An Aken S., Vogt C., Ward P.N., Wicktead B., Wortman J., White O.,
The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trypanosoma cruzi.
Bukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                 El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J., Aggarwal G., Caler E., Renauld H., Worthey E.A., Hertz-Fowler C., Ghedin E., Peacock C., Bartholomeu D.C., Haas B.J., Tran A.-N., Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Badger J., Bringaud F., Cadag E., Carlton J.M., Cerqueira G.C., Creasy T., Delcher A.L., Dikeng A., Embley T.M., Hauser C., Ivens A.C., Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J., Salzberg S.L., Shallom J., Silva J.C., Sundaram J., Westenberger S., White O., Melville S.E., Donelson J.E., Andersson B., Stuart K.D.,
                                                                                                                                                                                                                                                                                                                                                                                    CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                     "Comparative Genomics of Trypanosomatid Parasitic Protozoa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.8%; Score 36; DB 2; Length 597;
88.9%; Pred. No. 3.9e+02;
live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                        El-Sayed N., Bartholomeu D., Haas B.;
Submitted (JUN-2005) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AAHK01001015; EAN87570.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 597 AA; 67296 MW; 7D326736CF48E2B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2005, integrated into UniProtKB/TrEMBL.
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STRAIN-CL Brener;
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Science 0:0-0(2005).

NUCLEOTIDE SEQUENCE

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084H43 ALCDF
084H43;
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Q2LC71_9MI
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Distributed under the Creative Commons Attribution-NoDerivs License
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NUCLEOTIDE SEQUENCE.
STRAIN-CL Brener;
B1-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J.,
Aggarwal G., Caler E., Renauld H., Worthey E.A., Hertz-Fowler C.,
Ghedin E., Peacock C., Bartholomeu D.C., Haas B.J., Tran A.-N.,
Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A. Badger J.,
Bringaud F., Cadag E., Carlton J.M., Cerqueira G.C., Creasy T.,
Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivens A.C.,
Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J.,
Salzberg S.L., Shallom J., Silva J.C., Sundaram J., Westenberger S.
White O., Melville S.E., Donelson J.E., Andersson B., Stuart K.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 3.
Putative Rieske non-heme iron oxygenase alpha subunit (Fragment).
Arthrobacter 20. 3YC3.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Micrococcaceae; Arthrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=3YC3; Witzig R., Junca H., Hecht H.-J., Pieper D.H.; Witzig R., Junca H., Hecht H.-J., Pieper D.H.; "Toluene/biphenyl dioxygenase gene diversity in benzene-polluted soils: the environmental importance of the isopropylbenzene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
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                                                                                                                                                                                                                                                                                                                                     "Comparative Genomics of Trypanosomatid Parasitic Protozoa.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CL Brener;
El-Sayed N., Bartholomeu D., Haas B.;
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 791 AA; 88644 MW; 355C4DEAA84FF882 CRC64;
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GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0006725; P:aromatic compound metabolism; IEA.
GO; GO:0006118; P:electron transport; IEA.
Pfam; PF000848; Ring_hydr_doase_A.
Pfam; PF00848; Ring_hydroxyl_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.8%; Score 36; DB 2; 177.8%; Pred. No. 4.9e+02;
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Best Local Similarity 77.00
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483 KLLERIGAA 491
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Q3S4S6;
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SEQUENCE
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Q35456 9MICC
10 Q35456; 9A
AC Q35456; 9D
DT 11-0CT-2U
DF 11-0CT-2U
DF 07-FEB-2U
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                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative Rieske non-heme iron oxygenase alpha subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Witzig R., Junca H., Hecht H.-J., Pieper D.H., Proluene/biphenyl dioxygenase gene diversity in benzene-polluted solls: the environmental importance of the isopropylbenzene
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Alcaligenaceae, Alcaligenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Micrococcineae, Micrococcaceae, Arthrobacter.
                                         Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dioxygenase branch.";
Submitted (DEC-2005) to the EMBL/GenBank/DDBJ databases
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252 AA; 27999 MW; 79BB168D2164D0D9 CRC64;
                                         Score 35; DB 2; 1 Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.4%; Score 35; DB 2; 77.8%; Pred. No. 3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                             85.4%;
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Query Match
Best Local Similarity 77...
7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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81 KAIERLGAA 89
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07-FEB-2006, entry version 18.
10 days lactation, adult female mammary gland cDNA, RIKEN full-length enriched library, clone:D730033M24 product:similar to BCG INDUCED INTECRAL MEMBRANE PROTEIN BIGMO-103 (UP-REGULATED BY BCG-CWS).
Name=S1c39a8;
                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                               01-MAR-2003, integrated into UniProtKB/TrEMBL. 01-MAR-2003, sequence version 1.
                                                                    PRELIMINARY;
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                                                                    QBBUD6 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=W83,

MEDLINE-22829867; PubMed=12949112;

MEDLINE-22829867; PubMed=12949112;

Molson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,

Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,

Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,

Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,

Dewhirst F.E., Fraser C.M.;
                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                               Score 35; DB 2; Length 322;
Pred. No. 3.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of the oral pathogenic bacterium
Porphyromonas gingivalis strain W83.";
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                                                                                                                                                                                                                                                                                                               1; Indels
               EMBL; AY134843; AAN08490.1; -; Genomic DNA.
GO; GO:0016407; F:acetyltransferase activity; IEA.
GO; GO:0008122; P:metabolism; IEA.
InterPro; IPR012147; P Ac Bu_trans.
InterPro; IPR004614; PhpActrans.
InterPro; IPR004614; PhpActrans.
InterPro; IPR004614; PhA_PTB.
Pfam; PF01515; PTA_PTB.
PISSF, PISSF00481; PA_C, Trans; 1.
TIGRFAMS; TIGR00651; Pta; 1.
SEQUENCE 322 AA; 34524 MW; 229F7BD43B2965A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 AA; 35784 MW; AD41C5B42B743DBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=pta; OrderedLocusNames=PG1082; ORFNames=PG_1082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BioCyc; PGIN242619:PG1082-MONOMER; -.
GO; GO:0016407; F:acetyltransferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR012147; P Ac_Bu_trans.
InterPro; IPR012147; P Ac_Bu_trans.
InterPro; IPR002505; PTA_PTB.
InterPro; IPR002505; PTA_PTB.
PRO PRO : PTA_PTB; I.
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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TIGRFAMs; TIGR00651; pta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-2003, sequence version 1. 07-FEB-2006, entry version 12. Phosphotransacetylase.
                                                                                                                                                                                                                                                                   85.4%;
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RA Carninci P., Kasukawa T., Kacayama S., Gough J., Frith M.C., Maeda N., Ra Carninci P., Kasukawa T., Kacayama S., Gough J., Frith M.C., Maeda N., Bajic V. B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Bajic V. B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidnins V., Allen J.E., Davis M.J., Wilming L.G., Aidnins V. A., Allen J.E., Rabesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Rabesi-Impiombato A., Clutterbuck D.R., Choudhary V., Christoffela A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Dalla Gatta G., A. Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Dalla Gatta G., A. Fletcher C.F., Fukuchima T., Engeron P., Fagololin M., Faulkner G., R. Fletcher C.F., Fukuchima T., Engeron M., Ruesch T. K., Hirokawa N., R. Hill D., Humindecki L., Iacono M., Ikeo K., Harokawa N., A. Hill D., Humindecki L., Iacono M., Ikeo K., Hirokawa N., A. Hill D., Humindecki L., Iacono M., Ikeo K., Hirokawa N., A. Kitanura A., Katch M., Kawasawa Y., Kelso J., Kitamura H., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., R. Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., A. Matsuda H., Matsuda Babu M., Madera M., Marchionni L., R. Mottagui-Tabar S., Miki H., Mignon P., Miyake S., Morris K., A. Mottagui-Tabar S., Mishikawa S., Nori F., Ohara O., R. A. Norialiam S., Mishikawa S., Nori F., Ohara O., Shengic C., Sekiguchi K., Sandelin A., Schneider C., Sekiguchi K., Sample C.A., Sandelin A., Schneider C., Sekiguchi K., Sample C.B., Sandelin S., Stupka B., Sulva D., Sinclair B., A. Tammoja K., Shimada H., Shim
STRAIN=CS7BL/6J; TISSUE=Mammary gland; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hispahizaki Y.; Hispahizaki Y.; Mispahizaki Y.; Methods Enzymol. 303:19-44(1999).
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PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005).
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUB=Mammary gland;
PubMed=16141072; DOI=10.1126/science.1112014;
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RA Vorzaki N., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Riadido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Ragikk. Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T., Radadrelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Bladarelli R., Hill D.P., Bult C., Hume D.A., Cackenbush J., Cousins S., An Baldare J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Radasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Ranai A., Kawaji H., Kawasawa N., Jackson I.J., Jarvis B.D., Kanai A., Kaurichi H., Wawasawa N., Jackson I.J., Jarvis B.D., Kanai A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Madcahis L., Maltais L., Marchionni L., McKenzie L., Miki H., Rawashuma T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Ramachandran S., Sandelin A., Schneider C., Semple C.A., Setcu M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Sultana R., Takenaka T., Konno H., Namaira M., Yang I., Yang I., Yang I., Wati K., Kawai J., Aizawa K., Azakawa I., Rukada S., Hara A., Hashizume W., Imotani J., Aizawa K., Shinagawa A., Sakai K., Sasaki D., Shibata K., Shinagawa I., Birney E., Hayashizaki Y., Rayai I., Rayashizaki Y., Itoh M., Kagawa I., Birney E., Hayashizaki Y., Rayasi J., Shibata K., Shinagawa A., Birney E., Hayashizaki Y., Bultana R., Takana I., Mallysis of the mouse transcriptome based on functional annotation of R. Narine A., Aller A., Shinagawa R., Arakawa T., Rohnol R., Narine A., Shinagawa R., Arakawa T., Rukada S., Birney E., Hayashizaki Y., Rayasi J., Shibata K., Shinagawa B., Hayashizaki Y., Rayasi J., Shibata K., Shinagawa B., Hayashizaki Y., Rayasi J., Shibata K., Shinagawa B., Rayashizaki Y., Rayasi J., Shibata K., Shinaga B., Rayashizaki Y., Rayasi J., Shibata K., Shinaga K., Shinaga K.
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RAMAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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A Arakawa T., Hara A., Shibata K., Komo H., Kadchi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

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Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

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Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Bromstein M.J., Bult C., Fletcher C., Fuljita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sakai H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wilttaker C., Wilming L.,

Wannshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordon P., Wang K.H., Weitz C., Mittaker C., Wilming L.,

Wannshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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STRAIN-C57BL/6J; TISSUE-Mammary gland;
MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        annotation of a full-length mouse cDNA collection.";
                                                                                                                                                  MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
"Antisense Transcription in the Mammalian Transcriptome.", Science 309:1564-1566 (2005).
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                   NUCLEOTIDE SEQUENCE.
STRAIN-C57BL/6J; TISSUE=Mammary gland;
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NUCLEOTIDE SEQUENCE
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Distributed under the Creative Commons Attribution-NoDerivs License
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                         NOUZELOID SIZEGENE.

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Haraka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Makamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=16643691, DOI=10.1073/pnas.0504930102;
Feil H., Feil W.S., Chain P., Larimer F., Dibartolo G., Copeland A., Lykidis A., Trong S., Nolan M., Goltsman E., Thiel J., Malfatti S., Loper J.E., Lapidus A., Detter J.C., Land M., Richardson P.M., Kyrpides N.C., Ivanova N., Lindow S.E.; and G., Richardson P.M., Lymparison of the complete genome sequences of Pseudomonas syringae pro. syringae and pv. tomato DC3000.";
Proc. Natl. Acad. Sci. U.S.A. 102:11064-11069(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas syringae pv. syringae (strain B728a).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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77.8%; Pred. No. 3.8e+02;
ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02535; Zip; 1.
SEQUENCE 341 AA; 37465 MW; 90633BFES9004E51 CRC64;
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0046873; F:metal ion transporter activity; IEA.

GO; GO:0030001; P:metal ion transport; IEA.

InterPro; IPR003689; ZIP.
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NCBI_TaxID=205918;
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Hypothetical protein.
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Tissue=Liver;

M. Tissue=Liver;

A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A tluschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max. Schaefer C.F., Bhat N.K.,

Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brahleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Maley J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimmood J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimmishi M. Maran M.A.,

Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Rohner A., Schein J.E., Schauter M.A.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                             Gaps
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01-MAR-2005, sequence version 1.
07-FEB-2006, entry version 9.
Solute carrier family 39 (Metal ion transporter), member 8
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                                                                                                                                                                           85.4%; Score 35; DB 2; Length 393; 77.8%; Pred. No. 4.3e+02; Live 2; Mismatches 0; Indels
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EMBL; CP000075; AAY35405.1; -; Genomic_DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 393 AA; 43107 MW; A784AC3154C1721E CRC64;
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Pfam; PF02535; Zip; 1.
SEQUENCE 462 AA; 50171 MW; 954467170797180F CRC64;
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GO; GO:001620; C:membrane; IEA.
GO; GO:0046873; F:metal ion transporter activity; IEA.
GO; GO:0030001; P:metal ion transport; IEA.
InterPro; IPR003689; ZIP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     462 AA.
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Best Local Similarity 77.8
Matches 7; Conservative
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NIH MGC Project;
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                                                                                                                                                       2589679 segs, 457216429 residues
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                                          model
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ABU54283
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                                                                                                            QLQHQRLVRL 10
                                                         June 29, 2006,
                                                                                                                                                                                                                                                      A_Geneseq_8:*
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 Hypoxia-i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and polynucleotides encoding them for treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to peptides which are partial sequences of stor/lok family proteins. The present sequence is one such peptide. The peptides are useful for producing vaccines for the treatment of cancer, including colon cancer and small-cell lung cancer.
                                                                                                                                                                                                                                                  Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinase-associated signal transduction; diabetes; cancer; obesity; restenosis; bone healing; alopecia; osteoporosis; enviodegenerative disease; autoimmune disease; inflammation; atherosclerosis; skin disorder; central nervous system disease; inflammatory disorder; autoimmune disease; cardiovascular disease.
 Abp65101 F
Abu62101 F
Add18694 F
Abm85767 F
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                                                                              ALIGNMENTS
            ABU62101
ADD18694
ABM85767
 ABP65101
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                                                                                                                                            AAB73129 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 70; 75pp; Japanese
                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000; 2000WO-JP005220
                                                                                                                                                                                                                                                                                                                                                                                 99JP-00222101
                                                                                                                                                                                                                        Tumour antigen peptide #13
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                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                     AAB73129;
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                                                                                                                                                                                                                                                                                                        Identifying compounds for modulating kinase-associated signal transduction and treating cancer, by synthesizing compounds having short sequences identical to native sequences appearing in specific region of a
                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises a method for identifying compounds for the modulation of kinase-associated signal transduction. The invention also comprises a number of peptides which modulate kinase-associated signal transduction. The method of the invention is useful for identifying compounds for the modulation of kinase-associated signal transduction. The kinase-associated signal transduction modulating peptides of the invention are useful for treating idabetes; cancer; obesity; bone healing; alopecia; osteoporoasis; albetes; cancer; obesity; bone healing; alopecia; osteoporoasis; atheroselerosis; skin disorders; central nervous system disease; inflammation; restenosis; and manatory disorders; diseases; and cardiovascular diseases. The peptides ABJ04160 represent the kinase-associated signal transduction modulating peptides
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                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Fig 3; 143pp; English
                                                                                                                     11-DEC-2001; 2001WO-US047443.
                                                                                                                                                      11-DEC-2000; 2000US-00734520
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                                                WO200248336-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11 AA;
                                                                                                                                                                                                                                           Ben-Sasson S;
                Unidentified
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Identifying compounds for modulating kinase-associated signal transduction and treating cancer, by synthesizing compounds having short sequences identical to native sequences appearing in specific region of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention comprises a method for identifying compounds for the modulation of kinase-associated signal transduction. The invention also comprises a number of peptides which modulate kinase-associated signal transduction. The method of the invention is useful for identifying compounds for the modulation of kinase-associated signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              healing; alopecia; osteoporosis; neurodegenerative disease; autoimmune disease; inflammation; restenosis; atherosclerosis; skin disorders; central nervous system disease; inflammatory disorders; autoimmune diseases; and cardiovascular diseases. The peptides ABJ04169 - ABJ04300 represent the kinase-associated signal transduction modulating peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention are useful for treating: diabetes; cancer; obesity; bone healing; alopecia; osteoporosis; neurodegenerative disease; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The kinase-associated signal transduction modulating peptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiovascular disease; dermatological; neuroprotective;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Fig 1; 143pp; English.
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                                                                                                                                   11-DEC-2001; 2001WO-US047443.
                                                                                                                                                                                        11-DEC-2000; 2000US-00734520
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                         WO200248336-A2
                                                                                                                                                                                                                                                                                                                           Ben-Sasson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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Matches
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention discloses compounds, or variants of them, and methods for identifying and synthesising the candidate compounds which comprise a peptide region in the protein kinase A-region (PKA). This region is determined by aligning catalytic subunits of the kinase and PKA-Calpha and determining the sequence of the kinase corresponding to positions 92-109 of PKA-Calpha. The capacity of the compound to modulate the signal transduction associated with the kinase semediate signal transduction in a wide variety of cellular events, such as cell proliferation, differentiation, oncogenesis and immune/inflammatory responses. Enhanced stimulation can lead to proliferative diseases, such as cancer, arteriosclerosis, psoriasis and septic shock. The methods and compositions are useful for detecting A-region ligands and for treating a composition of a signal transduction associated with a kinase, where the kinase from which the Aregion and where the kinase associated with the signal transduction, and where the disease is diabbetes, cancer, with the signal transduction, and where the disease is diabbetes, cancer, with the signal transduction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   obesity, restenosis, tissue remodeling including improved bone healing, prevention of alopecia, reduced scarring, osteoporosis, neurodegenerative disease, autoimmune disease, inflammation, atherosclerosis, skin disorders, diseases of the central nervous system and cardiovascular diseases. The sequences presented in ABUS41215-ABUS4336 are the A-region peptides disclosed in the invention which are N-myristylated and C-
                                                                                                                                                                                                                                                                                                                                         Identifying candidate compounds for the modulation of kinase-associated signal transduction, useful for treating diabetes, cancer, obesity, osteoporosis, autoimmune disorders, atherosclerosis and cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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heurodegenerative disease; autoimmune disease; inflammation;
atherosclerosis; skin disorder; central nervous system disease;
inflammatory disorder; autoimmune disease; cardiovascular disease.
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                   26-SEP-2002.
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100.0%; Score 49; DB 5; Length 18; 100.0%; Pred. No. 0.054; Live 0; Mismatches 0; Indels

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The invention discloses compounds, or variants of them, and methods for identifying and synthesising the candidate compounds which comprise a peptide region in the protein kinase A-region (PKA). This region is so determined by aligning catalytic subunits of the kinase and PKA-clapha and determining the sequence of the kinase corresponding to positions 92-109 of PKA-Calpha. The capacity of the compound to modulate the signal transduction associated with the kinase sea corresponding to positions 92-109 of PKA-Calpha. The determined. Protein kinases mediate the signal transduction in a wide variety of cellular events, such as cell transduction in a wide variety of cellular events, such as cell transduction, differentiation, oncogenesis and immune/inflammatory responses. Enhanced stimulation can lead to proliferative diseases, such as cancer, arteriosclerosis, psoriasis and septic shock. The methods and compositions are useful for detecting A-region ligands and for treating a disease where a therapeutically beneficial effect may be evident by the modulation of a signal transduction, and where the disease associated with the signal transduction, and where the disease associated with the signal transduction, and where the disease is diabettes, cancer, obesity, restenosis, tissue remodeling including improved bone healing, prevention of alopecia, reduced scarring, osteoporosis, neurodegenerative diseases, autoinmune disease, inflammation, atherosclerosis, skin diseases, autoinmune disease, inflammation, atherosclerosis, skin diseases. The sequences presented in ABUS4155-ABUS4336 are the A-region and cardiovascular diseases. The sequences presented in ABUS4155-ABUS4336 are the A-region and cardiovascular diseases disconsed in the invention which are N-myristylated and C-pariety and and cardiovascular and cardiovas
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                                                                                                                                                                                                                                                                                                                                                                     Identifying candidate compounds for the modulation of kinase-associated
                                                                                                                                                                                                                                                                                                                                                                                                        signal transduction, useful for treating diabetes, cancer, obesity, osteoporosis, autoimmune disorders, atherosclerosis and cardiovascular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Fig 1; 79pp; English.
                                                                                                                                              (CHIL-) CHILDRENS MEDICAL CENT
                                                                     11-DEC-2000; 2000US-00734520.
11-DEC-2001; 2001US-00012034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                            WPI; 2003-110601/10.
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                                                                                                                                                                                                                       Ben-Sasson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5958784-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular scaffold; nuclear hormone receptor; TNF receptor; G-protein coupled receptor; methyl transferase; ligase; LCK tyrosine kinase; enzyme.
                                                                                                                                                                                                                                                                                                                                         Predicting the folded structure of proteins.
                                                                                                                                                                                                                                                                                                                                                                                                       Col 253-256; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR88385 standard; protein; 263 AA.
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16-SEP-2002; 2002US-041139BP.
20-SEP-2002; 2002US-0412341P.
02-JAN-2003; 2003US-0437929P.
                          92US-00857224
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                                                                                        92US-00857224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 QLQHQRLVRL
                                                                                                                                                                                                                                                                              WPI; 1999-570766/48
                                                                                                                                                  SA.
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                                                                                                                                                  (BENN/) BENNER
                                                                                    25-MAR-1992;
                          25-MAR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                   Benner SA;
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                                                                                                     The present invention relates to a method of designing a ligand binding to a target molecule. The method involves identifying as molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesising ligand. The invention is useful for designing drug products and for designing ligand binding to target molecules such as nuclear hormone receptors, TNF receptors, G-protein coupled receptors, methyl transferases, ligases, etc. The present sequence is the LCK tyrosine kinase protein. This sequence is used to illustrate the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Wild-type D substituted with N. This position is 364 in the full-length sequence (see ABR56202 for the
molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme Src-family protein tyrosine kinase; T-cell; immune response; mutein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant Lymphocyte Cell Kinase, Lck, fragment (237-501, D364N)
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                                                                                                                                                                                                                                                                                                                                              DB 8; Length 263;
                                                                                                                                                                                                                                                                                                                                                       Hirst GC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.8
Mismatches
                                                                    Disclosure; SEQ ID NO 24; 186pp; English.
                                                                                                                                                                                                                                                                                                                                       100.0%; Score 49; 100.0%; Pred. No.
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nes 10; Conservative
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                                    synthesizing ligand
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                                                                                                                                                                                                                                                                                                       Sequence 263 AA;
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                                                                                                                                                                                                                                                                      invention.
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             The present invention relates to a crystalline polypeptide (I), comprising the catalytic domain of human Lymphocyte Cell Kinsae (Lck) protein. Lck is a Src-family protein tyrosine kinsae expressed primarily in T-cells and plays an essential role in immune response. (I) is useful for identifying a compound which is an inhibitor of human Lck protein. The present sequence is a mutated fragment of the human Lck sequence, which approximately comprises the catalytic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type D substituted with N. This position is 364 in the full-length sequence (see ABR56202 for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a crystalline polypeptide (I), comprising the catalytic domain of human Lymphocyte Cell Kinsae (Lck) protein. Lck is a Src-family protein tyrosine kinase expressed primarily in T-cells and plays an essential role in immune response. (I) is useful for identifying a compound which is an inhibitor of human Lck protein. The present sequence is a mutated fragment of the human Lck sequence, which approximately comprises the catalytic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, protein co-ordinate data, Lymphocyte Cell Kinase; Lck; enzyme, Src-family protein tyrosine kinase; T-cell; immune response; mutein;
                                                                                                                                                                                                                Gaps
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                                                                                                                                                                              100.0%; Score 49; DB 7; Length 265; 100.0%; Pred. No. 0.87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 ABR56204 standard; protein; 271 AA.
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                                                                                                                                                                                                                                                                               QLQHQRLVRL
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                                                                                                                                                                                               Local Similarity
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                                                                                                                                               Sequence 265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                  ABR56204;
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                                                                                                                                                                                                                                                                                 28
                                                                                                                                                                                Query Match
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The invention relates to a new kinase scaffold library comprises at least 1 set of compounds, each set comprising at least 1 N-heterocyclic compound of formulae (1)-(VII) given in the specification. Also included are a system for fitting compounds in binding sites of protein kinases (comprising at least 1 collection of electronic representations of [I]-(VII), where the scaffold library is embedded in a computer device and the electronic representations of the compounds can be selectively cerrieved and functionally connected with computer software adapted to fit electronic representations of compounds in an electronic representations of which compounds can be selectively cerrieved and functionally connected with computer software adapted to fit electronic representations of compounds in an electronic conficulation of a binding site of a kinase), obtaining improved ligands binding to the kinase with greater for specificity for the particular kinase (which comprises has greater for specificity for the particular kinase than (I)-(VII)), developing ligands specific for a particular kinase (which comprises has greater for specificity for the particular kinase than (I)-(VII), developing ligands binding to a kinase (which comprises of the corystals with the kinase, identifying chemical structures of the scaffolds, that, when modified, change the binding affinity and/or specificity between the scaffold and kinase and synthesizing a ligand in which are least 1 chemical structures of the scaffolds is modified).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kiname; protein co-ordinate data; protein structure; cancer; cytostatic; neoplasm; inflammation; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New scaffold library used for identifying and developing ligands for protein kinases and treating kinase associated disorders e.g. cancer, comprises set of compounds comprising N-heterocyclic compounds.
                                                                                                     100.0%; Score 49; DB 7; Length 271; 100.0%; Pred. No. 0.89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bremer RE, Gillette SJ, Hurt CR, Ibrahim PL;
                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catalytic domain of PIM kinase-like protein LCK.
                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 170-174; 236pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADY85449 standard; protein; 279 AA.
                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-SEP-2004; 2004WO-US030360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-SEP-2003; 2003US-0503277P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                             64 OLOHORLVRL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PLEX-) PLEXXIKON INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2005-273155/28.
                                                                                                                                                                                                                                                          1 QLQHQRLVRL
                               Sequence 271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2005028624-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zuckerman RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Artis DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADY85449;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADY85449
ID ADY85,
XX
AC ADY85,
XX
DE Catal.
XX
KW Kinas,
KW Kinas,
KW Kinas,
XX
KX
Catal.
XX
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X S
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kinase (which comprises determining if a derivative compound including a core structure (I) (VII) binds to the kinase with changed binding affinity and/or specificity, a co-crystal of a kinase and a binding compound (I) (VII), preparation of co-crystals of Pin-1 with (I) (VII), identifying potential kinase binding compounds (which comprises fitting electronic representations of (I) (VII) in an electronic representation of a kinase binding compound to an attachment component (which comprises identifying energetically allowed sites) component at the allowed site), modified compounds (comprise) (I) (VIII) and attachment of the compound or derivative to the attachment (I) (VIII) and attachment at the allowed site), modified compounds (comprising (I) (VIII) comprising conserved residues matching at least on of Pim-1 residues 49, component at the allowed site), and developing a ligand for a kinase comprising conserved residues matching at least on of Pim-1 residues 49, component an attached linker group, and developing a ligand for a kinase comprising conserved residues matching at least on of Pim-1 residues 49, component and the factor receptor, endothelial growth factor receptor, endothelial growth factor receptor, endothelial growth factor receptor, endothelial growth factor receptor, condition associated with abnormal kinase activity e.g. cancer, condition associated with abnormal kinase activity e.g. cancer, condition associated with abnormal kinase activity and specificity towards kinase. The co-crystals of kinase activity and specificity or a condition associated with abnormal kinase activity e.g. cancer, chinase resulting in ligands having high affinity and specificity towards kinase. The co-crystals of kinase and the binding compound are of sufficient size and quality to allow structural determination of at least constitutions amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein kinase homologue; human; PKH; diagnosis; therapy; cancer; AIDS; autoimmune disorder; inflammatory disorder; reproductive defect; asthma; diabetes mellitus; infertility; ovulatory defect; endometriosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Azimzai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding a human protein kinase homolog useful for
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 49; DB 9; Length 279; 100.0%; Pred. No. 0.92; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein kinase homologue, PKH-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY76750 standard; protein; 346 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guegler KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00173581.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polycystic ovary syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QLQHQRLVRL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 QLQHQRLVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JL, Yue H,
Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-136321/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ86794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 279 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US6013455-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY76750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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This sequence represents a human protein kinase homolog (PKH) of the invention. The PKH sequences may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PKH expression such as cancers, autoimmune/inflammatory disorders and reproductive defects. They may be used to treat disorders associated with decreased PKH expression such as cancers (e.g. lymphoma, melanoma and cancers of the breast lung and prostate), autoimmune/inflammatory disorders (e.g. AIDS, asthma and diabetes mellitus), and reproductive defects (e.g. AIDS, asthma and diabetes mellitus), and reproductive defects (e.g. AIDS, asthma and diabetes mellitus), and reproductive defects (e.g. AIDS, asthma and diabetes mellitus), so administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of syndrome). The DNA may be administered to treat diseases by rectifying mutations or fell-ions in a patient's genome that affect the activity of product PKH, according to standard recombinant DNA methodology, by produce PKH, according to standard recombinant DNA methodology, by produce PKH, according to standard recombinant DNA methodology, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. Conversely, antisense mutation of proventing their expression. The DNA, and antisense sequences may also be used to study the expression. The DNA, and antisense sequences may also be used to study the expression and function of ERH polypeptides and duantitate the presence of similar nucleic acid sequences in samples, and hence which patients may be in need of restorative therapy. They may also be used to study the expression and function of ERH antibodies and attained the presence of similar nucleic acid sequences in calculate the production of antibodies against PKH and in assays to identify.

CHALLED PKH antibodies and pKH antagonists may also be used to down regulate for detecting the presence of PKH expression and activity. The samiles
   preventing, diagnosing and treating cancer, autoimmune/inflammatory
                                 disorders and reproductive defects
                                                                                              Claim 1; Col 47-50; 38pp; English.
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100.0%; Score 49; DB 3; Length 346; 100.0%; Pred. No. 1.2; 0; Indels Mismatches ; Conservative 131 QLQHQRLVRL 140 1 QLQHQRLVRL 10 Local Similarity tes 10; Conserv Sequence 346 AA; Query Match Matches 셤 ઠે

AAE06208 standard; protein; 346 AA. (first entry) 25-SEP-2001 AAE06208; RESULT 12 AAE06208

Human protein kinase homolog-3 (PKH-3).

Human, protein kinase homolog-3; PKH-3; cytostatic, protein therapy; vaccine; immunosuppressive; antisclerotic; antiabortive; adenocarcinoma; Acquired Immune deficiency Syndrome; AlDS; melanoma; cancer; bone; liver; breast; autoimmune disorder; multiple sclerosis; drug screening; anaemia; Crohn's disease; ectopic pregnancy; tubal disease; inflammatory disorder; reproductive disorder; polycystic ovary syndrome; asthma

Homo sapiens

125. .333 /note= "Signature sequence" Location/Qualifiers

Region

US6264947-B1.

24-JUL-2001.

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The present sequence is human protein kinase homolog-3 (PKH-3). Human protein kinase homologs (PKH) and their cDNA molecules are used in the prevention, diagnosis and treatment of diseases associated with increased or decreased expression of PKH. Examples of such disorders include, cancer (e.g. adenocarcinoma, melanoma and bone, breast and liver cancer), ancer (e.g. adenocarcinoma, asthma, Crohn's disease and multiple sclerosis) and reproductive disorders (e.g. tubal disease, ectopic pregnancy and reproductive disorders (e.g. tubal disease, ectopic pregnancy and colycystic ovary syndrome). PKH, its catalytic or immunogenic fragment are used for screening libraries of compounds in any of the drug screening techniques. PKH nucleic acids are used to generate hybridisation probes useful in mapping the naturally occurring genomic sequences. PKH are also used as antigens in the production of antibodies against protein kinases (PK) and in assays to identify modulators of PK expression and activity. PKH is also used in protein therapy
                                                                                                                                                                                                                                                                                 diagnosing and treating cancers, autoimmune/inflammatory disorders and reproductive disorders.
                                                                                                                                 Corley NC;
                                                                                                                                                                                                                                                           Human protein kinase proteins and homologs, useful for preventing,
                                                                                                                                 Guegler KJ,
                                                                                                                                 Yue H,
                                                                                                                            Hillman JL,
                                                                                                                                                                                                                                                                                                                                               Claim 1; Col 47-50; 38pp; English.
                                                                                                                                 Bandman O, Tang YT, Hillman JL
Gorgone GA, Azimzai Y, Lu DAM;
  99US-00420915.
                                            98US-00173581
                                                                                      (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                               2001-450728/48
                                                                                                                                                                                                                     N-PSDB; AAD11845.
20-OCT-1999;
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Gaps . 0 100.0%; Score 49; DB 4; Length 346; 100.0%; Pred. No. 1.2; 0; Indels 0; Mismatches Query Match Best Local Similarity 100.

Sequence 346 AA;

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131 OLÓHÓRLVRĽ 140 ò 셤

1 QLQHQRLVRL 10

; 0

Gaps

; 0

Human protein kinase homologue from clone 507669. 08-NOV-2002 (first entry) ABB84435;

ABB84435 standard; protein; 346 AA.

RESULT 13 ABB84435 Protein kinase homologue; PKH; cytostatic; immunosuppressive; antifungal; antiinflammatory; antiallergic; antiasthmatic; antianaemic; antidiabetic; antiarteriosclerotic; antithyroid; dermacological; nephrocropic; human; antigout; thyromimetic; nootropic; osteopathic; antiarthritic; allergy; antithrumatic; ophthalmological; antiucer; antiarthritic; allergy; antiprotozoal; antiparasitic; antihelmintic; ankylosing spondylitis; antiprotozoal; antiparasitic; antihelmintic; ankylosing spondylitis; adult respiratory distress syndrome; AIDS; Addison's disease; anyloidosis; autoimmune haemolytic anaemia; autoimmune thyroiditis; bronchitis; cholecystitis; contact dermatitis; Crohn's disease; atopic dermatitis; dermatcomyositis; diabetes melitus; emphysema; atrophic gastritis; gout; glomerulonephritis; diabetes melitus; emphysema; atrophic gastritis; gout; glomerulonephritis; Goodpasture's syndrome; Graves' disease, psoriasis; Hashimoto's thyroiditis; hypereosinophilia; irritable bowel syndrome; multiple sclerosis; myschenia gravis; myocardial inflammation; uveitis; pericardial inflammation; osteoarthritis; osteoporosis; pancreatitis; polymyositis; Raiter's syndrome; hetwated atribitis; scleroderma; SLE; Sjogren's syndrome; systemic bupus erythematosus; systemic sclerosis; thrombocytopenic purpura; ulcerative colitis; Werner syndrome; infection;

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ovulatory defect; endometriosis; oestrous; menstrual cycle; gene therapy; uterine fibroid; autoimmune disorder; polycystic ovary syndrome; enzyme; ovarian hyperstimulation syndrome; ectopic pregnancy; teratogenesis;
     extracorporeal circulation; infertility; tubal disease;
haemodialysis;
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Homo sapiens

US2002081290-A1

27-JUN-2002

30-MAY-2001; 2001US-00870962.

98US-00173581. 99US-00420915 15-OCT-1998; 20-OCT-1999;

(INCY-) INCYTE PHARM INC.

Corley NC; Guegler KJ, Yue H, Hillman JL, Y, Lu DAM; Bandman O, Tang YT, Hi Gorgone GA, Azimzai Y,

WPI; 2002-655433/70.

N-PSDB; ABQ76288

Nucleic acids encoding a human protein kinase homolog useful for preventing, diagnosing and treating cancer, autoimmune/inflammatory disorders and reproductive defects.

Claim 47; Page 27; 43pp; English.

Copyagetides which have cytostatic, immunosuppressive, antilitlammatory, antiallergic, antiasthmatic, antianaemic, antiarteriosclerotic, antiallergic, antiasthmatic, immunosuppressive, antiallergic, antiasthmatic, mostropic, antiarthritic, antithoratic, nootropic, osteopathic, antiarthritic, antithematic, cophthalmological, antiparasitic and antiarthritic, antithematic, cophthalmological, antiparasitic and antiarthritic activity. The polypeptide is used for treating a disease or condition associated with decreased expression of functional PKH The polypeptide is used to screen for agonists and antagonists of PKH whitch can also be used in disease.

Corputed immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, antivolumne haemolytic anaemia, asthma, atherosclerosis, autoimmune thyroiditis, bronchitis, cholecystitis, cancer, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, antoimmune thyroiditis, bronchitis, cholecystitis, cancer, contact dermatitis, crohn's disease, atopic dermatitis, dermatomyositis, disease, atopic dermatitis, dermatomyositis, cholecystitis, contact dermatitis, arritable bowel syndrome, multiple sclerosis, thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, thyroiditis, osteoporosis, pancreatitis, polymyositis, psoriasis, cereoarthritis, osteoporosis, pancreatitis, polymyositis, polymyositis, psoriasis, cereoarthritis, osteoporosis, pancreatitis, molymositis, pancreatitis, protection, viral, brancolalysis, and extracorporeal circulation, viral, brancolalysis, and extracorporeal circulation viral, brancolalysis, and extracorporeal circulation viral, brancolalysis, and extracorporeal circulation syndrome, economical and paramited and paramited solutions of the ostroors, undermy defects, and endometrial and ovarian tumours, uterine fibroids, autoimmune disorders, ectopic prequencies, and teratogenesis. The polypeptides of the invention contact dermatory. This sequence represents a PKH from clone of fr from non-adherent peripheral blood mononuclear cells collected from a pool of male and female donors This invention describes a novel protein kinase homologue (PKH)

Sequence 346 AA;

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                             Gaps
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100.0%; Score 49; DB 5; Length 346; 100.0%; Pred. No. 1.2;
                             0; Indels
                             0; Mismatches
              Best Local Similarity 100.
Matches 10; Conservative
 Query Match
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Gietzen D;
                                                                                                                                       gene therapy; human diagnostic and therapeutic polynucleotide; dithp
                                                                                                                                                                                                                                                                                                                                            Kirton ES
                                                                                                                                                                                                                                                                                                                         Gerstin EH;
                                                                                                                                                                                                                                                                                      Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin E Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton I Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gettin S, Shi X, Suarez CJ;
                                                                                                                   Human diagnostic and therapeutic pprotein SEQ ID NO:3229.
                                                       ABM82980 standard; protein; 355 AA.
                                                                                                                                                                                                                     12-SEP-2003; 2003WO-US028227.
                                                                                                                                                                                                                                         12-SEP-2002; 2002US-0410259P. 12-SEP-2002; 2002US-0410260P.
                                                                                               18-NOV-2004 (first entry)
131 OLOHORLVRL 140
                                                                                                                                                                                                                                                                                                                Mooney ... Stevens KA, Blancus... Stevens KA, Anderson S Peralta CH, Anderson S ... Spiro PA, ...
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-329368/30.
                                                                                                                                                                                                                                                                        (INCY-) INCYTE CORP.
                                                                                                                                                                               WO2004023973-A2.
                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                  25-MAR-2004.
                                                                            ABM82980;
                                      RESULT 14
                                               ABM82980
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New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosting a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.

N-PSDB; ACN41632

Claim 27; Page; 190pp; English.

The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorders, autoimmune/inflammatory disorders, developmental disorders, or disorder, neurological disorders, dastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

Sequence 355 AA;

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Gaps
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0
100.0%; Score 49; DB 8; Length 355; 100.0%; Pred. No. 1.2; ive 0; Mismatches 0; Indels
                                  10; Conservative
                  Local Similarity
   Query Match
                                 Matches
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modulates Tlymphocyte activation. The method comprises contacting a Cell comprising an A-raf-1 or TCPTP/PTRN2 polypeptide with a compound, where the A-raf-1 or TCPTP/PTRN2 polypeptide with a compound, call comprising an A-raf-1 or TCPTP/PTRN2 polypeptide with a compound, acid that hybridises to a nucleic acid encoding a polypeptide having a sequence selected from two 606-amino acid sequence and a 415-amino acid sequence given in the specification. The method of the invention has immunosuppressive, antiasthmatic, antiallargic, and antiinflammatory activity. The method is useful for identifying compounds that modulate lymphocyte activation and migration, and for monitoring changes in cell surface marker expression, cytokine production, antibody production, proliferation and differentiation, and apoptosis, using either cell lines or primary cells. The A-raf-1 or TCPTP/PTRN2 proteins may be used as activation and migration, eag. for the treatment of diseases in which modulation of the immune response is desired such as delayed type hypersensitivity reactions, asthma, allergies, graft versus host disease, and acute and chronic inflammation. Modulators of lymphocyte activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying a compound that modulates T lymphocyte activation, useful for monitoring changes in cell surface marker expression, comprises contacting a T cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with
                                                                                                                                                                                                                                                                          Human; T lymphocyte activation; T-cell; A-raf-1; TCPTP/PTPNZ; asthma; immunosuppressive; antiasthmatic; antiallergic; antiinflammatory; lymphocyte activation; lymphocyte migration; cytokine production; cell surface marker expression; antibody production; apoptosis; allergy; antibody proliferation; antibody differentiation; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to a novel method for identifying a compound that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        are useful for treating disorders related T and B cell activation migration. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao H;
                                                                                                                                                                                                                                                                                                                                                                              graft versus host disease; inflammation; ps6lck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pardo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 64; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Masuda E,
                                                                                                                  ABR59690 standard; protein; 363 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2002; 2002WO-US031618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-2001; 2001US-0327212P
                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li C, Liao XC,
(RIGE-) RIGEL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-363276/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003029277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ACC81082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                  25-JUL-2003
                                                                                                                                                                                                                                         Human p561ck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a compound
                                                                                                                                                           ABR59690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chu P,
                                                                                                  ABR59690
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The invention relates to a compound targeted to a nucleic acid molecule encoding the human lymphocyte specific tyrosine kinase (Lok) polypeptide. The compound is an antisense oligonucleotide that specifically hybridises with the nucleic acid and inhibits expression of the polypeptide. The antisense oligonucleotide comprises at least one modified internucleoside linkage i.e. a phosphorothioate linkage, at least one modified sugar moiety, preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase comprising a 5-methylcytosine. The antisense compounds are useful for modulating the expression of the human Lck polypeptide and in preparation of a composition for treating human Lck polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preventing and/or treating diseases or conditions associated with aberrant expression or activity of Lck, such as hyperproliferative
                                                                                                                                                                                                       Human lymphocyte specific tyrosine kinase (Lck) polypeptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense oligonucleotide compounds, useful for diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 49; DB 8; Length 363; 100.0%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                   antisense oligonucleotide, phosphorothioate linkage, 2'-O-methoxyethyl sugar moiety; 5-methylcytosine, hyperproliferative disorder; cancer; cytostatic; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,
0
                                                                                                                                                                                                                                     Human; lymphocyte specific tyrosine kinase; Lck;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 17; SEQ ID NO 75; 40pp; English.
                                                                                                        ADP48375 standard; protein; 363 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR14201 standard; protein; 417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                               10-DEC-2002; 2002US-00316515.
                                                                                                                                                                                                                                                                                                                                                                                                                                              10-DEC-2002; 2002US-00316515.
                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                294 QLQHQRLVRL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 ÓLÓHÓRLVRL 303
1 QLQHQRLVRL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QLQHQRLVRL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Freier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-498280/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADP48372.
                                                                                                                                                                                                                                                                                                                                                  US2004116365-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 363 AA;
                                                                                                                                                                        09-SEP-2004
                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borchers AH,
                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders.
                                                                                                                                         ADP48375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR14201;
                                                                           RESULT 16
ADP48375
ID ADP48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 17
AAR14201
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8
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Gaps

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100.0%; Score 49; DB 6; Length 363; 100.0%; Pred. No. 1.2; ive 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 10; Conservative

Query Match

a

Key

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The invention discloses isolated human nucleic acid alternative splicing variants that are all tumour-involved genes (TIGS). The nucleic acids and polypeptides are useful for determining the level of a nucleic acid or polypeptide in a biological sample, for deterting a variant nucleic acid or polypeptide sequence in a biological sample, for determining the level of variant nucleic acid or polypeptide sequences in a biological sample and for variant between the level of variant sequence in a first biological sample and for raising antibodies. A pharmaceutical composition comprising a carrier and the nucleic acid, is useful for the variant diseases (e.g. cancer) that can be ameliorated or cured by increasing the level of the encoded protein. The nucleic acids are also useful for diagnostic purposes, especially for detecting cancer or a predisposition to cancer, for evaluating the state or aggressiveness of cancer disease, in basic research, for understanding the physiological function of the original TiG in targeting or developing pharmaceuticals, for distinguishing various stages in the life cycle of the same type of cells which may be helpful for the development or or predispositions cancer stages in which cell cycle is noncommal, for determining mutations in tumour-involved genes and in gene therapy. The polypeptides are useful for identifying compounds capable of binding to the variant product and modulating its activity and for modulating endochelial differentiation and proliferation, as well as to modulate apoptosis either ex vivo or in vivo. The sequences presented in Assistants (NV) 1-36 proteins of the TIGs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian; nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic; immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
                                                                                                                                                                                                                                                                                           Novel nucleic acid sequence, which is an alternative splicing variant of tumor involved genes, useful for detecting cancer, predisposition to cancer, for evaluating cancer state and in gene therapy for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 49; DB 5; Length 437; llarity 100.0%; Pred. No. 1.5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                       Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 68-69; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC99048 standard; protein; 458 AA
                                                                                                                                                                                       Romano C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human KPP protein - SEQ ID 1.
                   14-MAR-2000; 2000IL-00135402.
16-MAY-2000; 2000IL-00136154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 QLQHQRLVRL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QLQHQRLVRL 10
                                                                                                     DAVID A.
ROMANO C.
BERNSTEIN J.
                                                                                                                                                                                       David A,
                                                                                                                                                                                                                                 WPI: 2002-635679/68
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nes 10; Conserv
                                                                                 LEVINE Z.
                                                                                                                                                                                                                                                       N-PSDB; ABS65202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-2004
                                                                                                                                                                                       Levine Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disclosed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC99048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                     (DAVI/)
(ROMA/)
(BERN/)
                                                                                 (LEVI/)
                                                                                                                                                                                                                                                                                                                                                                 cancer
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Matches
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fused polypeptide - has amino acid sequence of beta-galactosidase with a LCK gene conjugated to the N-terminal via DNA having multi-cloning site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          galactósidase gene fused with the lck gene. It is produced by E.coli transformed with a recombinant vector (see AAQ13983). It is useful for producing an antibody specifically immunoreactive with only a lck genederived polypeptide in T cells. The antibody may recognise lck genederived polypeptides in human cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical composition; cancer; diagnostic; tumour; gene therapy; endothelial cell; cell differentiation; cell proliferation; apoptosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence consists of the N-terminal amino acids of the beta-
                                                           (Beta-galactosidase N-terminal) - (1ck gene prod.) fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour involved gene (TIG) splice variant protein, NV-3.
                                                                                                                                                                                                             1. .26
/note= "beta-galactosidase fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; splice variant; tumour-involved gene; TIG;
                                                                                                                                                                                                                                                                         /note= "lck gene polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 49; 100.0%; Pred. No.
                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG79672 standard; protein; 437 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 4,2; 15pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                         89JP-00338268
                                                                                                                                                                                                                                                                                                                                                                                                                                               89JP-00338268
                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TOKU ) TOKUYAMA SODA KK
                                                                                                                                                                                                                                                       27. .417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 QLQHQRLVRL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLQHQRLVRL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-300980/41.
                                                                                                     Multi-cloning site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ14201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 417 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2002086384-A1
                                                                                                                                                                                                                                                                                                                   JP03201994-A
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                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                               28-DEC-1989;
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                   13-DEC-1991
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                                                                                                                                                                                                                                                                                                                                                               03-SEP-1991
                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Н
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RESULT 18

à g ABG79672 1D ABG7 AC ABG7 XX XX XX XX XX XX XX XW Whuming phaning widen wi

Human; lymphocyte kinase; protein co-ordinate data; lck; crystal.

(first entry)

02-MAR-2001

AAB37700:

Human lymphocyte kinase.

19-MAY-2000; 2000WO-US013881.

WO200070030-A1.

23-NOV-2000.

Homo sapiens.

99US-0134965P

19-MAY-1999;

(KINE-) KINETIX PHARM

WPI; 2000-687708/67

Zhu X;

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', Duggan BM;
'd AE, Griffin JA;
'ee EA, Lee SY;
DB, Arvizu CS;
'. Tang YT;
'Yao MG, Yue H;
                osteopathic; antiarthrific; antiparasitic; antihelminthic; antipsoriatic; uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial; virucide; protozoacide; fungicide; kinase; phosphatase; KPP; cancel proliferative disorder; atherosclarosis; cirrhosis; hepatitis; cancer; developmental; mental retardation; neurological; haltinamatory; Crohn's; alzaheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's; diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan; helminthic infection; transgenic; gene therapy; human; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides, agonists and antagonists are useful for diagnosing, treating or preventing cell proliferative disorders such as atherosclerosis, cirrhosis, hepatitis and cancer, developmental disorders e.g. mental retardation, neurological disorders including Alzheimer's disease and Parkinson's disease and inflammatory disorders such as Crohn's disease and diabetes mellitus and finally, viral, bacterial, fungal, parasitic, protozoan or helminthic infections. Furthermore, the polymucleotides encoding KPP may be useful for creating transgenic animals to model human disease, as well as during gene therapy procedures. The current sequence is that of the human KPP protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel isolated polypeptide which is a human
antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disor (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Grif Gururajan R, Hafalia AJA, Khan FA, Lial PG, Lee EA, Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 1; 424pp; English.
                                                                                                                                                                                                                                                                                                                                                    2001US-0345474P.
2001US-0343910P.
2001US-0333098P.
                                                                                                                                                                                                                                                                                                                                                                                                             16-NOV-2001; 2001US-0332424P.
                                                                                                                                                                                                                                                                                                                17-OCT-2002; 2002WO-US033723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-403214/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADC99100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 458 AA;
                                                                                                                                                                                                                                      WO2003033680-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zebarjadian Y;
                                                                                                                                                                                                                                                                                                                                                    19-OCT-2001;
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         02-NOV-2001;
13-NOV-2001;
                                                                                                                                                                                                                                                                            24-APR-2003
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Crystal of a protein-ligand complex for identifying kinase inhibitors, comprises a truncated lymphocyte kinase and a ligand, and diffracts X-rays to determine atomic coordinates at a resolution greater than 5

Claim 1; Page 434-5; 438pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enzymes involved in their pathology
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es 10; Conservative
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Gaps

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100.0%; Score 49; DB 7; Length 458; 100.0%; Pred. No. 1.5; tive 0; Mismatches 0; Indels

Conservative

Local Similarity les 10; Conser

Matches

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Query Match

AAB37700 standard; protein; 508 AA.

RESULT 20 AAB37700 ID AAB3 XX

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which respresents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a carrier issue of the polynucleotide sequence that is differentially expression of the polynucleotide sequence the is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypucleotides of ridentifying a compound or small molecule that regulates the activity in an animal of one or more of the polypucles of the identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating bain and a pharmaceutical composition comprising the one or more composition computation the compound that molypeptides or their antibodies. The polypucleotide or the compound that molypeptides or their antibodies. The polypucleotide or the compound that molypeptide in an animal merve injury (fund), changed medicament for treating pain (e.g. spinla segmental nerve injury (fund), an animal decomposition comprising a method or decomposition comprising a method or decomposition comprising a method or decomposition computation or or more or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page; 1017pp; English.
                                                                                                                          14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
                                                                          14-AUG-2002; 2002WO-US025765.
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                                                                                                                                                                                                                             (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
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GENBANK; P06239.
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comprising the vector comprising the movel polynuclectide, a host cell comprising the vector, a method for identifying a nuclectide dequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynuclectide sequence that increases or decreases the expression of the polynuclectide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynuclectide sequence which is differentially expression of a polynuclectide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynuclectides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of polypeptides or their antibodies. The polynuclectide or the compound that composition a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more configurates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene for the sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note:

The sequence data for this patent did not form directly from WIPO at the print of the printed or the composition or meaning the configuration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragme derivative or allelic variation of the nucleic acid sequence. Also
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spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                         Befort K,
                                                                                                                                                                                                                  14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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                                                                                                                                                                                                                                                                                                        (GEHO ) GEN HOSPITAL CORP
(FARB ) BAYER AG.
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Best Local Similarity 100.
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                                                                                        WO2003016475-A2
                                               Homo sapiens.
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Gaps

Crystal of protein-ligand complex useful for identifying an inhibitor of lymphocyte kinase (Lck), comprises truncated Lck and a ligand.

WPI; 2003-810380/76.

(AMGE-) AMGEN INC

Zhu X;

Claim 1; SEQ ID NO 1; 295pp; English.

21-MAY-2001; 2001US-00862154. 19-MAY-2000; 2000US-0205510P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for identifying a ligand (L), which binds to an inactive conformation of target protein kinase (T). The method involves contacting inactive conformation of (T), which contains or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bonding to the reactive group thus forming a kinase-(L) conjugate (C). The method is useful for identifying protein kinase inhibitors that preferentially bind to inactive conformation of a target protein kinase. The present sequence is a protein kinase which may be modified via an amino acid substitution, for use in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fungicide, nootropic, neuroprotective, kinase inhibitor; crystal; protein-ligand complex; lymphocyte kinase; Lck; Lck ligand; kinase inhibitor; therapeutic; kinase-mediated physiological event; cancer; autoimmunological; metabolic; inflammatory; infection; central nervous system degenerative disease; transplant rejection; human; globular core; protein co-ordinate data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; immunosuppressive; antiinflammatory; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                               Identifying ligand binding to inactive conformation of target protein kinase (T) comprises contacting the conformation modified (T) which contains reactive group at binding site, with ligands and detecting kinase-ligand conjugate formation.
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                                                  Human; protein kinase; enzyme; inhibitor; LCK.
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 41; 260pp; English.
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                                                                                                                                                                                                                                                           (SUNE-) SUNESIS PHARM INC
                                                                                                                                                                                                                                                                                               Braisted A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match . 100.
Best Local Similarity 100.
Matches 10, Conservative
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                 Human kinase LCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 508 AA;
                                                                                                                    WO2003081210-A2
                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                               Prescott JC,
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Comprises a sequence (S1) of residues 225-508 of a 508 amino acid sequence, given in specificater than 5.0 angstroms, and truncated Lck comprises a sequence (S1) of residues 225-508 of a 508 amino acid sequence, given in specification and retains the globular core of full-length Lck. (I) is useful in an inhibitor screening assay and to identify, design, select, and evaluate potential inhibitors of kinases that would be useful as therapeutics for diseases or symptoms of diseases that are associated with kinase-mediated physiological events. The inhibitors identified by the methods may also be useful for inhibition of kinase activity of one or more enzymes. The inhibitors are also useful criminate in the biological activity of any enzyme comprising greater than 70% sequence homology with a kinase sequence. The inhibitors are useful criminate for treating disease or disease symptoms mediated by any enzyme that binds ATP and thus for treating disease or disease symptoms mediated by any enzyme that binds ATP inhibitors are useful in inhibiting kinase activity and are useful in treating kinase enclosed disease or disease symptoms in a marmal particular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mammal, particularly a human e.g., cancer, autoimmunological, metabolic, inflammatory, infection, (bacterial, viral, yeast, fungal, etc.), central nervous system degenerative disease etc. The inhibitors are useful in treating or preventing diseases, including, transplant rejection etc. This is the amino acid sequence of a human lymphocyte kinase (Lck)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human protein of a TNF-alpha signalling pathway protein complex SeqID 3.
                                                                                                                                                                                                                                                                                                                                                    The invention describes a crystal (I) of a protein-ligand complex (C) comprising a truncated lymphocyte kinase (Lck) and a ligand, where (I) effectively diffracts X-rays for determination of atomic coordinates of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein complex; tumour necrosis factor-alpha signalling pathway; TNF-alpha; chronic inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; infectious disease; septic shock; bacterial infection; neurological disease; stroke-induced inflammation; neurodegenerative disease; cancer; antiinflammatory; antiarthritic; antirheumatic; cytostatic; antibacterial; gene therapy; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide comprising the Lck globular core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADS88148 standard; protein; 508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 QLQHQRLVRL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QLQHQRLVRL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 508 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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US6589758-B1

08-JUL-2003

Homo sapiens

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Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer; kinase substrate; immunosuppressive disorder; proliferative disease; HIV infection; AIDS; immunodeficiency; autoimmune disease; systemic lupus erythematosus; Src-family.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY49420 standard; protein; 509 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKA substrate, Src-family protein.
                     24-SEP-2003; 2003WO-EP050655.
                                    26-SEP-2002; 2002EP-00021809.
10-FEB-2003; 2003EP-00100274.
                                                                          Huhse B, I
, Kruse U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    293 QLQHQRLVRL 302
                                                                                                                                                                                                                                                                                                                                                                           1 QLQHQRLVRL 10
                                                                                                 WPI; 2004-348460/32.
                                                           (CELL-) CELLZOME AG
                                                                                                                                        diseases or cancer.
                                                                          Bouwmeester T, H
Superti-Furga G,
                                                                                                                                                                                                                                                                                                                             Sequence 508 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
       29-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY49420;
                                                                                                                                                                                                                                                                                                                                             Query Match
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This invention relates to novel protein complexes of the tumour necrosis factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to methods for preparing these complexes comprising at least two component proteins, as well as screening methods to identify modulators of the proteins, as well as screening methods to identify modulators of the pathway, which include antibodies, agonists and antagonists thereof. The pathway, which include antibodies, agonists and antagonists thereof. The clasmosing, prognosing or treating chronic inflammatory diseases such as septic shock and bacterial infections; neurological diseases such as serior shock and bacterial infections; neurological diseases such as stroke-induced inflammation in neurons; neurodegenerative diseases and cancer. Accordingly, these complexes can be used for the development of pharmaceutical compositions that exhibit antihilammatory, antiarthritic, antirheumatic, cytostatic and antibacterial activities and can be used for gene therapy purposes. In particular, the invention further provides is IRNA-oligonucleotides useful for inhibiting protein expression for in vitro or cell culture assays. This polypeptide is a human protein that can be used in combination with other proteins provided in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                               New protein complex comprising at least one first and second protein of
the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
diagnosing or treating inflammation, neurological diseases, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Bauch A, Ruffner H, Bauer A, Kuester B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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The invention provides a novel method of altering the activity of the protein kinase A (PKA) signaling pathway in a cell that comprises a tering the extent of phosphorylation of one or more PKA substrates, or kinase substrates downstream in the PKA signaling pathway. Pharmaceutical compositions containing a nucleic acid molecule that encodes a PKA compositions containing a nucleic acid molecule that encodes a PKA compositions containing a nucleic acid molecule that encodes a PKA composition by PKA can be used for treating a disorder exhibiting phosphorylation by PKA can be used for treating a disorder so a proliferative diseases. They can be used for treating e.g. HIV infection, AIDS, common variable immunodeficiency or cancers. Conditions in which upregulation of the PKA pathway is required, such as autoimmune disease, e.g. systemic lupus erythematosus, may also be treated. The present sequence represents a PKA subserate, wherein the subserate is in the Srcfamily, preferred the stream of the PKA PKA, PKA, Wark PKA, Wark

Fyk, Src-1 or Src-2

Altering the activity of protein kinase signaling pathways, used for treating immunosuppressive disorders, e.g. AIDS, proliferative disorders,

Claim 23; Page 95-96; 111pp; English. e.g. cancers or autoimmune diseases.

Skalhegg BS, Sundvold V;

Hansson V, Levy FO, Mustelin T, Skalht Tasken K, Vang T, Altman A, Munshi A;

(LAUR-) LAURAS AS. (JONE/) JONES E L.

WPI; 2000-086801/07.

N-PSDB; AAZ46491

99WO-GB001680. 98NO-00002419.

27-MAY-1999; 27-MAY-1998; 30-DEC-1998;

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                                                                                                                                                                                                                                                                                                                                                                                              Human, cancer; diagnosis, screening, modulator, leukaemia; ischaemia; heart disease, atherosclerosis; endometriosis.
                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                                   100.0%; Score 49; DB 3; Length 509; 100.0%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  Human cancer related protein SEQ ID NO:356
                                                                                                                                                                                                                                                                                                                                            ABR58699 standard; protein; 509 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-SEP-2001; 2001US-0323469P.
20-SEP-2001; 2001US-0323887P.
13-NOV-2001; 2001US-0350666P.
                                                                                                                                                                                                                                                                                                                                                                      09-JUL-2003 (first entry)
                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                      294 QLQHQRLVRL 303
                                                                                                                                                                                                                                                                                              1 OLOHORLVRL 10
                                                                                                                                                                                                                                                       Sequence 509 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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ADE40449
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                                                                                                                                                                                                                                                                                                                                                                                                                                           related gene nucleotide sequences which encode the proteins given in ABR58521 to ABR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a cut general assay. The nucleic acid is useful as diagnostic markers or therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus). Wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in a colon of the processing and condendarily for identifying agents for treating these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                  The present invention describes an isolated nucleic acid molecule, which
                                                                                                                                                     New genes that are up-regulated or down-regulated in cancers, useful as markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                                                                                                                                             comprises the sequence of any of the genes that are up-regulated or d regulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme; Src-family protein tyrosine kinase; T-cell; immune response.
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                                                                            Wilson KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 49; DB 6; Length 509; 100.0%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                           Aziz N, Gish KC, Hevezi PA, Mack DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                         Claim 12; Page 762; 767pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR56202 standard; protein; 509 AA
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0
                                                   (EOSB-) EOS BIOTECHNOLOGY INC.
08-FEB-2002; 2002US-0355145P.
08-FEB-2002; 2002US-0355257P.
12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-2002; 2002WO-US024546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2001; 2001US-0310051P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Matches 10; Conservative
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294 QLQHQRLVRL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QLQHQRLVRL 10
                                                                                                                WPI; 2003-354600/33.
                                                                                                                             N-PSDB; ACC72850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 509 AA;
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                                                                                        Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                           Afar D,
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                                                                                                                                                                                               New crystalline polypeptide comprising ligand binding domain or catalytic domain of Lck protein, for determining three-dimensional structure of catalytic domain of Lck, has predetermined unit cell parameters.
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                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a crystalline polypeptide (1), comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck) protein. Lck is a Src-family protein tyrosine kinase expressed primarily in T-cells and plays an essential role in immune response. The present sequence is the full-length sequence of human Lck (1-509). (1) is useful for identifying a compound which is an inhibitor of human Lck protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus; HIV-related disorder; differential expression; drug screening; viral replication modulation; diagnosis; prognosis; predisposition; anti-HIV; gene therapy; antiesnse therapy; human; proto-oncogene Tyr protein kinase LCK; enzyme.
                                                           Hrnciar P, Loew A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human proto-oncogene Tyr protein kinase LCK (gene ID 1611) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 49; DB 7; Length 509; 100.0%; Pred. No. 1.7; 0; Mismatches 0; Indels
                                                           Hirst GC,
                                                           Dixon RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE40449 standard; protein; 509 AA.
                                                                                                                                                                                                                                                                                                                    Claim 5; Fig 1; 994pp; English.
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2002US-0380249P.
2002US-0391306P.
2002US-0406297P.
2002US-0412007P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002US-0432318P
                                                           ۵,
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    Calderwood
Ritter K;

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                                                                                                                                            WPI; 2003-300872/29
(ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADE40448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 509 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003070883-A2.
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19-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-DEC-2002;
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25-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-FEB-2002;
                                                        Borhani DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE40449;
                                                                                         Leung A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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Identifying a candidate p21 or p53 pathway modulating agent using an assay system having a modulator of p21 or p53 (MP2153) polypeptide or nucleic acid, useful for diagnosing or treating cancer, such as colon or
           Claim 1; SEQ ID NO 28; 167pp; English
                                                                                                                                                          Local Similarity 100 les 10; Conservative
                                                                                                                                                                                        294 ÓLOHÓRLVRL 303
                                                                                                                                                                              1 OLOHORLVRL 10
polypeptide activity.
                                                                                                                                                                                                                                                                                                                                                           (EXEL-) EXELIXIS INC
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-180653/17.
                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADL22890
                                                                                                                                         Sequence 509 AA;
                                                                                                                                                                                                                                                                                               WO2004015069-A2
                                                                                                                                                                                                                                                                                                                                                                                                                              oreast cancer.
                                                                                                                                                                                                                                                20-MAY-2004
                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                   ADL22907;
                                                                                                                                                     Query Match
                                                                                                                                                                                                          Matches
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The invention relates to a method of identifying a compound useful in the treatment of AIDS (acquired immunodeficiency syndrome) or an HIV (human immunodeficiency virus) related disorder. The invention involves assaying the ability of a test compound to modulate the activity or expression of 26 human proteins. These proteins and nucleic acids encoding them (ADE4022-ADE40473) are differentially expressed in tissues relating to AIDS or an HIV-related disorder compared to their expression in normal tissues. The invention also relates to the use of the compounds clanified to modulate viral replication in a cell and to treat a patient with AIDS or an HIV-related disorder. The invention further discloses methods for the diagnostic evaluation and prognosis of various HIV-related disorders, and for the identification of individuals exhibiting a predisposition to such conditions. The modulatory compounds identified using the method of the invention may be small organic molecules, the invention are useful in diagnosing, preventing or treating AIDS or HIV-related disorders. The present sequence represents a human protein which is differentially expressed in AIDS or HIV-related disorders.

Gaps ö 100.0%; Score 49; DB 7; Length 509; 100.0%; Pred. No. 1.7; 0; Indels Mismatches .,

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Human MP2153 polypeptide sequence SEQ ID NO: 27. ADL22907 standard; protein; 509 AA. (first entry)

human; MP2153; p21; p53; cancer. 07-AUG-2002; 2002US-0401701P. 16-SEP-2002; 2002US-0411017P. 30-DEC-2002; 2002US-0437107P. 06-AUG-2003; 2003WO-US024505.

Belvin M; Francis-Lang H, Friedman L, Kidd T, Roche S, Plowman GD, Lickteig K, Zhang H, Amundsen CD;

Example 3; Page 94-96; 110pp; English

ö The present invention relates to a method of identifying a candidate p21 or p53 pathway modulating agent. This comprises providing an assay system comprising a modulator of p21 or p53 (MP2153) polypeptide or nucleic acid, contacting the assay system with a test agent, where in its presence the system provides a reference activity, and detecting a test agent-biased activity of the assay system, wherein a difference between the test agent-biased activity and the reference activity identifies the test agent biased activity of the present invention are useful for the diagnosis and/or treatment of diseases or conditions associated with aberrant expression or activity of the p21 or p53 pathway, such as cancer, preferably colon or head and neck cancer. The present sequence is a human MP2153 protein sequence of the invention. Gaps ., 0 100.0%; Score 49; DB 8; Length 509; 100.0%; Pred. No. 1.7; tive 0; Mismatches 0; Indels completed: June 29, 2006, 09:13:03 Local Similarity 100 nes 10; Conservative 111111111 294 QLQHQRLVRL 303 1 QLQHQRLVRL 10 Sequence 509 AA; Query Match Best Loca Matches Search Job time 888888888888888888 ઠ

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Cybuscription: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP Cybuscription: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP CySuperfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology CyKeywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho F; 68-116/Domain: SH3 homology cSH3> F; 68-116/Domain: SH3 homology cSH3> F; 68-116/Domain: SH2 homology cSH3> F; 217-224/Domain: SH2 homology cSH3> F; 217-224/Domain: protein kinase ATP-binding motif F; 251-259/Region: protein kinase ATP-binding motif F; 25/Modified site: myristylated amino end (Gly) (in mature form) #status predicted F; 23/Modified site: myristylated amino end (Gly) (covalent) #status predicted F; 23/Active site: Lys #status predicted F; 23/Active site: Lys #status predicted F; 23/Active site: Lys #status predicted F; 23/Active site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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Cell 43, 393-404, 1885
A;Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpress A;Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpress A;Reference number: A23639; MUID:86079521; PMID:2416464
A;Accession: A23639
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A;Accession: A23639
A;Accession: BANA
A;Residues: 1-282, VP',285-509 cMAR>
A;Accession: A23639
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A;Accession: A23639
A;Accession: BND-361031
B;A;Accession: UNIPARC:UPI0000172586; GB:MI2056; NID:g198763
A;Accession: UNIPARC:UPI0000172586; GB:MI2056; NID:g198763
A;Accession: NIA-4413, 1987
A;Attle: Two lock transcripts containing different 5' untranslated regions are present in A;Reference number: I57629; MUID:88142832; PMID:3501824
A;Accession: I57629; MUID:88142832; PMID:3501824
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KGarvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A;Title: Structure of the murine 1ck gene and its rearrangement in a murine lymphoma cel
A;Reference number: IS7636; MUID:89096891; PMID:2850479
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A;Cross-references: UNIPARC:UPI000016CE9E; GB:M21511; NID:g198768; PIDN:AAA39422.1; PID::
A;Cross-references: UNIPARC:UPI000016CE9E; GB:M21511; NID:g198768; Protein kinase homology
C;Kuperfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphosylation; blocked amino end; kinase-related transforming prof
P;68-116/Domain: SH3 homology <SH3>
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F;243-501/Domain: protein kinase homology <KIN>
F;251-255/Region: protein kinase ATP-binding motif
F;251-255/Region: protein kinase ATP-binding motif
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C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-2000 #sequence revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: 148845; A23639; IS7629; I77452
Nature 319, 682-685, 1986
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Pred. No. 0.14;
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A;Molecule type: DNA
A;Residues: 1-11 <VOR>
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A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-509 <VORL>
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Best Local Similarity 100.0%;
Matches 10; Conservative 0
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A; Molecule type: mRNA
A; Residues: 368-471, "H, 473-509 «VEI»
A; Cross-references: UNIPARC:UPI000016ABFC; EMBL:X06369; NID:g34288; PIDN:CAA29667.1; PII
R; Trevillyan, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Linna, T.J.
Bilochim. Biophys. Acta 888, 286-295, 1986
A; Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56(LSTRA). A; Reference number: S07143; MUID:87000726; PMID:3489486
A; Accession: S07143
A; Molecule type: mRNA
A; Residues: A; 376-509
A; Molecule type: mRNA
A; Residues: A; 376-509
A; Title: Structure of the two promoters of the human lck gene: differential accumulation
A; Reference number: A32797; MUID:89313764; PMID:2787474
                                                                                                                                                                                             protein-tyrosine kinase (BC 2.7.1.112) lck - human N;Alternate names: kinase-related transforming protein (lck) C;Species: Homo aspiens (man) C;Species: 30-Sep-1992 meaquence revision 30-Sep-1992 #text change 05-Oct-2004 C;Accession: UQ0152; S07822; $07200; S01879; S07143; A32797; I57636 R;Rouer, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R. A;Title: Structure of the human lck gene: differences in genomic organisation within src A;Reference number: JQ0152; MUID:90108697; PMID:2558056
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A;Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other n A;Reference number: S01879; MUID:88217332; PMID:2835736
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A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel A;Reference number: I57636; MUID:89096891; PMID:2850479
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C;Comment: Protein tyrosine kinases play important roles in the control of cell growth a
C;Genetics:
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A,Molecule type: mRNA
A,Molecule type: mRNA
A,Fesidues: 1-86, '9. 88-509 <PER>
A,Cross-references: UNIPARC:UPI0000163BD5; EMBL:X13529; NID:g34294; PIDN:CAA31884.1; PI
A,Cross-references: UNIPARC:UPI0000163BD5; EMBL:X13529; NID:g34294; PIDN:CAA31884.1; PI
R,Coga, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.
Bur. J. Immunol. 16, 1643-1646, 1986
A,Title: A human T cell-specific DNA clone (YTI6) encodes a protein with extensive hom
A;Reference number: S07200; MUID:87133831; PMID:3493153
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A;Map position: 1p35-1p34.3
A;Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
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A,Molecule type: DNA
A,Molecule type: DNA
A,Rolecules: 1-509 <RCUJ>
A,COSS-references: UNIPROT:P06239; UNIPARC:UPI0000151F17; EMBL:X14053
R,Perlmutter, R.M.; Marth, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, J. Cell. Biochem. 39, 117-126, 1988
A,Title: Structure and expression of lck transcripts in human lymphoid cells.
A,Reference number: S07822; MUID:89123626; PMID:3265417
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lecule type: mRNA

A;Accession: S07200 A;Molecule type: mRJ

A; Status: translated from GB/EMBL/DDBJ

A; Accession: I57636

A; Molecule type: DNA A; Residues: 1-35 <TAK>

A; Molecule type: DNA A; Residues: 1-35,'VR' <RES>

A;Gene: GDB:LCK

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Gaps

Query Match

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protein-tyrosine kinase (EC 2.7.1.112) tkl [similarity] - chicken
N/Alternate names: kinase-related transforming protein (tkl); T-cell surface antigen ass
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A;Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBIP:88833)
R;Strebhardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987
A;Title: Additional member of the protein-tyrosine kinase family: the src-and lck-relate
A;Reference number: A39939; MUID:88097370; PMID:3321053
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A;Residues: 52-507 <STR>
A;Cross-references: UNIPARC:UPI00001713B3; GB:J03579; NID:g212712; PIDN:AAA490B1.1; PID:
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;66-114/Domain: SH3 homology <SH3>
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F:241-499/Domain: protein kinase homology <KIN>
F:249-257/Region: protein kinase ATP-binding motif
F:249-257/Region: protein kinase ATP-binding motif
F:240-257/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 05-Oct-2004
C;Accession: T51736
R;Jouannic, S.
submitted to the EMBL Data Library, August 1998
A;Reference number: 225444
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Gallus gallus (chicken)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: Ag1226; A393939
Mol. Cell. Biol. 12, 1226-1333, 1992
Mol. Cell. Biol. 12, 1226-1333, 1992
A;Title: tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene. A;Title: tkl is the A2126; MUID:92186854; PMID:1545804
F_i 2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted F_i 269/Active site: Lys #status predicted
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A;Residues: 1-88 <CHO>
A;Cross-references: UNIPARC:UP10000172587; GB:M85043
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A;Molecule type: mRNA
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larity 88.9%; Pred. No. 17;
Conservative 0; Mismatches
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Pred. No.
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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                                            (by autophosphorylation) #status pred
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S.Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type, protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;S9-107/Domain: SH3 homology <SH3.
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A;Cross-references: UNIPROT:P51451; UNIPARC:UPI0000163B22; EMBL:Z33998; NID:g601951; PID
C;Genetics:
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C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; tyro
C;Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; tyro
F;55-113/Domain: SH2 homology <SH3->
F;124-220/Domain: SH2 homology <SH2->
F;239-497/Domain: protein kinase homology <KIN->
F;247-255/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-499 <DYM>
A;Cross-references: UNIPROT:P16277; UNIPARC:UP10000151F18; GB:M30903; NID:g202076; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;233-491/Domain: protein kinase homology <KIN>F;24-249/Region: protein kinase ATP-binding motif
F;24-249/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;263/Active site: Lys #status predicted
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C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: A40092
R;Dymecki, S.M.; Niederhuber, J.E.; Desiderio, S.V.
Science 247, 322-336, 1990
A;Fitle: Specific expression of a tyrosine kinase gene, blk, in B lymphoid of A;Reference number: A40092; MUD:90117147; PMID:2404338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                           Length 509;
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88.9%; Pred. No. 4.6;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A40092
protein-tyrosine kinase (EC 2.7.1.112) blk [validated] - mouse
                                                                                                                                                                                                                   1; Indels
                                                                                                                      Score 43; DB 1;
Pred. No. 2;
0; Mismatches
                                   F,394,505/Binding site: phosphate (Tyr) (covalent)
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A;Cross-references: GDB:454114; OMIM:191305
F;273/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;59-107/Domain: SH3 homology <SH3>
F;118-214/Domain: SH2 homology <SH2>
                                                                                                                           87.8%;
90.0%;
                                                                                                                                                                  Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity
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Genetics:

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A, Residues: 1-608 <ANT>
A, Residues: 1-608 <ANT>
A, Cross-references: UNIPROT:081470; UNIPARC:UP100000A1A9F; EMBL:AF076275; NID:g3293582, A, Cross-references: Cultivar Columbia
B, Covic, L.; Lew, R.R.
Bjochim. Blophys. Acta 1305, 125-129, 1996
A, Title: Arabidopsis thaliana cDNA isolated by functional complementation shows homology A, Reference number: $65789; MUID:96180314; PMID:8597596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 'YVRE',119-236,'LDPLLIIGDRLG',248-338,'V',340-358,'G',360-369,'EVEALKNPYNREG
A;Cross-references: UNIPARC:UP1000017A45B; EMBL:L43125; NID:g871811; PIDN:AAA99196-1; PI
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R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, Bubmitted to the Protein Sequence Database, April 1999
A;Reference number: Z15789
A;Accession: T06609
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C;Superfamily: DNA-binding protein WRKY1
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A;Cross-references: UNIPROT:09SZ67; UNIPARC:UP1000009F5B5; EMBL:AL049638; GSPDB:GN00062;
A;Experimental source: cultivar Columbia; BAC clone F16J13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Introns: 353/2; 381/3; 402/3; 455/2; 479/3; 499/3; 537/3
A;Note: T15F16.5
C;Keywords: AFP; phosphotransferase; serine/threonine-specific protein kinase F;331-587/Domain: protein kinase homology <KIN>F;331-587/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
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C;Species: Yersinia pestis
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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                      submitted to the EMBL Data Library, August 1998
A; Description: The sequence of A. thaliana TISF16.
A;Reference number: Z14443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 2; Pred. No. 21; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.6%; Score 38; DB 77.8%; Pred. No. 65; iive 1; Mismatches
                                                                                                                                                                            A;Status: translated from GB/EMBL/DDBJ
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77.8%;
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Best Local Similarity 7/...
A Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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388 QLQHQNIVR 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                    probable mitogen-activated protein kinase [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Peb-2004) (Peb-2004) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine/threonine-specific protein kinase ARA.KIN homolog T15F16.2 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 05-Oct-2004
C;Accession: T01836
R;Antoniou, B.; Le, T.
submitted to the BMBL Data Library, August 1998
A;Description: The sequence of A. thaliana T15F16.
A;Reference number: Z14443
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A;Introns: 156/2; 241/2; 323/2; 351/3; 372/3; 425/2; 449/3; 481/3; 519/3
A;Note: T15F16.2
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Pred. No. 19;
1; Mismatches 1; Indels
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                                         Indels
                                         1;
   ed. No. 18;
Mismatches
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A;Molecule type: DNA
A;Residues: 1-572 <ANT>
                                     1,
. 88;
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Best Local Similarity 77.8
Matches 7; Conservative
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                  333 QLQHQNIVR 341
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                                                                                                            QLQHQRLVR
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A; Residues: 1-560 <STO>
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Genetics:

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iron uptake in Yersinia pestis
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A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI000003DEC; GB:AL590842; PIDN:CAC89109.1;
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C;Species: Yersinia pestis
C;Accession: AH0078
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0031
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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                                 A;Molecule type: DNA
A;Residues: 2-260 <BUC.
A;Cross-references: UNIPARC:UP10000DCDCO; EMBL:AL031866; PIDN:CAA21402.1
A;Experimental source: strain 6/69
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                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 2-260 <BU2-
A;Cross-references: UNIPARC:UP10000DCDC0; EMBL:AL031866; PIDN:CAA21334.1
A;Experimental source: strain 6/69
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                                                                                                                                                                                                                                                                                                                                                        RiFetherston, J.D.; Bertolino, V.J.; Perry, R.D. Mol. Microbiol. 32, 289-299, 1999
A,Title: YbtP and YbtO: two ABC transporters required for A;Reference number: 218782; MUID:99248409; PMID:10231486
A;Accession: T17450
                                                                                                                                                           A,Accession: T46991
A,Status: preliminary; translated from GB/EMBL/DDBJ
      preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 13;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Genome: plasmid
A;Mobile element: insertion sequence
A;Note: plasmids pMT1 and pCD1
C;Superfamily: DNA replication protein dnaC
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A,Gene: YP00248
C;Superfamily: DNA replication protein dnaC
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70.0%;
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70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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A; Residues: 164-260 <FET>
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A; Status: preliminary
A; Molecule type: DNA
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                       A;Accession: S43107
A;Status: preliminary
A;Moilotule type: DNA
A;Residues: 1-219 <PIL>
A;Cross-references: UNIPROT:Q56968; UNIPARC:UPI00000B43AB; EMBL:X78302; NID:g467611; PIC
C;Superfamily: DNA replication protein dnaC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable transposase - Yersinia pestis plasmid pWT1 and pCD1 insertion sequence C.Species: Yersinia pestis C.Species: Versinia pestis C.Date: 20-Sep-1999 #sequence revision 20-Sep-1999 #text_change 09-Ju1-2004 C.Accession: T14971; T15009; T42855; T14648; T47569; T47559; T46991; T17450 R.Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R. Thifect. Immun. 66, 5731-5742; 1998 A.Fitle: Complete DNA sequence and detailed analysis of the Yersinia pestis KIM5 plasmid A.Reference number: Z18268; MUID:99043898; PMID:9826348
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A; Residues: 2-260 <LI2>
A; Residues: 2-260 <LI2>
A; Cross-references: UNIPARC: UPI0000DCDC0; EMBL: AF074611; NID: 93883003; PID: 93883092; PI
R; Perry, R.D.; Straley, S.C.; Petherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R.
Infect. Immun. 66, 4611-4623, 1998
A; Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia p
A; Reference number: Z22273; MUID: 98427122; PMID: 9746557
A; A; Rocession: T42855
A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: UNIPARC:UPI0000DCDC0; EMBL:AF053947; NID:g2996286; PID:g2996299; PI
A;Experimental source: plasmid pMT1
R;Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubaker
J. Bacteriol. 180, 5192-5202, 1998
A;Title: Structural organization of virulence-associated plasmids of Yersinia pestis.
A;Reference number: Z22578; MUID:98422474; PMID:9748454
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A; Cross-references: UNIPARC:UPI000003DEC; EMBL:AF074612; NID:g3822037; PIDN:AAC69770.1;
A; Cross-references: UNIPARC:UPI000003DEC; EMBL:AF074612; NID:g3822037; PIDN:AAC69770.1;
A; Experimental source: strain KIMS, plasmid pCD1
R; Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Carrano, submitted to the EMBL Data Library, March 1998
A; Description: Structural organization of virulence determinants in three Yersinia pesti
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A;Experimental source: strain KIM, plasmid pCD1
B;Buchrieser, C.; Rusnick, C.; Couve, B.; Frangeul, L.; Billault, A.; Kunst, F.; Carniel submitted to the EMBL Data Library, October 1998
A;Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.
A;Reference number: 224348
A;Reference number: 224348
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A; Accession: T14971
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-260 «LIN»
A; Residues: 1-260 «LIN»
A; Cross-references: UNIPROT: Q9R315; UNIPARC: UP1000003DEC; EMBL: AF074611; NID: 93883003;
A; Experimental source: plasmid pMT1
A; Accession: T15009
A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Accession: T14648
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A, Status: preliminary; translated from GB/EMBL/DDBJ
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ELQHQRLMAL 12
A; Reference number: S43106
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A; Residues: 2-260 <HUZ>
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C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 0.2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AF0065
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. R;Parkhill, J.; Wren, B.W.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
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R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Ctillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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C,Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
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A;Reference number: AB0001; MUID:21470413; PMID:11586360
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                                       75.5%; Score 37; DB 70.0%; Pred. No. 13; iive 2; Mismatches
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C;Superfamily: DNA replication protein dnaC
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C;Superfamily: DNA replication protein dnaC
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A;Status: preliminary
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A;Molecule type: DNA
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A.Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A.Reference number: AB0001; MUID:21470413; PMID:11586360

A.Accession: A10197

A.Status: preliminary

A.Nolecule type: DNA

A.Residues: 1-260 < KUR>
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A,Residues: 1-260 «KUR»
A,Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI000003DEC; GB:AL590842; PIDN:CAC89491.1;
C,Genetics:
A,Gene: YPO0638
C,Superfamily: DNA replication protein dnaC
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C;Genetics:
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A;Title: Genome sequence of Yersinia peetis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI000003DEC; GB:ALS90842; PIDN:CAC92179.1;
C;Genetics:
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deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AI0197
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Pred. No. 13;
2; Mismatches
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C;Superfamily: DNA replication protein dnaC
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Superfamily: DNA replication protein dnaC
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Local Similarity 70.0%;
les 7; Conservative
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ELOHORLMAL 13
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insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A,Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A,Reference number: AB0001; MUID:21470413; PMID:11586360
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               A; Cross-references: UNIPROT: Q9R3L5; UNIPARC: UPI0000003DEC; GB: AL590842; PIDN: CAC93168.1
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE0174
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                                                                                                                                                           Length 260;
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Pred. No. 13;
2; Mismatches 1; Indels
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2; Mismatches
                                                                                                                                                           Score 37;
Pred. No.
                                       C;Genetics:
A;Gene: YPO3700
C;Superfamily: DNA replication protein dnaC
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C,Superfamily: DNA replication protein dnaC
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C,Superfamily: DNA replication protein dnaC
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70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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A;Molecule type: DNA
A;Residues: 1-260 <KUR>
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A;Molecule type: DNA
A;Residues: 1-260 <KUR>
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession. AC0185
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Title: Genome AC0185
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Status; preliminary
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH0047
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
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C;Genetics:
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C;Genetics:
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insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
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A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0450
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD0450
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A;Accession: AH0047
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-260 <KUR>
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C; Superfamily: DNA replication protein dnaC
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C;Superfamily: DNA replication protein dnaC
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les 7; Conservative
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Matches 7; Conservative
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ELQHQRLMAL 13
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A;Molecule type: DNA
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Matches
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insertion sequence IS100,

A, Reference number: Al A, Accession: AC0070 A, Status: preliminary A, Molecule type: DNA

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A;Accession: AH0436
A;Status: preliminary
A;Molecule type: DMA
A;Residues: 1-260 «KOR»
A;Residues: 1-260 «KOR»
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI000003DEC; GB:AL590842; PIDN:CAC92820.1;
C;Genetics:
A;Gene: YP03592
C;Superfamily: DNA replication protein dnaC
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A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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C;Accession: AE0124
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Bavis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Species: Yersinia pestis
C,Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
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A;Reference number: AB0001; MUID:21470413; PMID:11586360
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C;Superfamily: DNA replication protein dnaC
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C;Superfamily: DNA replication protein dnaC
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4 ELQHQRLMAL 13
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4 ELQHQRLMAL 13
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A;Molecule type: DNA
A;Residues: 1-260 <KUR>
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A; Residues: 1-260 < KUR>
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A; Thitle: Genome sequence of Yersinia pestis, the causative agent of plague. A; Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI000003DEC; GB:AL590842; PIDN:CAC89422.1;
C;Genetics:
A;Gene: YPO0566
C;Superfamily: DNA replication protein dnaC
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
R;Packhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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C;Genetics:
                                                                                                                                                                                                                                                 Ribarkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Ji, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                               ATP-binding protein [imported] - Yersinia pestis (strain C092)
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                                                                                                                                                 C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0070
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Pr
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C;Superfamily: DNA replication protein dnaC
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1 QLQHQRLVRL 10

8 g Best Local Similarity 70.0 Matches 7; Conservative

Query Match

A; Molecule type: DNA A; Residues: 1-260 < KUR>

Accession: AH0231 Status: preliminary

1 QLQHQRLVRL 10

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1 QLQHQRLVRL 10

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C. Species: Yersinia pestis
C. Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C. Accession: AD013
C. Accession: AD013
R. Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, B.P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A.Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A.Tacles Genome sequence of Yersinia pestis, the causative agent of plague.
A.Accession: AD013
A.Stetus: preliminary
A.Molecule type: DNA
A.Residues: 1-260 «KUR»
A.Gross-references: UNIPROT: Q9R3L5; UNIPARC: UP10000003DEC; GB:AL590842; PIDN:CAC89767.1; C. Superfamily: DNA replication protein dnaC
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE0459
E;Parthill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AE0459
                                                                                                                                                                                    insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
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A;Molecule type: DNA
A;Keidues: 1-260 «KUR»
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UP10000003DEC; GB:AL590842; PIDN:CAC93241.1;
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A;Gene: YPO3773
C;Superfamily: DNA replication protein dnaC
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LCK_CHICK

032EHE_ACTSC

032EHE_ACTSC

032EHE_ACTSC

032EHE_ACATH

084W26_ARATH

081470_ARATH

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081470_ARATH

081470_ARATH

081470_ARATH

081470_ARATH

080499_ECOLI

078TY2_ECOLI

078TY2_ECOLI

078TY2_ECOLI

078TY2_ECOLI

078TY3_EECOLI

078TY3_EECOLI

078TY3_EECOLI

078TY3_EECOLI

077ARK4_YERPE

081W92_ECOLI

077ARK4_YERPE

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077ARK4_YERPE

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081W93_ECOLI

087AFFE

067VV7_ORYSA

065AFFE

065VV7_CORYSA

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QBSH3UG_XANOR
004191_ARATH
QZMZNS_MOUSE
06547G_ARATH
QZRZU4_ORYSA
Q4TC30_TETNG
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(c) 1993 - 2006 Biocceleration Ltd.
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095M3Z_9PRIM
032CM0_BOVIN
0573B4_HUMAN
0573B4_HUMAN
047R7Z_TETNG
1.CKC_87A_MOUSE
047EX6_RAT
045TV0_BRARE
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Q9U8V6_EPTBU
Q6L576_ORYSA
Q93411_XENLA
Q6104_BRARE
Q7QS13_GIALA
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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dechloromon desulfotale clostridium vibrio vuln glycine max carica papa

lampetra re homo sapien uncultured

burkholderi oryza sativ

frankia sp.

homo sapien homo sapien xanthomonas

mus musculu arabidopsis

oryza sativ

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tetraodon n arabidopsis mus musculu

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arabidopsis oryza sativ oryza sativ

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-!-FUNCTION: Tyrosine kinase that plays an escential role for the mature T-cell function. Is constitutively associated with the mature T-cell function. Is constitutively associated with the cytoplasmic portions of the CD4 and CD8 surface receptors and plays a key role in T-cell antigen receptor (TCR)-linked signal transduction pathways. Association of the TCR with a peptide antigen-bound MHC complex facilitates the interaction of CD4 and CD8 with MHC class II and class I molecules, respectively, and thereby recruits the associated LCK to the vicinity of the TCR/CD3 complex. LCK then phosphorylates tyrosines residues within the immunoreceptor tyrosines-based activation motifs (ITPMS) in the cytoplasmic tails of the TCRgamma chains and CD3 subunits, initiating the TCR/CD3 signaling pathway. In addition, contributes to signaling by other receptor molecules. Associates directly with the cytoplasmic tail of CD2, and upon engagement of the CD2 molecule. LCK undergoes hyperphosphorylation and activation. Also plays a role in the IL2 receptor-linked signaling pathway that controls T-cell proliferative response. Binding of IL2 to its receptor results in increased activity of LCK. Is expressed at all stages of thymocyte development and is required for the regulation of maturation events that are governed by both pre-TCR and mature alpha beta TCR (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine phosphate.
SUBUNIT: Binds to the cytoplasmic domain of cell surface receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD12. Also binds to effector molecules, such as P14K, VAV1, RASA1, FYB and to other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds to phosphatidylinositol 3'-kinase (PT3K) from T lymphocytes through its SH3 domain and to the tyrosine phosphorylated form of KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.

Interacts with phosphorylated LIME1. Interacts with CBLB (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
                                                                                                                                                                                                                     08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
08-NOV-2005, sequence version 3.
07-MAR-2006, entry version 13.
Proteoncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK) (Lymphocyte cell-specific protein-tyrosine kinase).
Name=LCK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULĀR LOCATION: Cytoplasmic and attached to the membrane. Present in lipid rafts in an unactive form (By similarity). DOMAIN: The SH2 domain mediates interaction with SQSTM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the Tyr protein kinase family. SRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [MRNA].
Perez-Quintero L.A., Vernot J.P.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 SH2 domain. SIMILARITY: Contains 1 SH3 domain.
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InterPro; IPR000719; Prot kinase.

InterPro; IPR002290; Ser Thr pkinase.

InterPro; IPR001980; SH2.

InterPro; IPR001452; SH3.

InterPro; IPR001245; Tyr pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aotus nancymaae (Ma's night monkey)
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=37293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
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                                                                                                                                       AOTNA
                                                                                                                                                                              QSPXS1;
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similarity).
Phosphotyrosine (negative regulation) (By
similarity).
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDLINE-87133831; PubMed-3493153;
Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
Mak T.W.;
"A human T cell-specific cDNA clone (YT16) encodes a protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proto-oncogene tyrosine-protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK) (Lymphocyte cell-specific protein-tyrosine kinase) (LSK) (T cell-specific protein-tyrosine kinase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-myristoyl glycine (By similarity).
S-palmitoyl cysteine (By similarity)
S-palmitoyl cysteine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50002; SH3; 1.
ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
Auchectide-binding; Palmitate; Phosphorylation; Proto-oncogene;
CH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
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P06239; P07100; Q12850; Q13152; Q5TDHB; Q5TDH9; Q96DW4; Q9NYTB; Q1-JAN-1988, integrated into UniProtKB/Swiss-Prot. O1-PEB-1994, sequence version 8.5. O7-MAR-2006, entry version 87.
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Interactions with CD4 and CD8 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proton acceptor (By similarity). ATP (By similarity).
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PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50001; SH2; 1.
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                                                                  PFam; PF00018; SH3 1; 1
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00402; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Proc. Kinase; 1.
ProDom; PD0000093; SH2; 1.
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Pfam; PF07714; Pkinase Tyr;
Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                ProDom, PD000001; Prot_kina
ProDom, PD000063; SH2; 1.
ProDom, PD0000066; SH3; 1.
SWART; SM00252; SH2; 1.
SWART; SM00326; SH3; 1.
SWART; SM00326; SH3; 1.
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Matches 10; Conservative
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INIT MET 0
CHAIN 1
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126
244
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CR HOMO

CC BUKAX

OC HOMO

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TISSUE=Lymph;

WEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Featigold E.A., Grouse L.H., Derge J.G.,

A Altachul S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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A Capleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Gennerch A., Schein J.E., Jones S.J.M., Marra M.A.;

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R. Gennerd A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Gennerd A., Schein J.E., Jones S.J.M., Marra M.A.;
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MEDLINE=90108697; PubMed=2558056; DOI=10.1016/0378-1119(89)90144-3;
ROUGE E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
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TISSUE-Leukemia;
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  extensive homology to a family of protein-tyrosine kinases.";
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Human chromosome 1 international sequencing consortium;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
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"An aberrant lck mRNA in two human T-cell lines.";
Biochim. Biophys. Acta 1264:168-172(1995).
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                        16:1643-1646 (1986)
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                                                                       NUCLEOTIDE SEQUENCE [MRNA]
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Gene 84:105-113(1989).
                        Eur. J. Immunol.
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NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
MEDLINE-89313764; PubMed=2787474;
Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,

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MEDLINE=92347326; PubMed=1639064; Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A., Amrein K.E., Autero M., Burn P., Alitalo K.; "The human p50csk tyrosine kinase phosphorylates p561ck at Tyr-505 and down regulates its catalytic activity."; EMBO J. 11:2919-2924(1992).
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MEDLINE-88217332; PubMed-2835736;
Veillette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.;
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"Lck protein tyrosine kinase is a key regulator of T-cell activation
                        the human lck gene: differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLECTIDE SEQUENCE [MRNA] OF 374-508.
MEDLINE-87000726; PubMed=3489486; DOI=10.1016/0167-4889(86)90228-4;
Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Park I., Chung J., Walsh C.T., Yun Y., Strominger J.L., Shin J., "Phosphotyrosine-independent binding of a 62-kDa protein to the src homology 2 (SH2) domain of p56-lck and its regulation by phosphorylation of Ser-59 in the lck unique N-terminal region.", Proc. Natl. Acad. Sci. U.S.A. 92:12338-12342(1995).
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                                                                                                                 TISSUE=Peripheral blood lymphocyte;
MEDLINE=20462621; PubMed=11009097;
MODI=10.1002/1521-4141(200009)30:9<2632::AID-IMMU2632>3.0.CO;2-C;
Boncristiano M., Majolini M.B., D'Elios M.M., Pacini S., Valensir
Ulivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
Baldari C.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Greenway A.L., Azad A., Mills J., McPhee D.A.;
"Human immunodeficiency virus type 1 Nef binds directly to LCK a
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Miyamoto N.G., Mak T.W.; "Structure of the human lck gene: differ accumulation of two classes of lck transcripts in T cells.";
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                                                                                                 NUCLEOTIDE SEQUENCE [MRNA] OF 13-508.
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J. Biol. Chem. 270:2506-2511(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                Oncogene Res. 1:357-374 (1987).
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INTERACTION WITH KHDRBS1.
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PubMed=10848956;
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PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
es 10; Conservative
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294 QLQHQRLVRL 303
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                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00017; SH2; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-22289034; PubMed=12401726; Mervi S., Nicodeme S., Gartioux C., Atlan C., Lathrop M., Reviron D., Naquet P., Matsuda F., Imbert J., Vialettes B.; Matsuda F., Inchert J., Vialettes B.; Matsuda F., Inchest J., Vialettes B.; Matsuda F., Inchest J., No. association between lck gene polymorphisms and protein level in
target for signal intervention by Herpesvirus saimiri and other
                                                                                                                                                                                                                                                                                                                                                                                                    "LIME: a new membrane raft-associated adaptor protein involved in CD4
                                                                                                                                                                                                                                                                                                                              INTERACTION WITH LIME1.
PubMed=14610046; DOI=10.1084/jem.20031484;
Brdickova N., Brdicka T., Angelisova P., Horvath O., Spicka J.,
Brdickova V., Sameoni L., Kliche S., Merten C., Schraven B.,
Horejsi V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                           MASS SPECTROMETRY.

12 SUB-Mammary cancer;

MEDLINE=218.9512; Pubmed=11840567;

DOI=10.1002/1615-9861(200202)2:2<212::AID-PROT212>3.0.CO;2-H;

DOI=10.1002/1615-9861(200202)2:2<212::AID-PROT212>3.0.CO;2-H;

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Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.

Zvelebil M.J.
                                                                                                                                                                                                                                                                           "Cluster analysis of an extensive human breast cancer cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                 Yamada T.,
                                                                 PubMed=12218089;
Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.
Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kobugi A.;
"Fyn is essential for tyrosine phosphorylation of Csk-binding
protein/phosphoprotein associated with glycolipid-enriched
microdomains in lipid rafts in resting T cells.";
J. Immunol. 169:2813-2817(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       type 1 diabetes.";
Diabetes 51:3326-3330(2002).
-!- MISCELLANEOUS: The sequence shown here is derived from an
EMBL/GenBank/DDBJ third party annotation (TPA) entry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 49; DB 1; Length 508; 100.0%; Pred. No. 1.1;
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                     Eur. J. Biochem. 267:3413-3421 (2000) [19]
                                                                                                                                                                                                                                                                                       protein expression map database.";
Proteomics 2:212-223(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
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                                                      SUBCELLULAR LOCATION
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NUCLEOTIDE SEQUENCE.
                 gene products
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Q7RTZ3;
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  and a
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Ensembl; ENSG00000182866; Homo Bapielle.

G0; G0:0002421; Cilpid raff; ISS.
G0; G0:0000242; Cipericentriolar material; ISS.
G0; G0:0000242; P:protein serine/threonine phosphatase activity; ISS.
G0; G0:0004713; P:protein-tyrosine kinase activity; ISS.
G0; G0:0005919; P:SHZ domain binding: ISS.
G0; G0:0005917; P:hemopolesis; ISS.
G0; G0:0007242; P:hemopolesis; ISS.
G0; G0:0007242; P:intracellular signaling cascade; ISS.
G0; G0:0006802; P:positive regulation of T cell receptor sign. .; ISS.
G0; G0:000726; P:positive regulation of T cell receptor sign.
G0; G0:000074; P:regulation of lymphocyte activation; ISS.
G0; G0:000074; P:regulation of progression through cell cycle; ISS.
G0; G0:000074; P:regulation of progression through cell cycle; ISS.
G0; G0:000078; P:response to drug; ISS.
R0; G0:0006882; P:zinc ion homeosesia; ISS.
R1 InterPro; IPR000719; Prot_kinase.
R1 InterPro; IPR00079; Ser_thr_pkinase.
R2 InterPro; IPR000890; Ser_thr_pkinase.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hylobatidae, Hylobates.
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MEDLINE=22031236; PubMed=12033791; DOI=10.1006/viro.2002.1381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 49; DB 2; Length 509; 100.0%; Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 1.
SMORT; SM00219; TYPKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS500109; PROTEIN_KINASE_DOM;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001245; Tyr pkinase.
InterPro; IPR008266; Tyr pkinase_AS.
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PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot kinase; 1.
ProDom; P0000093; SH2; 1.
ProDom; P0000066; SH3; 1.
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O95M32 9PRIM

ID Q95M32 9PRIM

A Q95M32 9PRIM

DT O1-DEC-2001, integrated into Un:

O1 01-DEC-2001, sequence version 18.

O7 FEB-2006, entry version 18.

DE LCk protein.

GN Name=1ck;

CS Hylobates SP. (gibbon).

CC Mammalia; Eutheria; Buarchontog;

CC MATOBATIAE; Hylobates.

CC NCBL TaxID=9581;

RN | 11 |

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22031236; PubMed=120337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF07714; Pkinase Tyr; 1.
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EMBL; BC102046; AA102047.1; .., mRNA.

OR GO; GO:0045121; C:lipid raft; ISS.

OR GO; GO:0004222; F:protein raterial; ISS.

GO; GO:0004722; F:protein serial threonine phosphatase activity; ISS.

GO; GO:0004713; F:protein ryrosine kinase activity; ISS.

GO; GO:0004713; F:protein ryrosine kinase activity; ISS.

GO; GO:00042169; F:SH2 domain binding; ISS.

GO; GO:0006919; P:loaspase activation; ISS.

GO; GO:0006917; P:loaspase activation of real activation; ISS.

GO; GO:0006917; P:loaspase activation of T cell activation; ISS.

GO; GO:0006468; P:protein amino acid phosphorylation; ISS.

GO; GO:000045; P:protein amino acid phosphorylation; ISS.

GO; GO:000049; P:regulation of lymphocyte activation; ISS.

GO; GO:000049; P:regulation of progression through cell cycle; ISS.

GO; GO:000049; P:regulation of progression through cell cycle; ISS.

GO; GO:000049; P:regulation of progression through cell cycle; ISS.

GO; GO:000049; P:regulation of progression through cell cycle; ISS.

GO; GO:000049; P:regulation of progression through cell cycle; ISS.

GO; GO:000049; P:regulation of progression through cell cycle; ISS.

GO; GO:000049; P:regulation of progression through cell cycle; ISS.

GO; GO:000049; P:regulation of progression through cell cycle; ISS.

InterPro; IPR000199; Prot kinase.

InterPro; IPR001452; HY: pkinase.

InterPro; IPR001452; HY: pkinase.

InterPro; IPR001749; Primase.

INTERPRO; IPR001774; Primase.

INTERPRO; IPR001749; Primase.

INTERPRO; IPR00174
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                                                                                                                                                                                                                                                              STRAIN-Crossbred x Angus; TISSUE-Ileum;
Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.
Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
Matsuo C., Mayo M., Santos R.R., Stort J., Tsai M., Wong D.,
Siddiqui A., Holt R., Jones S.J., Marra M.A.;
Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                   Bos taurus (Bovine).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00017; SH2; 1.

Pfam; PF00018; SH3 1; 1.

PRINTS; PR00401; SH3DOMAIN.

PRINTS; PR00452; SH3DOMAIN.

PRINTS; PR00109; TYRKINASE.

ProDom; PD000001; Prot kinase; 1.

ProDom; PD000001; Prot kinase; 1.

ProDom; PD000005; SH2; 1.

SMART; SM00252; SH3; 1.

SMART; SM00219; TYRK; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 1.

PROSITE; PS00101; PROTEIN KINASE TYR; 1.
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         27-SEP-2005, sequence version 1. 07-MAR-2006, entry version 6. Hypothetical protein MGC126900.
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es 10; Conserv
                                                                                                                                                                                               NCBI_TaxID=9913;
                                                                           Name=MGC126900;
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SEQUENCE 5
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## SWR 1987821, 621991

## CO GO: 0004712; C:pericentriolar material; ISS.

## CO: GO: 0004712; C:pericentriolar material; ISS.

## CO: GO: 0004712; F:protein erine(threonine phosphatase activity; ISS.)

## CO: GO: 0004713; F:protein erine(threonine phosphatase activity; ISS.)

## CO: GO: 0004713; F:protein erine(threonine phosphatase activity; ISS.)

## CO: GO: 0006913; P: SHR domain binding; ISS.

## CO: GO: 0006913; P: Protein erine(threonine phosphatase activity; ISS.)

## CO: GO: 0006913; P: Protein erine(threonine phosphatase activity; ISS.)

## CO: GO: 0006913; P: Protein erine(threonine phosphatase activity)

## CO: GO: 0006913; P: Protein erine(threonine phosphatase activity)

## CO: GO: 0006913; P: Protein erine(threonine phosphatase)

## CO: GO: 0006914; P: Protein erine(threonine phosphatase)

## CO: GO: 0006917; P: Protein erine(threonine phosphatase)

## CO: GO: 0006917; P: Protein erine(threonine phosphatic)

## CO: GO: 0006917; P: Protein erine(threonine phosphatase)

## PROTEIN ERROUGH ## PROTEIN ERRORENE ARP; I.

## PRODEIN: PROTEIN ERRORENE ATP; I.

## PROSEIN: PRODEIN: PROTEIN ERRORENE ATP; I.

## PROSEIN: PRODEIN: PROTEIN ERRORENE ATP; I.

## PRO
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Picard C., Greenway A., Holloway G., Olive D., Collette Y.; "Interaction with simian Hck tyrosine kinase reveals convergent evolution of the Nef protein from simian and human immunodeficiency viruses despite differential molecular surface usage."; Virology 295:320-327(2002)
                                                                                                                                                                                     Thesis (2001), Department of Experimental Oncology laboratory, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                  EMBL, AJ320182; CAC44027.1; -; mRNA.
HSSP, P06229; ILCK.
SMR; Q95M32; 65-509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 ÓLÓHÓRLVRL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QLQHQRLVRL 10
                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                       Picard C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
Q3ZCM0 BOVIN
ID Q3ZCM0 BC
AC Q3ZCM0;
DT 27-SEP-2C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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. .; ISS.

ö Gaps ; 0 100.0%; Score 49; DB 2; Length 509; 100.0%; Pred. No. 1.1; Indels il protein.
509 AA; 58116 MW; CE0E80DCD6D0F2F8 CRC64; ö 9

g

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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 431:946-957(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q4RR72; 2-322
                                                                                                                                                                                NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
  SOLUTION NEW TONE TO THE PROPERTY OF THE PROPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine
                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=16107303; DOI=10.1016/j.gene.2005.06.018;
Nervi S., Guinamard R., Delaval B., Lecine P., Vialettes B.,
Naquet P., Imbort J.;
"A rare mRNA variant of the human lymphocyte-specific protein tyrosin kinaseLCK gene with intron B retention and exon 7 shipping encodes a putativeprotein with altered SH3-dependent molecular interactions.";
Gene 359:18-25(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ865079; CAI23831.1; -; mRNA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR00219; Prot kinase.

InterPro; IPR00199; Prot kinase.

InterPro; IPR001990; SH2.

InterPro; IPR001452; SH3.

InterPro; IPR001452; SH3.

InterPro; IPR001452; Tyr_pkinase.

InterPro; IPR001452; Tyr_pkinase.

InterPro; IPR00145; Tyr_pkinase.

R Pfam; PF0011; SH2; 1.

R Pfam; PF00017; SH2; 1.

R PRINTS; PR001401; SH319.1.

R PRINTS; PR001401; SH310PMAIN.

R PRINTS; PR001401; SH3DOMAIN.

R PRINTS; PR001401; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 49; DB 2; Length 516; 100.0%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   516 AA; 58333 MW; EB9A52D4EBDF14D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
Q4RR72 TETMG
D4RR72 TETMG
AC Q4RR72, DR D4RR72 TETMG
D7 19-JUL-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                 10-MAY-2005, integrated into UniProtKB/TrEMBL
                                                                                                                            516 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                             Proto-oncogene tyrosine-protein kinase LCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00252; SH2; 1.
SMART; SM00226; SH3; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS500109; PROTEIN KINASE TYR; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                          PRT;
                                                                                                                                                                                       10-MAY-2005, sequence version 1. 07-FEB-2006, entry version 5.
                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 QLQHQRLVRL 310
294 QLQHQRLVRL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QLOHORLVRL 10
                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50002;
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                        Q573B4_HUMAN
Q573B4;
                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                     Name=LCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kinase
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PubMed=15496914; DOI=10.1038/nature03025;

Ruducelis L. Bouneau L. Fischer C., Ozouf-Costaz C., Bernot A.,

Anicaud S., Jaffee D., Fischer C., Ozouf-Costaz C., Bernot A.,

Railon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

Macaud S., Jaffee D., Fischer C., Lutfalla G., Dossat C., Segurens B.,

Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

Rathouard V., Jubin C., Castelli V., Katinka M., Wacherie B.,

Riemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

Riemont C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,

Rand C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,

Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,

Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

"Market D., 1946-057,0004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
-- FUNCTION: Plays a key role in the control of the eukaryotic cell cycle. It is required in higher cells for entry into S-phase and mitosis. Component of the kinase complex that phosphorylates the repetitive c-terminus of RNA polymerase II. Catalytic component of MPF (By similarity).
-- CAMANYIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tyrosine phosphate.
-!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in mature oocytes (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
07-FBB-2006, entry version 6.
Chromosome 14 SCAF15003, whole genome shotgun sequence. (Fragment)
ORFNames=GSTENG00030294001;
                                                                                                                   Terraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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GO; GO:000524; P:ATP binding; IEA.
GO; GO:000166; P:nucleotide binding; IEA.
GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.
GO; GO:0016740; P:protein amino acid phosphorylation; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR002799; Ser thr pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001265; Tyr_pkinase.
PRINTS; PR00109; TYRKINAŠE.
PRINTS; PR00109; TYRKINAŠE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 AA; 36768 MW; BCOEDOB6DB1CBB2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS500109; PROTEIN KINASE TYR; 1.
ATP-binding; Kinase; Nucleotide-binding; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; CAAE01015003; CAG09110.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 2;
Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.9%;
90.0%;
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tyrosine phosphate.

-!- ENZYME REGULATION: Regulated by phosphatases.
-!- SUBUNIT: Binds to the cytoplasmic domain of cell surface receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also binds to effector molecules, such as PI4K, VAVI, RASAI, FYB and to other proteins kinases including CDC2. RAFI, ZAPYO and SYK. Binds to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes through its SH3 domain and to the tyrosine phosphorylated form of KHDRSSI/PYO through its SH2 domain. Interacts with phosphorylated LIMEI. Interacts with Dhosphorylated LIMEI. Interacts with CBLB (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane. Present in lipid rafits in an unactive form (By similarity).
-!- TISSUE SPECIFICITY: Expressed specificaly in lymphoid cells.
-!- DEVELORMENTAL STAGE: Levels remain relatively constant throughout
                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Buteleostomi,
Mammalia; Eutheria, Euarchontoglires, Primates, Platyrrhini, Cebidae,
Cebinae, Saimiri.
                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA], ENZYME REGULATION, AND INTERACTION WITH SAIMIRINE HERPESVIRUS 2 TIP. TISSUE=T-cell;
                                                                                                                                      Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK) (Lymphocyte cell-specific protein-tyrosine kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-cell ontogeny. DoMaIn: The SH2 domain mediates interaction with SQSTM1 \ensuremath{\mathsf{SQMIN}}
                                                                                                      integrated into UniProtKB/Swiss-Prot.
                                                                               508 AA.
                                                                                                                                                                         Saimiri sciureus (Common squirrel monkey).
                                                                               PRT;
                                                                                                                                                                                                                                                                           MEDLINE=21424508; PubMed=11533187;
                                                                                                                08-NOV-2005, sequence version 2.
                                                                                                                            07-MAR-2006, entry version 26.
                                                                               STANDARD;
QLQHQRLVRL 10
                     91
             ||||:|||||
QLQHERLVRL
                                                                                                                                                                                                                      NCBI_TaxID=9521;
                                                                                                   08-NOV-2005,
                                                                               SAISC
Н
                                                                                      095KR7;
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                             PTM: Phosphorylated on Tyr-504 presumably by CSK. This phosphorylation downrequiates catalytic activity. Phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proto-oncogene tyrosine-protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphotyrosine (by autocatalysis) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-myristoyl glycine (By similarity).
S-palmitoyl cysteine (By similarity)
S-palmitoyl cysteine (By similarity)
508BC64061853819 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
SH2 domain; Transferase; Tyrosine-protein kinase.
INIT MET 0 Probable.
CHAIN 1 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein kinase.
ATP (By similarity).
Interactions with CD4 and CD8 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proton acceptor (By similarity).
Interaction is regulated by Ser-58 phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 1; Length 508; Pred. No. 6.5; 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTId=PRO_0000088127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 1.
SMART; SM00216; TYPKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity)
                                                                                                                                                                                                                                                         InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR001980; SH2.
InterPro; IPR001452; SH2.
                                                                                                                                                                                                                          EMBL; AJ277921; CAC38871.1; -; mRNA.
                                                                                                                                                                                                                                                                                                      InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase_AS.
Pfam; PF07714; Pkinase_Tyr; 1.
Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00018; SH3 1; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD0000001; Proc. Kinase; 1.
ProDom; PD0000093; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
223
497
258
71
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272
393
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                                                                                                                                                                                                                                                  SMR; Q95KR7; 64-508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                      P06239; 1LKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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TISSUE-Mammary gland;

RA PUNDECALIDE SEQUENCE.

RA DEMONS SEQUENCE.

RAD SEGUENCE.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB=Mammary_gland,
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninol P., Hayashizaki Y.;
High-efficiency Hayashizaki Y.;
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                 11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 7.
Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched
11brary, clone:G830026006 product:lymphocyte protein tyrosine kinase,
full insert sequence. (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The transcriptional landscape of the mammalian genome.";
                                                                                                                                                                                         368 AA.
                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 309:1559-1563(2005).
                                                                                                                                                                                       Q3TLX4 MOUSE PRELIMINARY;
Q3TLX4;
                                                    293 QLQHKRLVRL 302
                        1 QLQHQRLVRL 10
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                      Name=Lck;
                                                                                                                                                                 COLOR CONTROL 
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REP NUCLECTIES STORMER.

READ MUCLECTIES STO
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L.H., Derge J.G., Schuler G.D., Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altachul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Alsochen M., More T., Max J.L., Wang J., Hsich F., Stapleron M., Soarses M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Toner D.M., Marra M.A., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
             Mammalia; Eutheria; Evarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH MGC Project;
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00252; SH2; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC099218; AAH99218.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pkinase_AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase_i
Pfam; PF07714; Pkinase_Tyr; 1.
Pfam; PF000171; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00109; TYRKINASE.
PRODOM; PROC Kinase; 1.
ProDom; P0000093; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyrosine-protein kinase.
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                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q4FZR6; 2-379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Thymus;
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SEQUENCE
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Arakawa T., Carninci P., Thotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N. Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Muramateu M., Hayashizaki Y., Sulaki Y., Sulaki Y., Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                MEDLINE=20500913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rikki integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0004674; F:protein serine/threonine kinase activity; RCA. InterPro; IPR000719; Prot kinase. InterPro; IPR00290; Ser_thr_pkinase. InterPro; IPR001290; SH2. InterPro; IPR001245; Tyr_pkinase. InterPro; IPR001245; Tyr_pkinase. Ffam; PF00714; Pkinase Tyr; 1. Pfam; PF00017; SH2: InterPro; IPR001245; Tyr_pkinase AS. Ffam; PF00017; SH2: I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.8%; Score 43; DB 2; Length 368; 90.0%; Pred. No. 11; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                 sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 AA; 42018 MW; 7AB6AE53AF1A5059 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP-binding; Kinase; Nucleotide-binding; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-2005, integrated into UniProtKB/TrEMBL. 30-AUG-2005, sequence version 1. 07-FEB-2006, entry version 7. Lck_mapped protein (Fragment). Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PRO0109; TYRKINASE.
ProDom; PD000019; Prot_kinase; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS50011; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS50010; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AK166263; BAE38668.1; -; mRNA.
MGI; MGI:96756; Lck.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 90.0
Les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 QLQHPRLVRL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QLOHORLVRL 10
                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
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Q4FZR6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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RRY RAPARA RAPAR

ö Gaps ö 87.8%; Score 43; DB 2; Length 379; 90.0%; Pred. No. 11; indels iive 0; Mismatches 1; Indels 379 AA; 43336 MW; 7CDEB573BAFB53AB CRC64; ATP-binding; Kinase; Nucleotide-binding; Transferase;

RESULT 10 Q4FZR6 RAT 1D Q4FZR AC 30-FZR DT 30-AU DT 07-FE DE LGK M GN Name= OS Rattu

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NUCLEOTIDE SEQUENCE [MRNA].
MEDLINE-86079521; PubMed=2416464; DOI=10.1016/0092-8674(85)90169-2;
Marth J.D., Peet R., Krebs B.G., Perlmutter R.M.;
"A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpressed in the murine T cell lymphoma LSTRA.";
                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea; Muridae, Murinae, Mus.
                                                                                                                                                                                Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK) (Lymphocyte cell-specific protein-tyrosine kinase) (LSK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (2]
NUCLEOTIDE SEQUENCE [MRNA].
NUCLOTIDE SEQUENCE [MRNA].
Voronova A.F., Sefton B.M.;
"Expression of a new tyrosine protein kinase is stimulated by retrovirus promoter insertion.";
Nature 319:682-685(1986).
LCK_MOUSE STANDARD; PRT; 508 AA. P06240; O61794; O61795; O62120; O91X65; O1-UAN-1988, integrated into UniProtKB/Swiss-Prot. 25-OCT-2005, sequence version 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [3]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                            Name=Lck; Synonyms=Lsk-t;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell 43:393-404(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
       C BERGER 
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ensembl; ENGRAGORO0007783; Danio rerio.

Resembl; ENSDARGORO00007783; Danio rerio.

Resembl; ENSDARGORO000007783; Danio rerio.

Resembl; ENSDARGORO000007783; Danio rerio.

Resembl; ENSDARGORO00007783; Danio rerio.

Resembl; ENSDARGORO00007783; Danio rerio.

Resembl; ENSDARGORO0007783; ENTRE Profession kinase activity; IEA.

Resembl; Resembl; Profession kinase activity; IEA.

Resembl; Profession Resemble R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dunn M.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         485 AA; 55644 MW; 3ED1878453666747 CRC64;
                                                                                                                                                                                                                                                                                                                                                                07-DEC-2004, sequence version 1.
07-FEB-2006, entry version 8.
07-FEB-2006, entry version 8.
Novel protein tyrosine kinase.
Name-si-lakey-33122.2.
0RFNames=DKEY-33122.2-001;
Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 2;
Pred. No. 15;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                     07-DEC-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                    485 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BX842684; CAH69080.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probom; PD000001; Prot. Kinase; 1.
Probom; PD0000093; SH2; 1.
Probom; PD000066; SH3; 1.
SWART; SM00252; SH2; 1.
SWART; SM00226; SH3; 1.
SWART; SM00219; TyrKc; 1.
PROSITE; PS500107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS50010; SH2; 1.
                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                            QSTYU7 BRARE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.88;
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                                                                        164 OLOHPRLVRL 173
       1 QLQHQRLVRL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
NUCLEOTIDE SEQUENCE.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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OFTUD BRA
10 TYOT BRA
11 O7T-DE
DT 07T-DE
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RC PREAINENCYLUE SCHOULD MINIOUS SCHOULD MINIOUS RC PREAINENCYLUE SCHOULD LIANGES SCHOULD MINIOUS TISSUE-Thymus; S. Goody J., Frith M.C., Maeda N., RA Carninci P., Kasukawa T., Katayama S., Goody J., Frith M.C., Maeda N., RA Oyama R., Ravens T., Lenhad B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Barenner S. E., Batalov S., Forrest A.R., Zavolan M., Radinis V.B., Brenner S. E., Batalov S., Forrest A.R., Zavolan M., Radesi-Impiombato A., Apwailer R., Aturaliya R.N., Balls Y T.L., Ambesi-Impiombato A., Apwailer R., Aturaliya R.N., Balls Y T.L., Radesi-Impiombato A., Apwailer R., Aturaliya R.N., Balls Y T.L., Choudhary V., Christoffels A., Cluterbook D.R., Chuk K.P., Choudhary V., Christoffels A., Cluterbook D.R., Chuk R.A., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., R. Gercher C.F., Fukushima T., Furuno M., Pheak J. Crowe M. E., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., R. Anstroich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Anstroich S., Harbers M., Katoh M., Kawasawa Y., Kelso J., Kitamo H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Iwand H., Kanapin A., Katoh M., Kawasawa Y., Kalson M., Makauchi H., McMilliam S., Madlan Babu M., Madera M., Marchionni L., Liu J., Ravesi G., Krishnan S., Main Babu M., Madera M., Makauchi H., Marusawa S., Miki H., Mighon R., Miraka S., Morti F., Ohara O., Schopsen C., Sekguchi S., Ramade H., Shimada H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUCLEOTIDE SEQUENCE [LARGE SCALE MENA].
STRAIN=FVB/N; TISSUE-Salivary gland;
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RESULT 12 LCK_MOUSE

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          Klausher R.D., Collins F.S., Wagner I., Derge J.G.,
Klausher R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buerow K.H., Schemfer C.F., Bhar N.K.,
Apkins R.F., Jordan H., Moore T., Wagner I., Shenmen C.M., Schuler G.D.,
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Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rohards S.M., McEwan P.J., McKernan K.J., Mallek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raha S.S., Loquellano M.A., Young A.C., Sheychenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Salska U., Smailus D.E.,
Mcharch A., Schein J.E., Jones S.J.M., Marra M.A.;
Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Rohner A., Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hurley T.R., Amrein K.B., Sefton B.M.; "Creation and characterization of temperature-sensitive mutants of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTIONS WITH CD4 AND CD8, AND MUTAGENESIS OF 2-CYS-4; CYS-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88142832; PubMed=3501824;
Voronova A.F., Adler H.T., Sefton B.M.;
"Two lck transcripts containing different 5' untranslated regions are
present in T cells.";
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"Avian recovirus mRNAs are nonfunctional in infected mon
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J. Virol. 66:7406-7413(1992).
                                                                                                                                                                                                                                                                                                              mouse cDNA sequences.
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MUTAGENESIS OF TYR-504.
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05-JUL-2004, sequence version 1.
07-FBB-2006, entry version 9.
Hypothetical protein OJ1063_D06.21.
Name=OJ1063_D06.21;
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PubMed=8371758; DOI=10.1038/365156a0;
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                                                                                                                                                                                                                                                                                                                                                   anchoring ATP.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995, sequence version 2.
07-MAR-2006, entry version 63.
Tyrosine-protein kinase BLK (EC 2.7.1.112) (B lymphocyte kinase) (p55-
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euzrchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96224819; Pubmed=8639560; DOI=10.1021/bi960157x; Metlat W.J., Leiting B., Pryor K., Mueller L., Farmer B.T. II; The three-dimensional solution structure of the SH2 domain from p55blk kinase."; Proverse of the SH2 domain from Biochemistry 35:6201-6211(1996).

-!- PUNCTION: May function in a signal transduction pathway that is restricted to B Lymphoid cells.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dymecki S.M., Niederhuber J.E., Desiderio S.V.; "Specific expression of a tyrosine kinase gene, blk, in B lymphoid
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80.0%; Pred. No. 37;
ive 1; Mismatches 1; Indels
                                                                                                                                     NUCLEOTIDE SEQUENCE.
Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                  56815 MW; 2C3B2BDA3745CA28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1990, integrated into UniProtKB/Swiss-Prot.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M30903; AAA40453.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90117147; PubMed=2404338;
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                                                                                                                                                                                                                                                                                      Gramene; Q6KA98; -.
InterPro; IPR001810; F-box.
Pfam; PF00646; F-box; 1.
PROSITE; PS50181; FEOX; 1.
Hypothetical protein.
SEQUENCE 490 AA; 56815 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [MRNA].
TISSUE=B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 247:332-336(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 QLEHQRLVEL 232
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P16277;
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                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC089654; AAH89654.1; -; mRNA.
GO; GO:0004713; F:ATP binding; IEA.
GO; GO:0004713; F:ATP binding; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR001999; SPC thr_pkinase.
InterPro; IPR001990; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001452; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase_AS.
Fēam; PF0714; PRinase_Tyr; I.
                                          Indels
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Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2005, integrated into UniProtKB/TrEMBL.
01-MAR-2005, sequence version 1.
07-FEB-2006, entry version 8.
                                                                                                                                                                                                                                                                                                                                                                                  498 AA
                                          1; Mismatches
   Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                      QSFW27 XENTR PRELIMINARY; PRT; QSFW27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PD000001; Prot_kinase; 1.
88.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00018; SH3 1; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
                                          8; Conservative
                                                                                                                                                              |||:|||||
284 LQHERLVRL 292
                                                                                                               2 LQHQRLVRL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGC107870 protein.
Name=MGC107870;
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OSFW27 XENTR

ID QSFW27 XENTR

OOF 01-MAR-2()

DT 01-MAR-2()

DT 01-MAR-2()

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DT 01-MAR-2()

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GN Name-MGC;

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RC STRAIN=NOD; TISSUE=Activated spleen;

RC Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Ayama R., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Ayama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Bajic V.B., Milming L.G., Addinis V., Allen J.E.,

Bayis M.J., Wilming L.G., Addinis V., Allen J.E.,

Bayis M.J., Wilming L.G., Addinis V., Allen J.E.,

Bayis M.J., Wilming L.G., Addinis V., Allen J.E.,

Bansal M., Baxer L., Basel K.W., Bersano T., Bono H., Chalk A.M.,

RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

Crowe M.L., Down T., Engstrom P., Fagiolini M., Fallkner G.,

R. Crowe M.L., Down T., Engstrom P., Furaki S., Gariboldi M.,

R. Hetcher C.F., Fukushima T., Furuno M., Furaki S., Gariboldi M.,

R. Hench T.K., Harbers M., Hayashi Y., Hensch T.K., Hirokawa T.,

R. Harbers M., Hayashi Y., Hensch T.K., Hirokawa T.,

R. Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,

R. Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,

R. Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,

R. Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,

R. Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,

Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,

Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,

R. Matsuda H., Nashiguchi S., Nishikawa S., Norri F., Ohara O.,

R. Asaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Senga L., Sheng Y., Salzberg S.L., Sandelin A., Schoneider C., Sekiguchi K., Semple J., Richana R., Takenaka Y., Taki K.,

Shibata Y., Shimada H., Shimada K., Silva D., Silcialis R., Taki K.,

Sperling S., Stupka E., Sugiura K., Sulvana R., Taki K., Taki K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=NOD; TISSUE=Activated spleen;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Activated spleen cDNA, RIKEN full-length enriched library,
clone:F830002A02 product:B lymphoid kinase, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 2; Length 498;
Pred. No. 38;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  56437 MW; 3C5B9CEED5A0DF00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           499 AA.
                                                                        SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 1.
SMART; SM00319; TYPKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS0001; SH2; 1.
PROSITE; PS50002; SH3; 1.
SEQUENCE 498 AA; 56437 MW; 3CSB9CEEDSA0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q3TAT8 MOUSE PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-OCT-2005, sequence version 1. 07-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.98;
ProDom; PD000093; SH2; 1. ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||:||||
283 LQHERLVRL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LQHQRLVRL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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R. Mannishi H., Zabarozenky E. Zhus D. Zhane A. Kai C., Sabati D. Tomaru Y.,

R. Mannishi H., Zabarozenky E. Jusach E. T., Brusic V., Omackenbush J.,

R. Mandiested C., Martick J. S., Hune D. A. Kai C., Sabati D. Tomaru Y.,

R. Mandiested C., Marmanori-Macepane M. Wat C., Sabati D. Tomaru Y.,

R. Mandiested C., Marmanori-Macepane M. Wat C., Sabati D. Tomaru Y.,

R. Mandiested C., Marmanori-Macepane M. Sabati M. Mandia M. Maki M. Maki M. Maki M. Maki M. Maki M. Maki K., Maralhiti A., Okamira-Oho Y., Suzuki H., Kawai J.,

R. Mandiested C., Maralhiti A., Okamira-Oho Y., Suzuki H., Kawai J.,

R. Mandiested C., Maralhiti A., Okamira-Oho Y., Suzuki H., Kawai J.,

R. Mandiested C., Maralhiti A., Okamira-Oho Y., Suzuki H., Kawai J.,

R. Mandiested C., Maralhiti A., Okamira-Oho Y., Suzuki H., Kawai J.,

R. Mandiested C., Maralhiti A., Okamira-Oho Y., Suzuki H., Kawai J.,

R. Mandiested M. Maki K., Watchild M. Mandia M. Mandiested M. Maki M. Maki K., Maralhiti M. Mali D. Mali M. Maki M. Maki K., Maralhiti M. Mali M. Maki M
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                                                                                                                                                                                                            STRAIN=NOD; TISSUE=Activated spleen;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-NOD; TISSUE-Activated spleen;
Arakwa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Nagadka K., Nagadka K., Nagadka N., Sasaki N., Carninci P., Sumata K., Itoh M., Aizawa K., Nagadka T., Tashiro H., Itoh M., Sumi N., Ishii K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamannoto H., Sakaguchi S., Inegami T., Kashiiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikiki integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                    Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AK171640; BAE42580.1; -; mRNA.
MGI; MGI:88169; Blk.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000290; Ser_thr_pkinase.
InterPro; IPR000980; SH2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56614 MW; E1C607564BB4FD6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
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Pred. No. 38;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00107; PROTEIN KINASE ATP; PROSITE; PS0011; PROTEIN KINASE DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00018; SH3_1; 1.
PRINTS; PR00401; SH2DOWAIN.
PRINTS; PR00452; SH3DOWAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot_kinase; 1.
ProDom; PD0000063; SH2; 1.
ProDom; PD0000065; SH3; 1.
SWART; SM00252; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001452; SH3.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF07714; Pkinase_Tyr; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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88.9%;
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PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                  Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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SEQUENCE
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Best Local S
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SMART; SM00326; SH3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUB-THYMUS;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Retausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausberg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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Rachery J., Helton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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Rotriguez A.C., Grimwood J., Schnutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR00290; SET.
InterPro; IPR001990; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001452; Tyr_pkinase.
InterPro; IPR00145; Tyr_pkinase.
InterPro; IPR00145; Tyr_pkinase.
InterPro; IPR00145; Tyr_pkinase.
IPEam; PF00018; SH3 1; 1.
IPEINTS; PR00401; SH2DOMAIN.
IPRINTS; PR00401; SH2DOMAIN.
IPRINTS; PR00402; SH2DOMAIN.
IPRINTS; PR00409; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                               02-AUG-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                     499 AA.
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                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                  02-AUG-2005, sequence version 1.
                                                                                                                                                                                                                                                                             07-FEB-2006, entry version 3 B lymphoid kinase.
                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                       285 LQHERLVRL 293
                 LOHORLVRL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
TISSUE=Thymus;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                Q4KM97_RAT
Q4KM97;
                                                                                                                                    RESULT 17
Q4KM97 RAT
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STRAIN-C57BL/G1; ITSSUE-Mammary gland;
STRAIN-C57BL/G1;
STRAIN-C57BL/G1;
STRAIN-C57BL/G1;
STRAIN-C57BL/G1;
STRAIN-C57BL/G1;
STRAIN-C57BL/G1;
STRAIN-C5.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2002, integrated into UniProtKB/TrEMBL.
01-0CT-2002, sequence version 1.
07-FEB-2006, entry version 27.
B lymphoid kinase (Blk protein) (Activated spleen cDNA, RIKEN full-length enriched library, clone:F830045C23 product:B lymphoid kinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 2; Length 499;
Pred. No. 38;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                          499 AA; 56648 MW; BABC593E15CAAFD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          499 AA.
SMART; SM00219; TYRKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
STRAIN=NOD; TISSUE=Activated spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBK2M8 MOUSE PRELIMINARY; PRT;
O8K2M8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                   83.7%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                Kinase
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REALINE ## 19979253; Pubbled-in194955; DOI=10.1016/S0076-6879(99)03004-99; RT "High-efficiency Mill-length Ty." A when when the Realization of the
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Sandellan, A. Schneider C., Sengle C.A., Setou M., Shimada K.,

Railtean R., Takenaka Y., Taylor M.S., Taeadale E.D., Tomita M.,

Verardo, R., Wagner L., Wahlested C., Wang Y., Matanabe V., Wells C.

R. Wiltean R., Takenaka Y., Taylor M.S., Taeadale E.D., Tomita M.,

Verardo, R., Wagner L., Wahlested C., Wang Y., Matanabe V., Wells C.

R. Winner C., Whenhaw Bortz M., Zamen T., Sandella E., Mangel L., Wang I.,

R. Hara A., Hashtune W., Takena M., Tahlid Y., Tahlid S., Mangel L., Wang I.,

R. Hara A., Hashtune M., Waterston R., Jahlid Y., Tohlid S.,

R. Hara A., Hashtune W., Materston R., Jahlid Y., Tohlid S.,

R. Hara A., Hashtune M., Waterston R., Jahlid Y., Tohlid S.,

R. Hara A., Hashtune M., Waterston R., Jahlid K., Jich M., Kagawa I.,

R. Mangasi A., Soblid M., Waterston R., Lander E.S., Rogers J.,

R. Mangasi C., the Mangase transcriptome based on functional annotation of M. Wangasis C. the Month C. M., Standam M., Mangasis C. The Mangasis of the Month C.

R. Mangasis of the Month C. M., Shindara M., Shondara M., Shindara M.

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PRINTS; PR00401; SH2DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLK_HUMAN STANDARD; PRT; 504 AA.
P51451; Q16291;
01-0CT-1996, integrated into UniProtKB/Swiss-Prot.
01-0CT-1996, sequence version 1.
07-MAR-2006, entry version 48.
Tyrosine-protein kinase BLK (BC 2.7.1.112) (B lymphocyte kinase) (p55-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLECTIDE SEQUENCE (MRNA).

MEDLINE=95123078; PubMed=7822795;

Islam K.B., Rabbani H., Larsson C., Sanders R., Smith C.I.;

"Molecular cloning, characterization, and chromosomal localization of a human lymphoid tyrosine Kinase related to murine Blk.";

J. Immunol. 154:1265-1272(1995).
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.
                                                                                                              Gaps
                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, 233998; CAA83965.1; -; mRNA.
REMBL, 233998; CAA83365.1; -; mRNA.
RISE, 137206.
RISE, 137206.
RISE, P16277; BLK.
SKR; P51451; 62-504
RISGOO00136573; Homo sapiens.
RICK, HGNC:1057; BLK.
RICK, HG
                                                       2; Length 499;
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [MRNA].
MEDINE=99148218; PubMed=7845672;
Drebin J.A., Hartzell S.W., Griffin C., Campbell M.J.,
Niederhuber J.E.;
                                                    Score 41; DB
Pred. No. 38;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
                                                    83.7%;
88.9%;
                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00018; SH3_1; 1.
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285 LQHERLVRL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tyrosine phosphate.
                                                                                                                                                             2 LQHQRLVRL 10
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                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=BLK;
                                                                                                                                                                                                                                                                                          RESULT 19

BLK HUMAN

ID PS1451

DT O1-0C

DT O1-0C

DT O1-0C

OC Manna

OC Homo

OC Manna

OC Homo

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TISSUB-Blood, and Lymph;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                  R SMART; SM0025; SH2; 1.

R SMART; SM00326; SH2; 1.

SMART; SM00326; SH3; 1.

R SMART; SM0019; TYRC; 1.

R PROSITE; PS0010; PROTEIN KINASE ATP; 1.

R PROSITE; PS0010; PROTEIN KINASE_DOM; 1.

R PROSITE; PS00002; SH3; 1.

R PROSITE; PS00002; SH3; 1.

M ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding; M Phosphorylation; SH2 domain; SH3 domain; Transferase; M Tyrosine-protein kinase.

T INIT MET 0 0 PTyrosine-protein kinase BLK.

T CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
Phosphotyrosine (by autocatalysis) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sımılarıty).
N-myristoyl glycine (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
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Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                              By similarity.
Tyrosine-protein kinase BLK./FTId=PRO_0000088061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 M -> V (in Ref. 2).
106 I -> Y (in Ref. 2).
57607 MW; BDB1DF50EC7370C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001, integrated into UniProtKB/TrEMBL. 01-DEC-2001, sequence version 1. 07-FEB-2006, entry version 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O<u>9</u>61N1 HUMAN PRELIMINARY; PRT;
Q961N1;
PRINTS; PRO0452; SH3DOMAIN.
PRINTS; PRO0109; TYRKINASE.
PRODOM; PD000001; Prot_kinase; 1.
ProDom; PD0000093; SH2; 1.
ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.7%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B lymphoid tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     493
359
268
388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1
286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP BIND
ACT SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIPID
CONFLICT
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                                                                                                                                       US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Methylobacillus flagellatus KT.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUCLEOTIDE SEQUENCE.
PubMed=15496914; DOI=10.1038/nature03025;
Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Micaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.; Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORFNames-GSTENG00032670001;
Tetraodon nigroviridis (Green puffer).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-FEB-2006, entry version 6.
Chromosome undetermined SCAF15024, whole genome shotgun sequence.
Bacteria, Proteobacteria, Betaproteobacteria, Methylophilales,
Methylophilaceae, Methylobacillus.
NCBL_TaxID=265072;
                                                                                                                                                                                                                                                                                                                                                 Larimer F., Land M.; "Annotation of the draft genome assembly of Methylobacillus flagellatus KT.";
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                            Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AADX02000002; EAN03635.1; -; Genomic_DNA.
InterPro; IPR006860; FecR.
InterPro; IPR012373; Ferrdict_sens_TM.
Pfam; PF04773; FecR; 1.
PIRSF; PIRSF018266; FecR; 1.
SEQUENCE 320 AA; 35823 MW; 24B1EF921196EFE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.6%; Score 40; DB 2;
100.0%; Pred. No. 36;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2005, integrated into UniProtKB/TrEMBL 19-JUL-2005, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         511 AA.
                                                                                                                                                                                                                                                                                                                                US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US DOE Joint Genome Institute (JGI-PGF);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 QHQRLVRL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data
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                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
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Q4RL31;
                                                                                                                                                                                                                                                                                                              STRAIN=KT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TETNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U.C., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Barra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
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& GO; GO:0005524; F:ATP binding; IEA.

& GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

& GO; GO:0006468; P:protein-tyrosine kinase activity; IEA.

& GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

& InterPro; IPR000719; Prot kinase.

InterPro; IPR000290; Ser_thr_pkinase.

InterPro; IPR001290; Ser_thr_pkinase.

InterPro; IPR001452; SH3.

InterPro; IPR001452; Tyr_pkinase.

Pfam; PF00171; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                             Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                  Director MGC Project;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         505 AA; 57706 MW; BSF739BEF8389176 CRC64;
                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 2;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-0CT-2005, integrated into UniProtKB/TrEMBL. 11-0CT-2005, sequence version 1. 07-FBB-2006, entry version 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000001; Proc. Kinase; 1.
ProDom; PD000093; SH2; 1.
ProDom; PD000066; SH3; 1.
SMART; SM00252; SH3; 1.
SMART; SM00326; SH3; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS50017; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC007371; AAH07371.1; -; mRNA.
EMBL; BC034713; AAH32413.1; -; mRNA.
HSSP; P16277; 1BLK.
SMR; Q96IN1; 63-505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feck protein.
ORFNames=MflaDRAFT_2314;
Methylobacillus flagellatus KT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q3XC39 METFL PRELIMINARY;
Q3XC39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF00018; SH3 1; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
                                                                                                                      and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 LQHERLVRL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LQHQRLVRL 10
                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
TISSUE=Blood;
                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                            TISSUE=Lymph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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03X39 METFL
03X39 METFL
AC 03X39 M
DT 11-0CT-20
DT 07-PEB-20
DT 07-PEB-20
DR PEGR Prof
DR ORNAMES
OS METPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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RAPARA RA

Kinase

ò a

ö

Gaps

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Length 320; 0; Indels

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Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Plays a key role in the control of the eukaryotic cell
cycle. It is required in higher cells for entry into S-phase and
mitosis. Component of the kinase complex that phosphorylates the
repetitive C-terminus of RNA polymerase II. Catalytic component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                      WOCHEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research;
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding, Kinase, Nucleotide-binding; SH3 domain; Transferase;
Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GG; GG:0005524; F:ATP binding; I; Genomic_Dna.

GG; GG:0005524; F:ATP binding; IEA.

GG; GG:0004713; F:Droclectide binding; IEA.

GG; GG:0004713; F:Droclectide binding; IEA.

GG; GG:0007242; F:Intracellular signaling cascade; IEA.

GG; GG:0007242; P:Intracellular signaling cascade; IEA.

GG; GG:0007242; P:Intracellular signaling cascade; IEA.

GG; GG:000668; P:Droclectin anino acid phosphorylation; IEA.

InterPro; IPR000799; Prot Kinase.

InterPro; IPR000990; Ser_thr_pkinase.

InterPro; IPR001452; SH3.

InterPro; IPR001452; Tyr_pkinase.

InterPro; IPR00156; Tyr_pkinase.

InterPro; IPR001856; Tyr_pkinase.

InterPro; IPR001856; Tyr_pkinase.

IPEan; PF00011; SH3:1:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.6%; Score 40; DB 2; Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               511 AA; 58279 MW; 9B7977111E4685AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; CAAE01015024; CAG10901.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00222; SH2; 1.
SMART; SM00225; SH3; 1.
SMART; SM00219; TYKK2; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mature oocytes (By similarity).
-!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD000001; Prot kinase; 1. ProDom; PD000093; SH2; 1. ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00452; SH3DOMAIN
PRINTS; PR00109; TYRKINASE
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                                                                                                                                                                                                                                                                                                                                                                        Nature 431:946-957(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPF (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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           SO TAWAR BURNERS BURNE
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05-JUL-2004, sequence version 1.
05-JUL-2004, sequence version 1.
07-FBB-2006, entry version 8.
Hypothetical protein OJ1008_D08.5.
Name=OJ1008_D08.5;
Name=OJ1008_D08.5;
Name=OJ1008_D08.5;
Serratophyta; Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP Clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                               Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T., "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey: isoform duplications around the divergence of cyclostomes and
                                                                                               Src-like A (Fragment).
Eptetretus burgeri (Inshore hagfish).
Eptetretus burgeri (Inshore tagfish).
Bukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
Myxinidae; Eptetretinae; Eptetretus.
NCBI_TaxID=7764;
                                                                                                                                                                                                                                                                                                                                   J. Mol. Evol. 49:601-608(1999).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB025546; BAA84736.1; -; mRNA.

HSSP; P06239; 1QPC.

S GNR; QQUBVG, 1.249.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0004713; F:protein amino acid phosphorylation; IEA.

GO; GO:0006469; P:protein amino acid phosphorylation; IEA.

RICERPO; PR001245; Tyr_pkinase.

RICERPO; PR001245; Tyr_pkinase.

REAM: PR07714; Pkinase Tyr; 1.

REAM: PR07714; Pkinase Tyr; 1.

REAM: PR07714; Pkinase Tyr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 AA; 28636 MW; D7F37EE197EA580C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.6%; Score 39; DB 2;
88.9%; Pred. No. 43;
trive 0; Mismatches
                                                                     into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                  PRT;
                                                                                                                                                                                                                                                MEDLINE=20020330; PubMed=10552041;
                                                                                  01-MAY-2000, sequence version 1.
07-FEB-2006, entry version 28.
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Q6L576;
                                 Q9U8V6_EPTBU PRELIMINARY;
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                                                                01-MAY-2000, integrated
                                                                                                                                                                                                                                                                                                                                                                         tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00219; TyrKc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LOHORLVRL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 LOHDRLVRL 43
                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                    gnathostomes.";
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Q6L576_ORY
RESULT :
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Gaps

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1; Indels

Pred. No. 60; 1; Mismatches

80.08;

8; Conservative

Matches

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Local Similarity

1 QLQHQRLVRL 10 :||| ||||| 258 KLQHDRLVRL 267

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Q66104_BRARE
Q66104;
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                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M., Chang S.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R., Cheng Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H., Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L., Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W., Wu H.-P., Shaw J.-F., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W., Submitted (JUN-2004) to the BMBL/GenBank/DDBJ databases.
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1-NOV-1998, sequence version 1.
07-FBB-2006, entry version 25.
Non-receptor protein tyrosine kinase laloo.
Non-receptor favis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniala, Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                            Gramen; Q6L576, -...
GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
GO; GO:0006629; P:lipid metabolism; IEA.
InterPro; IPRO1087; Lipase_GDSL.
Pfam; PF00657; Lipase_GDSL, 1.
Hypothetical protein.
SEQUENCE 371 AA; 42000 MW; 01AA0FD3200A8D28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
Weinstein D.C., Marden J., Carnevali F., Hemmati-Brivanlou A.;
"FGF-mediated mesoderm induction involves the Src-family kinase
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GO; GO: 000471; 54.496.

GO; GO: 000471; 54.496.

GO; GO: 0004871; F: Parceptor activity; IEA.

GO; GO: 0004872; F: Perceptor activity; IEA.

GO; GO: 0007242; P: Pintracellular signaling cascade; IEA.

GO; GO: 0006488; P: Pintracellular signaling cascade; IEA.

InterPro; IPR000290; Ser_thr_pkinase.

InterPro; IPR001980; SH3.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR0011; SH2.

IPEm; PF0011; SH2.

IPEm; PF0011; SH2.

REM; PR0011; SH3.

REM; PR00451; SH3DOWAIN.

REM; PRNTS; PR00401; SH2DOWAIN.

REM; PRNTS; PR00401; SH2DOWAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.6%; Score 39; DB 2; Length 371; 77.8%; Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       496 AA.
                                                                                                                                                                                                                                                                                                                                                                EMBL; AC104705; AAT44173.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF081803; AAC31209.1; -; mRNA.
HSSP; P06239; 1QPC.
SMR; O93411; 54-496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    093411_XENLA PRELIMINARY; PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae; Xenopus; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||||:|||
306 QLQHERVVR 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QLQHQRLVR 9
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093411 XEN
10 093411 XEN
10 001-NG
DT 001-NG
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MEDINES 250. PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899; Atlausher R.D., Colling F.S., Wagger L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haish F., Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Arapa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Abramson R.D., Mullahy S.J., Ancher B. S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Arilaton D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Willaton D.K., Muzny D.W., Sodergren B.D., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anthing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Abraeley R.W., Touchman J.W., Green E.D., Dickson M.C., Abraeley R.W., Touchman J.W., Green E.D., Dickson M.C., Abraeley R.W., Touchman J.W., Green E.D., Dickson M.C., Abraeley R.W., Krzywinski M.I., Skalska U., Smailus D.E., Benterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., M. Generzation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OŘFNames=zgc:92124;
Brachydanio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                    496 AA; 56275 MW; 96223A6F99689965 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                            79.6%; Score 39; DB 2;
88.9%; Pred. No. 91;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2004, integrated into UniProtKB/TrEMBL. 11-OCT-2004, sequence version 1. 07-FBB-2006, entry version 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                510 AA.
SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 1.
SMART; SM00319; TYRK2: 1.
PROSITE; PS00107; PROTEIN KINASE ATF; 1.
PROSITE; PS50011; PROTEIN KINASE DOW; 1.
PROSITE; PS50010; PROTEIN KINASE TYR; 1.
PROSITE; PS50001; SH3; 1.
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Ensembl; ENSDARG0000031715; Danio rerio.
ZFIN; ZDB-GENE-040912-7; zgc:92124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC081601; AAH81601.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 79.6
Best Local Similarity 88.9
Matches 8; Conservative
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Director MGC Project;
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                                                                                                                                                                                                                                                                                                                Kinase, Receptor
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1 OLOHORLVRL 10
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QEKAA1;
                                                                                                                                                       Rubrerythrin.
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Q6KAA1 ORY
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Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D., Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-:- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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GO; GO:0005524; P:ATP binding; IEA.

GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR00209; Ser_thr_pkinase.

InterPro; IPR001452; SH3.

InterPro; IPR001652; SH3.

InterPro; IPR001652; SH3.

R PRINTS; PR00109; TYKINASE.

PRODOM; PD0000093; SH3; 1.

R ProDom; PD0000065; SH3; 1.

R PRODOM; PD0000065; SH3; 1.

R SWART; SM00252; SH3; 1.

R SWART; SM00252; SH3; 1.

R PROSITE; PSS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PSS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PSS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PSS00109; SH07FIN KINASE TYR; 1.

R PROSITE; PSS00109; SH07FIN KINASE TYR; 1.

R PROSITE; PSS00109; SH07FIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-2003, sequence version 1.
07-FEB-2006, entry version 8.
GLP 228 4192 2252.
Glardia lamblia ATCC 50803.
Eukaryota, Diplomonadida, Hexamitidae, Giardiinae, Giardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.6%; Score 39; DB 2; Length 646; 70.0%; Pred. No. 1.2e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                               79.6%; Score 39; DB 2; Length 510; 88.9%; Pred. No. 94; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AACB01000126; EAA37797.1; -; Genomic_DNA.
InterPro; IPR002110; ANK.
PRINTS; PR01415; ANKYIN.
SMART; SM002415; ANK; 1.
SEQUENCE 646 AA; 71121 MW; 00AB6794E2516E55 CRC64;
                                                                                                                                                                                                                                                                                                                                        58258 MW; SEE8F68226569BA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-2003, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 88.9 es 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       295 LOHDRLVRL 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary data.
                                                                                                                                                                                                                                                                                                                                       510 AA;
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                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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GIALA
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05-UL-2004, sequence version 1.
07-FEB-2006, entry version 5.
07-FEB-2006, entry version 5.
Name=CJ1063_D06.18.
Name=CJ1063_D06.18.
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Spermatophyta; Niridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
NCBL TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-2CP-C;
US DOE Joint Genome Institute;
US DOE Joint Genome Institute;
US DOE Joint Genome Institute;
US DOE Joint Genome Instituck S., Brettin T., Bruce D., Han C.,
Hammon N., Israni S., Pitluck S., Brettin T., Bruce D., Han C.,
Tapia R., Gilna P., Kiss H., Schmutz J., Larimer F., Land M.,
Kyrpides N., Anderson I., Sanford R.A., Ritalahti K.M., Thomas H.S.,
Kirby J.R., Zhulin I.B., Looeffler F.E., Richardson P.;
"Complete sequence of Anaeromyxobacter dehalogenans 2CP-C.";
Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                             ORFNames=Adeh 2075;
Anaeromyxobacter dehalogenans 2CP-C.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.6%; Score 38; DB 2; Length 175; 77.8%; Pred. No. 46; tive 2; Mismatches 0; Indels
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; CP000251; ABC81845.1; -; Genomic_DNA.
SEQUENCE 175 AA; 19497 MW; 3CDB642B8F604347 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l protein.
327 AA; 38081 MW; 90DCDF0AEBA8AF50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cystobacterineae; Myxococcaceae; Anaeromyxobacter
                                                                                                                                                                                                                                                   07-MAR-2006, integrated into UniProtKB/TrEMBL. 07-MAR-2006, sequence version 1.
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Q2IJLI;
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4atches 7; Conservative
382 EVQHQRLARL 391
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142 ELKHQRLVR 150
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TRAINS-HW-1:IMSS.

CY PubMed=15729342; DOI=10.1038/nature03291;

UX Loftus B.J., Anderson I., Davies R., Alsmark U.C., Samuelson J.,

A Medeo P., Roncaglia P., Berriama M., Hirt R.P., Mann B.J., Nozaki T.,

A Medeo P., Roncaglia P., Berriama M., Hirt R.P., Leippe M.,

A Suh B., Pop M., Duchene M., Ackers J., Tannich B., Leippe M.,

A Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,

RA Hofer M., Bruchhaus I., Willhoeft U., Brattacharya A.,

RA Ghillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,

RA Whitchead S., Quail M.A., Rabbinowitsch B., Norbertczak H., Price C.,

RA Whitchead S., Quail M.A., Rabbinowitsch B., Norbertczak H., Price C.,

RA Whitchead S., Quail M.A., Rabbinowitsch B., Norbertczak H., Price C.,

RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,

RA Barrall B.G., Frager C.M., Hall N.;

RT Genome of the protist parasite Entamoeba histolytica.";

RA Loure 433:865-868(2005).

CC EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
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                                     Gaps
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GO; GO:0005224; F:ATP binding; IEA.
GO; GO:000466; F:nucleotide binding; IEA.
GO; GO:000466; F:nucleotide binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR008271; Ser_thr pkin AS.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001645; Tyr_pkinase.
InterPro; IPR001645; Tyr_pkinase.
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-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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Pred. No. 93;
2; Mismatches 1; Indels
                                  1; Indels
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Serine/threonine-protein kinase; Transferase.
SEQUENCE 335 AA; 38352 MW; 765FABA2D3D27D5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          07-JUN 2005, integrated into UniProtKB/TrEMBL. 07-JUN 2005, sequence version 1. 07-JUN 2005, entry version 7. Protein kinase, putative. ORFNames=72 t00027, Entamobe histolytica HM-1:IMSS. Eukaryota; Entamobebidae; Entamobeba.
                                                                                                                                                                                                                                                                                                                                    335 AA.
   Pred. No. 90;
2; Mismatches
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SMART; SM0220; S TKc; 1.
PROSITE; PS00101; PROTEIN KINASE ATP; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
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Best Local Similarity 70.0
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   Best Local Similarity 70.0
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91 QVEHQRLVEL 100
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ADM864601
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97 98 99

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Sequences AAV43902-Y44015 represent proteins used in a novel method of predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure, active sites, and parsing segments. Secondary structural units are assigned by identifying periodicity in the assignments, and assembled into globular form using distance conscraints imposed by disulfide bridges, active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein molecule, as interaction of a protein with other molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prediction; secondary structure; alignment; evolutionary conservation; homology; periodicity; co-variation analysis; antigenic site; site directed mutagenesis; interaction.
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                                                                                                                                                                                                                                 Predicting the folded structure of proteins.
                                                                                                                                                                                                                                                                Disclosure; Col 255-258; 113pp; English.
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Best Local Similarity 100.
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                                                                                                          25-MAR-1992;
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                   US5958784-A.
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                                               28-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Benner SA;
                                                                                                                                                                     Benner SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY43955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY43955
ID AAY4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
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Ady84080 Human Src
Abg23778 Novel hum
Abm88001 Rice abio
Abm87949 Rice abio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and polynucleotides encoding them for treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to peptides which are partial sequences of stor/lck family proteins. The present sequence is one such peptide. The peptides are useful for producing vaccines for the treatment of cancer, including colon cancer and small-cell lung cancer.
                                                                                                                                                                                                                                                                                               Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prediction; secondary structure; alignment; evolutionary conservation; homology; periodicity; co-variation analysis; antigenic site; site directed mutagenesis; interaction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 41; DB 4; Length 9; 100.0%; Pred. No. 2.1e+06; tive 0; Mismatches 0; Indels
                                                                                          ALIGNMENTS
                 ABG23778
ABM88001
   ADY84080
                                               ABM87949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 70; 75pp; Japanese.
                                                                                                                                                                     AAB73130 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000; 2000WO-JP005220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-00222101
                                                                                                                                                                                                                                                                Tumour antigen peptide #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity luv.
9; Conservative
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                                                                                                                                                                                                                                                                                                                             Homo sapiens
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33344
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AAB73130
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                                                                                                                          Sequences AAY43902-Y44015 represent proteins used in a novel method of predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure, active sites, and parsing segments. Secondary structural units are assigned by identifying periodicity in the assignments, and assembled into globular form using distance constraints imposed by disulfide bridges, active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein molecule, as guides for site directed mutagenesis studies, and for understanding the interaction of a protein with other molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Designing a ligand binding to a target molecule, comprises identifying as molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method of designing a ligand binding to a target molecule. The method involves identifying as molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesising ligand. The invention is useful for designing drug products and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular scaffold; nuclear hormone receptor; TNF receptor; G-protein coupled receptor; methyl transferase; ligase;
Predicting the folded structure of proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 24; 186pp; English.
                                                              Disclosure, Col 253-256; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR88385 standard; protein; 263 AA
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16-SEP-2002; 2002US-0411398P.
20-SEP-2002; 2002US-0412341P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCK tyrosine kinase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G-protein coupled receptor;
LCK tyrosine kinase; enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 259 AA;
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Best Local S:
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild-type D substituted with N. This position 364 in the full-length sequence (see ABR56202 for the wild-type full length sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New crystalline polypeptide comprising ligand binding domain or cataly domain of Lck protein, for determining three-dimensional structure of catalytic domain of Lck, has predetermined unit cell parameters.
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Human, protein co-ordinate data, Lymphocyte Cell Kinase, Lck, enzyme,
Src-family protein tyrosine kinase, T-cell, immune response, mutein,
designing ligand binding to target molecules such as nuclear hormone receptors, TNF receptors, G-protein coupled receptors, methyl transferases, ligases, etc. The present sequence is the LCK tyrosine kinase protein. This sequence is used to illustrate the method of
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                                                                                                                   100.0%; Score 41; DB 8; Length 263; 100.0%; Pred. No. 2.1; 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dixon RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                     ABR56203 standard; protein; 265 AA.
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                                                                                                                                                  9; Conservative
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                                                                                                                                   Local Similarity
                                                                                                                                                                              1 KLLDMAAQI
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                                                                                       Sequence 263 AA;
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Misc-difference
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Synthetic.
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                                                             invention
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                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       mutant.
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ADY85449 standard; protein; 279 AA.

RESULT 7 ADY85449 16-JUN-2005 (first entry)

ADY85449;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Loew A;
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
Src-family protein tyrosine kinase; T-cell; immune response; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New crystalline polypeptide comprising ligand binding domain or cat domain of Lck protein, for determining three-dimensional structure catalytic domain of Lck, has predetermined unit cell parameters.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant Lymphocyte Cell Kinase, Lck, fragment (231-501, D364N).
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      DB 7; Length 265;
                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164
/note= "Phosphorylation site"
100.0%; Score 41; DB 7
100.0%; Pred. No. 2.1;
                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  ABR56204 standard; protein; 271 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-AUG-2002; 2002WO-US024546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-2001; 2001US-0310051P.
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                                                                   9; Conservative
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KLLDMAAQI 112
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Query Match
Best Local Similarity
                                                                                                                                1 KLLDMAAOI
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003020880-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
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                                                                Matches
                                                                                                                                                                                                                                                                                    RESULT 6
ABRE 66204
1D ABRE 66204
1D ABRE 66204
1D ABRE 66204
1D ABRE 66204
1B-I ABRE 66204
1B
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The inversion changes be actived to the formulation of formulae (1)-(VII) given in the specification. Also included are a system for fitting compounds in binding sites of protein kinases (comprising an electronic kinase scaffold, and a scaffold library computer of protein kinases (VII), where the scaffold library is embedded in a computer device and the electronic representations of the compounds can be selectively retrieved and functionally connected with computer software adapted to it electronic representations of a kinase (compounds in an electronic adapted to retrieved and functionally connected with computer software adapted to it electronic representations of a kinase (compounds in an electronic corresponds in a binding site of a kinase), obtaining if a derivative confidence of (1)-(VII) binds to the kinase with greater affinity and/or specificity than (VII), developing ligands specific for a particular kinase (which comprises determining if a derivative of (1)-(VII) that binds to the kinase with greater affinity and/or comprises has greater for specificity for the particular kinase than (1)-(VII), developing ligands specific for a particular kinase (which comprises has greater for specificity for the particular kinase than (1)-(VII), developing ligands binding to a kinase (which comprises of the scaffolds, that, when modified, change the binding affinity and/or specificity between the scaffold and kinase and synthesizing a ligand in which at least I chemical structure of the scaffold in a smoothied).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            developing ligands with increased specificity on a kinase (which comprises testing a derivative of a kinase binding compound (1)-(VII) for increased specificity on the kinase), identifying a ligand binding to a kinase (which comprises determining if a derivative compound including a core structure (1)-(VII) binds to the kinase with changed binding a faffinity and/or specificity), a co-crystal of a kinase and a binding compound (1)-(VII), preparation of co-crystals of Pin-1 with (1)-(VII), identifying potential kinase binding compounds (which comprises fitting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to a new kinase scaffold library comprises at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       electronic representations of (I)-(VII) in an electronic representation of a kinase binding site), attaching a kinase binding compound to an attachment component (which comprises identifying energetically allowed sites for attachment of the component on a kinase binding compound (I)-(VII) and attaching the compound or derivative to the attachment component at the allowed site), modified compounds (comprising (I)-(VIII)
                                                                                                                                                         Kinase; protein co-ordinate data; protein structure; cancer; cytostatic;
neoplasm; inflammation; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New scaffold library used for identifying and developing ligands for protein kinases and treating kinase associated disorders e.g. cancer, comprises set of compounds comprising N-heterocyclic compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gillette SJ, Hurt CR, Ibrahim PL;
                                                                                                     Catalytic domain of PIM kinase-like protein LCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 170-174; 236pp; English
                                                                                                                                                                                                                                                                                                                                                                                              15-SEP-2004; 2004WO-US030360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bremer RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PLEX-) PLEXXIKON INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-273155/28.
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                                                                                                                                                                                                                                     Unidentified
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Gaps

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0; Indels

0; Mismatches

9; Conservative

Local Similarity

Best Loc Matches

KLLDMAAQI 118

1 KLLDMAAQI

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with an attached linker group, and developing a ligand for a kinase comprising conserved residues matching at least on of Plm-1 residues 49, 52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds to the kinase. The kinases comprise Pim-1, Pyk2, C-Ab1, Her2, CMet, Creceptor, CKit, Pkobera, P38 Cdk2, Akt or Gak3beta. The kinase scaffold library is used for identifying and developing ligands binding to kinases, for modulating kinase activity and for treating disease. Condition associated with abnormal kinase activity e.g. cancer, inflammatory disease. The method identifies improved ligands binding to kinase resulting in ligands having high affinity and specificity towards kinase resulting in ligands having high affinity and specificity towards sufficient size and quality to allow structural determination of at least can sufficient to the present sequence is a catalytic domain from a PIM-like kinase. NOTE: It is not clear whether the sequence as presented
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represents a continuous amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 279 AA;
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. 0 DB 9; Length 279; 2.2; 0; Indels 100.0%; Score 41; DB 100.0%; Pred. No. 2.2 :ive 0; Mismatches Query Match 100. Best Local Similarity 100. Matches 9; Conservative KLLDMAAQI 118 σ KLLDMAAQI 110 ч 셤 ઠે

AAY76750 standard; protein; 346 AA. RESULT 8

AAY76750;

Human protein kinase homologue, PKH-3.

(first entry)

17-APR-2000

Protein kinase homologue; human; PKH; diagnosis; therapy; cancer; AIDS; autoimmune disorder; inflammatory disorder; reproductive defect; asthma; diabetes mellitus; infertility; ovulatory defect; endometriosis; polycystic ovary syndrome.

Homo sapiens

US6013455-A.

11-JAN-2000.

98US-00173581. 15-OCT-1998;

98US-00173581 15-OCT-1998;

(INCY-) INCYTE PHARM INC.

Corley NC, Gorgone GA, Azimzai Y; Guegler KJ; Yang YT, JL, Yue H, Bandman O, Hillman JL, Lu DAM,

WPI; 2000-136321/12 N-PSDB; AAZ86794 Nucleic acids encoding a human protein kinase homolog useful for preventing, diagnosing and treating cancer, autoimmune/inflammatory disorders and reproductive defects.

Claim 1; Col 47-50; 38pp; English.

This sequence represents a human protein kinase homolog (PKH) of the invention. The PKH sequences may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PKH expression such as cancers, autoimmune/inflammatory disorders and reproductive defects. They may be used to treat disorders associated with decreased PKH expression such as cancers (e.g. lymphoma, melanoma and cancers of the

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and quantitate the presence of similar nucleic acid sequences in samples, and hence which patients may be in need of restorative therapy. They may also be used to study the expression and function of PKH polypeptides and their role in metabolism. The PKH polypeptides may be used as antigens in the production of antibodies against PKH and in assays to identify modulators (agonists and antagonists) of PKH expression and activity. The
                    asthma and diabetes mellitus, and reproductive defects (e.g. infertility, ovulatory defects, endometriosis and polycystic ovary syndrome). The DNA may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PKH by expressing inactive proteins or to supplement the patients own production of PKH polypeptides. Additionally, the DNA may be used to production of PKH polypeptides. Additionally, the DNA may be used to produce PKH, according to standard recombinant DNA methodology, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. Conversely, antisense nucleic acid molecules may be administered to down regulate PKH expression by binding with the cells own PKH genes and preventing their expression. The DNA, and antisense sequences may also be used as DNA probes in diagnostic assays to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-PKH antibodies and PKH antagonists may also be used to down regulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKH expression and activity. The anti-PKH antibodies may also be used as diagnostic agents for detecting the presence of PKH polypeptides in
   breast lung and prostate), autoimmune/inflammatory disorders (e.g. AIDS
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Seguence 346 AA;

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Gaps

Gaps ö 100.0%; Score 41; DB 3; Length 346; 100.0%; Pred. No. 2.7; ive 0; Mismatches 0; Indels 9; Conservative Best Local Similarity Query Match

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185 σ 1 KLLDMAAQI KLLDMAAQI 177

8 g RESULT 9

AAE06208 standard; protein; 346 AA.

AAE06208;

25-SEP-2001 (first entry)

Human protein kinase homolog-3 (PKH-3).

Human, protein kinase homolog-3; PKH-3; cytostatic, protein therapy; vaccine; immunosuppressive, antisclerotic; antiabortive; adenocarcinoma; Acquired Immune deficiency Syndrome; AIDS; melanoma; cancer; bone; liver; breast; autoimmune disorder; multiple sclerosis; drug screening; anaemia; Crohn's disease; ectopic pregnancy; tubal disease; inflammatory disorder; reproductive disorder; polycystic ovary syndrome; asthma.

Homo sapiens

/note= "Signature sequence" Location/Qualifiers Region

US6264947-B1

24-JUL-2001.

99US-00420915 20-OCT-1999; 98US-00173581. 15-OCT-1998;

(INCY-) INCYTE GENOMICS INC.

Corley NC; Guegler KJ, Yue H, Hillman JL, Y, Lu DAM; Tang YT, Azimzai Bandman O, Gorgone GA,

WPI; 2001-450728/48. N-PSDB; AAD11845.

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30-MAY-2001; 2001US-00870962.

98US-00173581. 99US-00420915.

15-OCT-1998; 20-OCT-1999;

Human protein kinase proteins and homologs, useful for preventing, diagnosing and treating cancers, autoimmune/inflammatory disorders and reproductive disorders.

Claim 1; Col 47-50; 38pp; English

The present sequence is human protein kinase homolog-3 (PKH-3). Human protein kinase homologs (PKH) and their cDNA molecules are used in the prevention, diagnosis and treatment of diseases associated with increased or decreased expression of PKH. Examples of such disorders include, cancer (e.g. adenocarcinoma, melanoma and bone, breast and liver cancer), autoimmune/inflammatory disorders (e.g. Acquired Immune deficiency Syndrome (AIDS), anaemia, asthma, Crohn's disease and multiple sclerosis) and reproductive disorders (e.g. tubal disease, ectopic pregnancy and colycystic ovary syndrome). PKH, its catalytic or immunogenic fragment are used for screening libraries of compounds in any of the drug screening techniques. PKH nucleic acids are used to generate hybridisation probes useful in mapping the naturally occurring genomic sequences. PKH are also used as antigens in the production of antibodies adainst protein kinases (PK) and in assays to identify modulators of PK expression and activity. PKH is also used in protein therapy

Sequence 346 AA;

Gaps ö 100.0%; Score 41; DB 4; Length 346; 100.0%; Pred. No. 2.7; 0; Indels 0; Mismatches Query Match Best Local Similarity 100. Matches 9; Conservative ò

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σ 1 KLLDMAAQI

177 KLLDMAAQI 185

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ABB84435 standard; protein; 346 AA: 08-NOV-2002 (first entry) ABB84435; RESULT 10

Human protein kinase homologue from clone 507669.

Protein kinase homologue; PKH; cytostatic; immunosuppressive; antifungal; antinflammatory; antiallergic; antiasthmatic; antianemic; antidiabetic; antiarteriosclerotic; antityroid; dermatological; nephrotropic; human; antiarteriosclerotic; antityroid; osecopathic; antiarthritic; allergy; antiprotrozoal; antiprastic; antincer; antiviral; antibacterial; antiprastic; antiproducoal; antiparastic; antincer; antiviral; antibacterial; acquired immunodeficiency syndrome; AIDS; Addison's disease; amyloidosis; autoimmune haemolytic anaemia; autoimmune thyroiditis; bronchitis; autoimmune thaemolytic anaemia; autoimmune thyroiditis; bronchitis; wholecystitis; contact dermatitis; Crobh's disease; atopic dermatitis; wholecystitis; contact dermatitis; Crobh's disease; atopic dermatitis; whencows the solution and syndrome; draves disease; psoriasis; whencows thyroiditis; hypereosinophilia; irritable bowel syndrome; multiple sclerosis; myasthenia gravis; myocardial inflammation; uveitis; perioratial inflammation; osteoarthritis; osteoporosis; pancreatitis; polymyositis; Reiter's syndrome; rheumatoid arthritis; scleroderma; SLE; Sjogran's syndrome, systemic lupus erythematosus; systemic sclerosis; thrombocytopenic purpura; ulcerative colitis; Werner syndrome; infection; haemedialysis; extracorporaal circulation; infertility; tubal disease; ovulatory defect; endometriosis; oestrous; menstrual cycle; gene therapy; uterine fibroid; autoimmune disorder; polycystic ovary syndrome; enzyme; ovarian hyperstimulation syndrome; ectopic pregnancy; teratogenesis; cancer.

US2002081290-A1

27-JUN-2002

This invention describes a novel protein kinase homologue (PKH)

comital pergic, antiachmatic, antiantenic, antithyroid, dermatological, antidabetic, nephrotropic, antiphrout.

compthal mological, antiducer, antiviral, antibacterial, antidungal, antiphronogal, antiparastic and antihelmintic activity. The polypeptide is used for treating a disease or condition associated with decreased expression of functional PKH The polypeptide is used for treating a capaired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, anyloidosis, anaemia, asthma, atherosclerosis, autoimmune haemolytic canaemia, autoimmune thyroiditis, bronchitis, cholecystitis, cancer, contact dermatitis, Crohn's disease, atopic dermatitis, cancer, contact dermatitis, emphysema, atropic gastritis, glomerulonophitis, hyperessinophilla, irritable bowel syndrome, multiple sclerosis, hyperessinophilla, irritable bowel syndrome, multiple sclerosis, csteoarthritis, osteoporosis, pancreatitis, sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, systemic sclerosis, thrombocytopenic concenter, haemodalalysis, and extracorporael circulation, viral benefity, protozoal, and helminthic infections, infertility, cholucystic protozoal, and helminthic infections, infertility, colucynentic colitis, uveitis, multiple menstrial colucing tubal disease, ovulatory defects, and endometricals. polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian tumours, uterine fibroids, autoimmune disorders, ectopic pregnancies, and teratogenesis. The polypeptides of the invention can be used for gene therapy. This sequence represents a PKH from clone ID 207669 isolated from TMLR3DT02, a library constructed using RNA isolated from non-adherent peripheral blood mononuclear cells collected from a pool of male and female donors Nucleic acids encoding a human protein kinase homolog useful for preventing, diagnosing and treating cancer, autoimmune/inflammatory disorders and reproductive defects. Corley NC; Guegler KJ, Yue H, Hillman JL, Claim 47; Page 27; 43pp; English Y, Lu DAM; (INCY-) INCYTE PHARM INC. Tang YT, Azimzai N WPI; 2002-655433/70. N-PSDB; ABQ76288 Bandman O, Gorgone GA,

100.0%; Score 41; DB 5; Length 346; 100.0%; Pred. No. 2.7; Indels .; 0 Mismatches 0; 9; Conservative Best Local Similarity Query Match Matches

Sequence 346 AA;

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Gaps

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ABM82980 standard; protein; 355 AA. RESULT 11 ABM82980

ABM82980;

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Fused polypeptide - has amino acid sequence of beta-galactosidase with a LCK gene conjugated to the N-terminal via DNA having multi-cloning site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence consists of the N-terminal amino acids of the beta-galactosidase gene fused with the lck gene. It is produced by E.coli transformed with a recombinant vector (see AAQ13983). It is useful for producing an antibody specifically immunoreactive with only a lck genederived polypeptide in T cells. The antibody may recognise lck genederived polypeptides in human cells
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pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
endothelial cell; cell differentiation; cell proliferation; apoptosis;
                     (Beta-galactosidase N-terminal)-(lck gene prod.) fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 41; DB 2; Length 417; 100.0%; Pred. No. 3.3; ive 0; Mismatches 0; Indels
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                                                                                                                                                                          l. .26
/note= "beta-galactosidase fragment"
                                                                                                                                                                                                             27. .417
/note= "lck gene polypeptide"
                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                89JP-00338268
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                                                             Multi-cloning site.
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Best Local Similarity
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                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248
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                                                                                                                                                    Key
Region
                                                                                                                                                                                                                Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gietzen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                 gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kirton ES;
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                                                                                                                                                                                                                                                                                                                                                                                                     Wright RJ, Bruns CM, Marjanovic MM, Shen F;
TA, Suchorolski MT, Altus CM, Pites SJ, Elder LV;
Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Anderson SB, Rloux P, Shen EJ, Wu C, Stuve LL;
Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES,
M. Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietze
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                                         Human diagnostic and therapeutic pprotein SEQ ID NO:3229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR14201 standard; protein; 417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; Page; 190pp; English
                                                                                                                                                                                                                                                     12-SEP-2003; 2003WO-US028227
                                                                                                                                                                                                                                                                                            12-SEP-2002; 2002US-0410259P
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(first entry)
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N-PSDB; ACN41632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kwong M, Fo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in gene mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stevens KA,
Peralta CH,
                                                                                                                            Homo sapiens
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                                                                                                                                                                                                           25-MAR-2004
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Xu Y, Kwor
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RESULT 12 AAR14201

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The invention discloses isolated human nucleic acid alternative splicing variants that are all tumour-involved genes (TIGS). The nucleic acids and polypeptides are useful for determining the level of a nucleic acid or polypeptide in a biological sample, for detecting a variant nucleic acid or polypeptide sequence in a biological sample, for determining the level of variant sequence in a first biological sample and the level of variant sequence from which the variant has been varied by alternative splicing in a second biological sample and for raising antibodies. A pharmaceutical composition comprising antibodies. A pharmaceutical composition comprising antibodies. A pharmaceutical composition comprising a crarier and the nucleic acid, is useful for treating diseases (e.g. cancer) that can be ameliorated or cured by composition comprising the level of the encoded protein. The nucleic acids are also useful for diagnostic purposes, especially for detecting cancer or a predisposition to cancer, for evaluating the state or aggressiveness of cancer disease, in basic research, for understanding the physiological function of the original TIG in targeting or development of the original TIG in targeting or development of the same type of cells which may be helpful for the development of physiological functions and stages in which cell cycle is noncommal, for determining mutations in tumour-involved genes and in gene therapy. The polypeptides are useful for identifying compounds capable of therapy. The polypeptides are useful for identifying compounds capable of modulating endothelial differentiation and proliferation, as well as to modulate apoptosis either ex vivo or in vivo. The sequences presented in dispersed the new variants (NV) 1-36 proteins of the TIGs
                                                                                                                                                                                                                                                          Novel nucleic acid sequence, which is an alternative splicing variant of tumor involved genes, useful for detecting cancer, predisposition to cancer, for evaluating cancer state and in gene therapy for treating
                                                                                                                                                      Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 68-69; 180pp; English.
                                                                                                                                                      Romano C,
16-MAY-2000; 2000IL-00136154
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Best Local Similarity luv.
Fest Local 9; Conservative
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                                                                                                        BERNSTEIN J.
                                                                                                                                                 David A,
                                                                                                                                                                                            2002-635679/68
                                           LEVINE Z.
                                                               DAVID A.
ROMANO C.
                                                                                                                                                                                                                   N-PSDB; ABS65202
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                                           (LEVI/)
                                                                                    (ROMA/)
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anti-HIV; antiallergic; antinflammatory; antianaemic; antiparkinsonian; noctropic; anticonvulsant; antiarteriosclerotic; antiasthmatic; immunosuppressive; antihyroid; cytostatic; hepatotropic; dermaticial; antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective; osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic; Gaps ö 100.0%; Score 41; DB 5; Length 437; 100.0%; Pred. No. 3.5; ive 0; Mismatches 0; Indels ADC99048 standard; protein; 458 AA Human KPP protein - SEQ ID 1. (first entry) 01-JAN-2004 ADC99048; ADC99048

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AAB37700 standard; protein; 508 AA

AAB37700

RESULT 15
AAB37700
ID AAB37'
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AC AAB37'
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KLLDMAAQI 297 1 KLLDMAAQI 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial; virucide; protozoacide; fungicide; kinase; phosphatase; KPP; cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; cancer; developmental; mental retardation; neurological; Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's; diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan; helminthic infection; transgenic; gene therapy; human; enzyme.
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Arvizu CS;
Tang YT;
Yao MG, Y
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, Griffin JA;
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2001US-0333098P.
2001US-0332424P.
2001US-0334288P.
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Thornton MB, Ty
Zebarjadian Y;
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30-NOV-2001;
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us-10-062-257a-14.rag

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diffracts X-rays so that the atomic coordinates of the protein-ligand comprising a truncated lymphocyte kinase [1ck] and a ligand. The crystal diffracts X-rays so that the atomic coordinates of the protein-ligand complex can be determined to a resolution of greater than 5.0 Angstroms. The truncated lck used in the present invention comprises the globular core of the corresponding full-length lck. The present sequence is the full-length human lck protein. The crystal of the present invention may be used to identify kinase inhibitors in screening assays, in drug screening and drug design processes, to design, select or test inhibitors of kinase enzymes, where the inhibitors are used as therapeutics for the treatment and modulation of diseases, disease symptoms or the effect of other physiological events mediated by kinases, having one or more kinase enzymes involved in their pathology
                                                                                                                                                                                                                                                                                                                                                                                                    Crystal of a protein-ligand complex for identifying kinase inhibitors, comprises a truncated lymphocyte kinase and a ligand, and diffracts X-rays to determine atomic coordinates at a resolution greater than 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a crystal of a protein-ligand complex
                                                                         Human; lymphocyte kinase; protein co-ordinate data; lck; crystal
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Best Local Similarity 100.00
Garbar 9; Conservative
(first entry)
                                                                                                                                                                                                                                                                                         (KINE-) KINETIX PHARM INC
                                 Human lymphocyte kinase.
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                                                                                                            Homo sapiens
 02-MAR-2001
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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

Costigan M;

Befort K,

Woolf C, D'urso D, WPI; 2003-268312/26

GENBANK; P06239

01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P.

(GEHO) GEN HOSPITAL CORP. (FARB) BAYER AG.

14-AUG-2002; 2002WO-US025765 14-AUG-2001; 2001US-0312147P.

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Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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                                                                                                                                                                     ADE58802 standard; protein; 508 AA.
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RESULT 16
ADE58802
ID ADE58
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DT 29-JA
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KW Human
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KW Spina
KW Spina
KW Spina
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CS HOMO
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CS HOM
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CS
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27-FEB-2003

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal composition and polynucleotide sequence which is differentially expression of a polynucleotide sequence which is differentially expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more pain and a pharmaceutical composition comprising the one or more pain and a pharmaceutical composition comprising the one or more polynpeptides or their antibodies. The polynucleotide or the compound that complete in a sectivity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene the sequence data for this patent did not form part of the printed the sequence data for this patent did not form part of the printed the sequence data for this patent did not form part of the printed the sequence data for this patent did not form and the data for this patent did not form and the data for this patent did not form and the data for the sequence data for this patent did not form and the data for the sequence data for this patent did not form and data for the sequence data for this data for the sequence data for this data fo
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spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
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Homo sapiens

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a method for identifying a compound useful in the specification, a method for identifying a compound useful in the cativity in an animal of one or more of the polypeptides given in the cativity in an animal of one or more of the polypeptides given in the cativity in a method for identifying a compound useful in treating and a compound the cativity in an animal of one or more of the polypeptides given in the cativity in a method for identifying a compound useful in treating and a cativity in a method for identifying a compound useful in the cativity in a method for identifying a compound useful in treating and a cativity or method for identifying a compound useful in treating and a cativity in an animal composition or man and an animal composition or man a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Costigan M;
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                               14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                          14-AUG-2002; 2002WO-US025765
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-268312/26
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Best Local Similarity
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WO2003016475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENBANK; P06239
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ID ADF4
XX ADF4
AC ADF4
XX DT 12-F
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The present invention relates to a method for identifying a ligand (L), which binds to an inactive conformation of target protein kinase (T). The method involves contacting inactive conformation of (T), which contains or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bonding to the reactive group thus forming a kinase-(L) conjugate (C). The method is useful for identifying protein kinase inhibitors that preferentially bind to inactive conformation of a target protein kinase. The present sequence is a protein kinase which may be modified via an amino acid substitution, for use in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; immunosuppressive; antiinflammatory; antibacterial; virucide; fungicide; nootropic; neuroprotective; kinase inhibitor; crystal; protein-ligand complex; lymphocyte kinase; Lck; Lck ligand; kinase inhibitor; therapeutic; kinase-mediated physiological event; cancer; autoimmunological; metabolic; niflammatory; infection; central nervous system degenerative disease; transplant rejection; human; globular core; protein co-ordinate data.
                                                                                                                                                                                                                                                                                                                    Identifying ligand binding to inactive conformation of target protein kinase (T) comprises contacting the conformation modified (T) which contains reactive group at binding site, with ligands and detecting kinase-ligand conjugate formation.
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100.0%; Pred. No. 4;
tive 0; Mismatches 0
            Human; protein kinase; enzyme; inhibitor; LCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lymphocyte kinase (Lck) globular core.
                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 41; 260pp; English.
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                                                                                                                                                 20-MAR-2003; 2003WO-US008725.
                                                                                                                                                                               21-MAR-2002; 2002US-0366892P
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                                                                                                                                                                                                                  (SUNE-) SUNESIS PHARM INC.
                                                                                                                                                                                                                                                   Prescott JC, Braisted A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Best Local Similarity
9; Conserv?
                                                                                                                                                                                                                                                                                    WPI; 2003-865136/80.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 508 AA;
                                                                                WO2003081210-A2
                                                 Homo sapiens.
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                                                                                                                02-OCT-2003
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RESULT 21
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                                                                                                                                                                                                                  Comprising a truncated lymphocyte kinase (Lck) and a ligand, where (I) effectively diffracts X-rays for determination of atomic coordinates of (C) to a resolution of greater than 5.0 angstroms, and truncated Lck (C) to a resolution of greater than 5.0 angstroms, and truncated Lck (C) to a resolution of greater than 5.0 angstroms, and truncated Lck (C) to a resolution of greater than 5.0 angstroms, and truncated Lck comprises a sequence (S1) of residues 225-508 of a 508 amino acid (C) to a resolution of residues 225-508 of a 508 amino acid (C) to a resolution of sequence, given in specification and retains the globular core of full-length Lck. (I) is useful in an inhibitor screening assay and to identify, design, select, and evaluate potential inhibitors of kinases continued by the methods may also be useful for inhibition of that are associated with kinase-mediated physiological events. The inhibitors identified by the methods may also be useful for inhibition of kinase activity of one or more enzymes. The inhibitors are also useful for inhibiting the biological activity of any enzyme comprising greater than 70% sequence homology with a kinase sequence. The inhibitors are useful correction in treating disease or disease symptoms mediated by any enzyme that binds ATP. The inhibitors are useful in inhibiting kinase activity and mammal, particularly a human e.g., cancer; tungal, etc.), central mammal, particularly a human e.g., cancer; tungal, etc.), central nervous system degenerative disease etc. The inhibitors are useful in treating or preventing diseases, including, transplant rejection etc. This is the amino acid sequence of a human lymphocyte kinase (Lck) polypeptide comprising the Lck globular core.
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                                                                                                                                            Crystal of protein-ligand complex useful for identifying an inhibitor of lymphocyte kinase (Lck), comprises truncated Lck and a ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein of a TNF-alpha signalling pathway protein complex SeqID 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein complex; tumour necrosis factor-alpha signalling pathway; TNF-alpha; chronic inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; infectious disease; septic shock; bacterial infection; neurological disease; stroke-induced inflammation; neurodegenerative disease; cancer; antiinflammatory; antiarthritic; antirheumatic; cytostatic; antibacterial; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                          Claim 1; SEQ ID NO 1; 295pp; English
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                19-MAY-2000; 2000US-0205510P.
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Best Local Similarity 100.
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                                                                                                              WPI; 2003-810380/76
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                                              (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 508 AA;
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29-APR-2004

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This invention relates to novel protein complexes of the tumour necrosis factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to methods for preparing these complexes comprising at least two component proteins, as well as screening methods to identify modulators of the proteins, as well as screening methods to identify modulators of the pathway, which include antibodies, agonists and antagonists thereof. The creating complex and kit that are useful for diagnosing, prognosing or treating chronic inflammatory diseases such as recording arthritis and inflammatory bowel disease; infectious diseases cut as septic shock and bacterial infections; neurodegenerative diseases such as stroke-induced inflammation in neurons; neurodegenerative diseases and cancer. Accordingly, these complexes can be used for the development of pharmaceutical compositions that exhibit antihiflammatory, antiarthritic, antirheumatic, cytostatic and antibacterial activities and can be used for gene therapy purposes. In particular, the invention further provides is alkNA-oligonucleotides useful for inhibiting protein expression for in vitro or cell culture assays. This polypeptide is a human protein that can be used in combination with other proteins provided in the specification to form novel complexes of the TNF-alpha signalling pathway
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                                                                                                                                                                                                                                                                                                                                 New protein complex comprising at least one first and second protein of
the Tumor Necrosis Factor-alpha (TNF-alpha)-signaling pathway, useful for
diagnosing or treating inflammation, neurological diseases, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                 Kuester B;
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                                                                                                                                                                                                 Bauch A, Ruffner H, Bauer A,
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100.0%; Pred. No. 4;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; SEQ ID.NO 3; 1980pp; English.
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24-SEP-2003; 2003WO-EP050655.
                                                    26-SEP-2002; 2002EP-00021809.
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                                                                                                                                                                                              Huhse B, |
, Kruse U;
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                                                                                                                                                                                                                                                                                WPI; 2004-348460/32.
                                                                                                                                         (CELL-) CELLZOME AG
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                                                                                                                                                                                           Bouwmeester T, Hi
Superti-Furga G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the invention.
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12-APR-2002; 2002US-0372246P.
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                                                                                                WPI; 2003-354600/33.
N-PSDB; ACC72850.
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hes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 509 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathologies
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                                                        Afar D, Az
Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABR56202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 23
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                                                                                                                                                                                                                                                                The invention provides a novel method of altering the activity of the protein kinase A (PKA) signaling pathway in a cell that comprises a letering the extent of phosphorylation of one or more PKA substrates, or kinase substrates downstream in the PKA signaling pathway. Pharmaceutical compositions containing a nucleic acid molecule that encodes a PKA compositions containing a nucleic acid molecule that encodes a PKA substrate, or fragment, precursor or functionally equivalent variant, where the sequence is modified to alter its susceptibility to phosphorylation by PKA can be used for treating a disorder exhibiting abnormal PKA signaling activity, immunosuppressive disorders or proliferative diseases. They can be used for treating e.g. HIV infection, ALDS, common variable immunodeficiency or cancers. Conditions in which upregulation of the PKA pathway is required, such as autoimmune disease, e.g. systemic lupus erythematosus, may also be treated. The present sequence represents a PKA substrate, wherein the substrate is in the Srcfamily, preferably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk, C-tkl, Fyk, Src-1 or Src-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                Altering the activity of protein kinase signaling pathways, used for treating immunosuppressive disorders, e.g. AIDS, proliferative disorders, e.g. cancers or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
heart disease; atherosclerosis; endometriosis.
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                                                                                                Hansson V, Levy FO, Mustelin T, Skalhegg BS, Sundvold V; Tasken K, Vang T, Altman A, Munshi A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 41; DB 3; Length 509; 100.0%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cancer related protein SEQ ID NO:356.
                                                                                                                                                                                                                                           Claim 23; Page 95-96; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR58699 standard; protein; 509 AA.
             98NO-00002419.
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20-SEP-2001, 2001US-0323887P.
13-NOV-2001, 2001US-035666F
08-FEB-2002, 2002US-0355145P.
08-FEB-2002, 2002US-0355257P.
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                                                                                                                                         2000-086801/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KLLDMAAQI
                                                      (LAUR-) LAURAS AS.
(JONE/) JONES E L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 509 AA;
                                                                                                                                                        N-PSDB; AAZ46491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003025138-A2.
             27-MAY-1998;
30-DEC-1998;
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The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-cregulated in specific cancers (e.g. about 1031 genes up-regulated in a cutte lymphocytic leukemia). ACC7241 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ARRS851 to ARRS8709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically trargeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a patient by administering to the patient the antibody above; and (7) a cut greening a pathology, e.g. cancer (e.g. cancer of the bone marrow, therapeutic targets. In particular, the nucleic acid is useful for the appending a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, canceres, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in the care of the processing these actives are treating these
                                                                                                                                                                                                                                                                                                                                                                                  New genes that are up-regulated or down-regulated in cancers, useful markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, protein co-ordinate data, Lymphocyte Cell Kinase; Lck; enzyme; Src-family protein tyrosine kinase; T-cell; immune response.
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                                                                                                 Wilson KE;
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                                                                                            Mack DH,
                                                                                            Aziz N, Gish KC, Hevezi PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 762; 767pp; English.
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(EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2001; 2001US-0310051P.
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Claim 1; SEQ ID NO 28; 167pp; English.
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                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                        RESULT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a compound capable of diagnosing, preventing or treating AIDS or an HIV-related disorder comprises assaying the ability of the compound to modulate e.g. 1414, 1481 or 1553 nucleic acid expression or polypeptide activity.
                                                     catalytic
                                                                                                                                    protein. Lck is a Src-family protein tyrosine kinase expressed primarily in T-cells and plays an essential role in immune response. The present sequence is the full-length sequence of human Lck (1-509). (1) is useful for identifying a compound which is an inhibitor of human Lck protein
                                                                                                                                                                                                                                                                                                                                                                                                              AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus; HIV-related disorder; differential expression; drug screening; viral replication modulation; diagnosis; prognosis; predisposition; anti-HIV; gene therapy; antiesense therapy; human; proto-oncogene Tyr protein kinase LCK; enzyme.
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 Hrnciar P, Loew A;
                                                                                                                 The present invention relates to a crystalline polypeptide (1), comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
                                                                                                                                                                                                                                   Gaps
                                                  New crystalline polypeptide comprising ligand binding domain or cat domain of Lck protein, for determining three-dimensional structure catalytic domain of Lck, has predetermined unit cell parameters.
                                                                                                                                                                                                                                                                                                                                                                                           Human proto-oncogene Tyr protein kinase LCK (gene ID 1611) protein.
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0
                                                                                                                                                                                                            Score 41; DB 7; Length 509;
Pred. No. 4;
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Dixon RW, Hirst GC,
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                                                                                             Claim 5; Fig 1; 994pp; English.
                                                                                                                                                                                                             100.0%;
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25-UUN-2002; 2002US-0391306P,
27-AUG-2002; 2002US-0406297P
19-SEP-2002; 2002US-0412007P-
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 Calderwood D,
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Best Local Similarity الاست
الاستارة 9, Conservative
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N-PSDB; ADE40448.
                              WPI; 2003-300872/29
         Ritter K;
                                                                                                                                                                                                                                                     KLLDMAAQI
                                                                                                                                                                                         Sequence 509 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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10-DEC-2002;
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           Leung A,
 Borhani
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The invention relates to a method of identifying a compound useful in the treatment of AIDS (acquired immunodeficiency syndrome) or an HIV (human immunodeficiency virus). Felated disorder. The invention involves assaying the ability of a test compound to modulate the activity or expression of 26 human proteins. These proteins and nucleic acids encoding them (ADE40422-ADE40473) are differentially expressed in tissues relating to AIDS or an HIV-related disorder compared to their expression in normal tissues. The invention also relates to the use of the compounds identified to modulate viral replication in a cell and to treat a patient with AIDS or an HIV-related disorder. The invention further discloses methods for the diagnostic evaluation and prognosis of various HIV-related disorders, and for the identification of individuals exhibiting a predisposition to such conditions. The modulatory compounds identified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               using the method of the invention may be small organic molecules, peptides, antibodies or antisense nucleic acid molecules. The methods of the invention are useful in diagnosing, preventing or treating AIDS or HIV-related disorders. The present sequence represents a human protein which is differentially expressed in AIDS or HIV-related disorders.
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Zhang H, Amundsen
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16-SEP-2002; 2002US-0411017P.
30-DEC-2002; 2002US-0437107P.
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Plowman GD, Lickteig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-180653/17.
N-PSDB; ADL22890.
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acid, contacting the assay system with a test goett, where in its presence the system provides a reference activity, and detecting a test agent-biased activity of the assay system, wherein a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate p21 or p53 pathway modulating agent. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of diseases or conditions associated with aberrant expression or activity of the p21 or p53 pathway, such as cancer, preferably colon or head and neck cancer. The present sequence is a human MP2153 protein sequence of the invention.
p21 or p53 (MP2153) polypeptide or nucleic
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Sequence 509 AA;

ô Gaps . 0 100.0%; Score 41; DB 8; Length 509; 100.0%; Pred. No. 4; 0; Indels 0; Mismatches 9; Conservative Query Match Best Local Similarity Matches

σ 1 KLLDMAAQI

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ADP12458 standard; protein; 509 AA.

ADP12458;

12-AUG-2004 (first entry)

Protein encoded by mRNA of the invention #68.

transplant rejection; immune system; rheumatoid arthritis; lupus; inflammatory bowel disease; multiple sclerosis; HIV; AIDS.

Homo sapiens

WO2004042346-A2.

21-MAY-2004

24-APR-2003; 2003WO-US012946.

24-APR-2002; 2002US-00131831. 20-DEC-2002; 2002US-00325899.

(EXPR-) EXPRESSION DIAGNOSTICS INC.

Morris M; Ly N, Prentice J, Woodward R, Wohlgemuth J, Fry K, Rosenberg S;

WPI; 2004-400724/37.

Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes

Claim 65; SEQ ID NO 2467; 1762pp; English.

The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, according to mechanical transplant rejection, and individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a RESULT 26
ADP12458
ADP12458
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Gaps

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Indels

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100.0%; Score 41; DB 8; 100.0%; Pred. No. 4; tive 0; Mismatches 0

Query Match
Best Local Similarity luv...
9; Conservative

1 KLLDMAAQI

Length 509;

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The invention relates to a compound targeted to a nucleic acid molecule encoding the human lymphocyte specific tyrosine kinase (Lck) polypeptide. The compound is an antisense oligonacleotide that specifically hybridises with the nucleic acid and inhibits expression of the polypeptide. The antisense oligonucleotide comprises at least one modified internucleoside linkage i.e. a phosphorothioate linkage, at least one modified sugar moiety, preferably a 2'-0-methoxyethyl sugar moiety, or at least one modified nucleobase comprising a 5-methylcytosine. The antisense compounds are useful for modulating the expression of the human Lck polypeptide and in preparation of a composition for treating hyperproliferative disorders, e.g. cancer. This sequence represents a human Lck polypeptide of the invention.
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense oligonucleotide compounds, useful for diagnosing, preventing and/or treating diseases or conditions associated with aberrant expression or activity of Lck, such as hyperproliferative
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                                                                                                                                                                                                                                                                                                                                                              Human lymphocyte specific tyrosine kinase (Lck) polypeptide #1.
                                                                     Length 509;
                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Human, lymphocyte specific tyrosine kinase, Lck, antisense oligonucleotide, phosphorothioate linkage, 2'.-O-methoxyethyl sugar moiety, 5-methylcytosine, hyperproliferative disorder; cancer, cytostatic, enzyme.
protein that is encoded by the mRNA of the invention
                                                                     8;
                                                                 100.0%; Score 41; DB
100.0%; Pred. No. 4;
ive 0; Mismatches
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                                                                                                                                                                                                                                                           ADP48374 standard; protein; 509 AA.
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                                                                                                       Conservative
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                                                                                                                                                                       340 KLLDMAAQI 348
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Best Local Similarity
'... 9; Conserv?
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N-PSDB; ADP48301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes a method for identifying protein kinase inhibitors that preferentially bind to the inactive conformation of a target protein kinase. The inhibitors are identified by locking the target protein kinase. The inhibitors are identified by locking the identify inhibitors preferentially targeting the inactive conformation, and using Tethering to identify inhibitors preferentially targeting the inactive conformation. The method of the invention is useful for identifying a ligand which binds to an inactive conformation of a target protein kinase. The present sequence represents the human Tyr kinase Lck. Lck variants were used to demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                      protein kinase inhibitor; inactive conformation; Tethering; Tyr kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying ligand binding to inactive conformation of target protei kinase, by contacting inactive conformation of target with ligand candidates specific to target, detecting formation of kinase-ligand conjugate and identifying ligand.
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                                                                                                                                                                                                                                             Amino acid sequence of human Tyr kinase Lck.
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                                                                                                        ADZ51107 standard; protein; 509 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-SEP-2003; 2003WO-US029870.
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                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SUNE-) SUNESIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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340 KLLDMAAQI 348
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ARA35921
ID ARA35:
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The invention relates to a method (M1) for identifying, selecting and/or characterizing a compound which modulates Src family kinase (SFK) activity, by expressing nucleic acids encoding SFK or mutated SFK in cells, contacting cells with test compound and determining whether phenotype of cells is changed as compared with phenotype of cells not expressed with above nucleic acids, where difference in phenotype of cells in didentified, selected and/or characterized by (M1); and (2) a compound (I) identified, selected and/or characterized by (M1); and (2) a pharmaceutical composition (PC1) containing (I), and a carrier, adjuvant or vehicle. (I) is useful as a medicament, particularly for the treatment of diseases, which are at least in part caused by a Src family kinase.

(I) and PC1 are useful for producing a medicament for the treatment of diseases, which are at least in part caused by a Src family kinase, particularly by a dysfunction of a Src family kinase, in particular cancer, hypercalcemia, restenosis, osteoporosis, osteoparthritis, symptomatic treatment of bone metastasis, rheumatoid arthritis, symptomatic treatment of beautiful services.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying compound which modulates Src family kinase (SFK) activity, by contacting cells expressed with SFK or mutated SFK with test compound, where change in phenotype of cells indicates that test compound modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory bowel disease, multiple sclerosis, psoriasis, lupus, graft versus host disease, T-cell mediated hypersensitivity disease, Hashimoto's thyroiditis, Guillain-Barre syndrome, chronic obstructive pulmonary disorder, contact dermatitis, Paget's disease, asthma, ischemic or reperfusion injury, allergic disease, atopic dermatitis, transplant rejection or allergic rhinitis. The present sequence represents human Lck kinase, which is given in the exemplification of the present invention.
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                                                                     note= "constant amino acid K in domain SH2"
                                                                                                                                                                                                                   'note= "constant amino acid Y in domain SH1"
                                                                                                                                          note= "constant amino acid T in domain SH2"
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Mismatches
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Location/Qualifiers
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Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP, Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Lagace RB, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D; Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                     New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
                          gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
Human diagnostic and therapeutic pprotein SEQ ID NO:3230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; Page; 190pp; English.
                                                                                                                                                           12-SEP-2002; 2002US-0410259P.
12-SEP-2002; 2002US-0410260P.
                                                                                                                                  12-SEP-2003; 2003WO-US028227
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N-PSDB; ACN41633.
                                                                                                                                                                                                  (INCY-) INCYTE CORP
                                                                            WO2004023973-A2
                                                      Homo sapiens
                                                                                                      25-MAR-2004.
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Shen F; S.J. Elder LV;

The invention relates to novel diagnostic and therapeutic polymucleotides selected from one of the 2722 sequences defined in the specification. A polymucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polymucleotides (dithp) or polypeptides may be used to diagnost a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp conditions also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm Sequence 539 AA;

ö 100.0%; Score 41; DB 8; Length 539; 100.0%; Pred. No. 4.3; 0; Indels tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 9; Conservative

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Gaps

8 g Search completed: June 29, 2006, 09:13:11 Job time : 89.8313 secs

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protein-tyrosine k
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probable acyl-CoA
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probable rna matur
hypothetical prote
probable transcrip
phosphadenosine p
probable transcrip
phosphadenosine p
probable integral
methyltransferase
tagatose-6-phospha
protein-tyrosine k
MHC class I histoc
hypothetical prote

TVHUER TVMVRR A40092 A43806 A43806 A43806 A43806 A43806 A43806 A438119 A438119

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A;Molecule type: mRNA
A;Residues: 368-471,'H','473-509 <VEI>
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Best Local Similarity
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A; Molecule type: DNA
A; Residues: 1-11 < VOR>
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148845
protein-tyrosine kinase (EC 2.7.1.112) lck, lymphocyte - mouse
NyAlternate names: p56; protein-tyrosine kinase tck
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: 148845; A23639; I57629; I77452
R;Voronova, A.F.; Sefton, B.M.
Nature 319, 682-685, 1986
A;Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promote A;Reference number: 148845; MUID:86146842; PMID:3081813
A;Accession: 148845
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Residus: 1-509 «VORI»
A;Molecule type: mRNA
A;Residus: 1-509 «VORI»
A;Residus: 1-509 «VORI»
A;Residus: 1-509 «VORI»
A;Residus: 1-509 «VORI»
A;Accession: A19404, 1985
A;Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpres A;Reference number: A23639; MUID:86079521; PMID:2416464
A;Accession: A23639
A;Accession: 
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A/Cross-references: UNIPARC:UP10000172587; GB:M85043
A/Cross-references: UNIPARC:UP10000172587; GB:M85043
A/Note: sequence extracted from NCBLP, C: Ruebsamen-Waigmann, H.
Broc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987
A/Itle: Additional member of the protein-tyrosine kinase family: the src-and lck-relate A/Reference number: A39339; MUID:88097370; PMID:3321053
A/Molecule type: mRNA
A/Residues: 52-507 <STR>
A/Cross-references: UNIPARC:UP100001713B3; GB:J03579; NID:g212712; PIDN:AAA49081.1; PID: C/Repwords: APP: autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
                                        protein-tyrosine kinase (EC 2.7.1.112) tkl [similarity] - chicken
NyAlternate names: kinase-related transforming protein (tkl); T-cell surface antigen ass
Cyspecies: Gallue gallue (chicken)
Cyspecies: Gallue gallue (chicken)
Cybate: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
CyAccession: A42126; A39939
CyAccession: A42126; A39939
Mol. Cell. Biol. 12, 1226-1233, 1992
Ayritle: tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene.
Ayreference number: A42126; MUID:92186854; PMID:1545804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;125-222/Domain: SH2 homology <SH2>
F;241-499/Domain: protein kinase homology <KIN>
F;249-257/Region: protein kinase ATP-binding motif
F;249-257/Region: protein kinase ATP-binding motif
F;21/Modified site: myristylated amino end (dly) (in mature form) #status predicted
F;392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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A;Residues: 1-282,'VP',285-509 <MAR>
A;Cross-references: UNIPARC:UPI0000172586; GB:M12056; NID:g198763
A;Note: the sequence is revised in GenBank entry MUSLCK, release 116.0, (PIDN:AAB59674.1
R;Voronova, A.F.; Adler, H.T.; Sefton, B.M.
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A;Molecule type: mRNA
A;Residues: 1-88 <CHO>
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A;Reference number: 157629; MUID:88142832; PMID:3501824
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A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel A;Reference number: 157636; MUID:89096891; PMID:2850479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-35,'VR' <GAR>
A;Cross-references: UNIPARC:UPI000016CE9E; GB:M21511; NID:g198768; PIDN:AAA39422.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro F;63-124-Domain: SH3 homology <SH3>
F;212-224/Domain: SH3 homology <SH3>
F;221-259/Region: protein kinase homology <KIN>
F;251-259/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;273/Active site: Lys #status predicted
F;373/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #text change 05-Oct-2004
C;Accession: JQ0152; 807200; 801879; 807143; A32797; 157636
C;Accession: JQ0152; 807200; 801879; 807143; A32797; 157636
R;Rouer, B.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R.
Gene 84, 105-113, 1989
A;Titles Structure of the human 1ck gene: differences in genomic organisation within src
A;Reference number: JQ0152; MUID:90108637; PMID:2558056
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A; Residues: 1-86, P', 88-509 <PER>
A; Residues: 1-86, P', 88-509 <PER>
A; Cross-references: Unitabac: UPI000163BD5; EMBL:X13529; NID:g34294; PIDN:CAA31884.1; PID
R; Kogs, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.
Eur. J. Immunol. 16, 1643-1646, 1986
A; Title: A human T cell-specific cDNA clone (YT16) encodes a protein with extensive homo
A; Reference number: S07200; MUID:87133831; PMID:3493153
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A;Cross-references: UNIPARC:UPI000016B09E; EMBL:X05027; NID:g36807; PIDN:CAA28691.1; PID
B;Veillette, A.; Foss, F.M.; Sausville, E.A.; Bolen, J.B.; Rosen, N.
Oncogene Res. 1, 357-374, 1987
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R;Perlmutter, R.M.; Marth, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, J. Cell. Biochem. 39, 117-126, 1988
A;Title: Structure and expression of 1ck transcripts in human lymphoid cells. A;Reference number: S07822; MUID:89123626; PMID:3265417
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N;Alternate names: kinase-related transforming protein (lck)
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Mon

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F;93-351/Domain: protein Kinase homology <KIN>F;101-109/Region: protein kinase ATP-binding motif
F;123/Active site: Lys #status predicted
F;355/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
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A;Status: translation not shown
A;Residues: 1-526 xB0D-
A;Residues: 1-526 xB0D-
A;Genes: 1-526 xB0D-
A;Genes: arc
C;Genetics:
A;Gene: arc
C;Genetics:
A;Gene: arc
C;Genetics:
A;Gene: arc
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F;Rel-137/Domain: SH2 homology xSH3>
F;265-523/Domain: protein kinase homology xIN>
F;265-523/Domain: protein kinase ATP-binding motif
F;273-281/Region: protein kinase ATP-binding motif
F;273-281/Region: protein kinase predicted
F;295/Active site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: phosphate (Tyr) (covalent) (by autophosphorylation) #status
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A;Residues: 1-526 <CZE>
A;Cross-references: UNIPROT:P00524; UNIPARC:UPI0000170DC3; GB:L29199; GB:J02018; GB:J020
A;Experimental source: strain Schmidt-Ruppin
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Mature 301, 736-738, 1983
A;Title: Corrections to the nucleotide sequence of the src gene of Rous sarcoma virus.
A;Reference number: A38017; MUID:83141780; PMID:6298633
A;Accession: A38017
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Cell 32, 881-890, 1983
A;Title: Structure and sequence of the cellular gene homologous to the RSV sec gene
A;Reference number: A00630; MUID:83155664; PMID:6299580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
C;5pecies: Rous sarcoma virus
C;Date: 22-May-1981 #sequence revision 17-Dec-1982 #text_change 05-Oct-2004
C;Accession: A38017; A00631; S02726; A38018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rous sarcoma virus
C;Jate: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-
C;Accession: S09609
R;Bodor, J; Poliak, E; Pichrtova, J; Geryk, J; Svoboda, J.
Nucleic Acids Res. I7, 8869, 1899
A;Title: Complete nucleoride sequence of LTR, v-src, LTR provirus H-19.
A;Reference number: S09609; MUID:90067864; PMID:2587228
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                      Length 362
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N;Alternate names: kinase-related transforming protein src
                                                                                                                                                                                                                                                                                                                                            Score 34; DB 2;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                         F;1-70/Domain: SH2 homology (fragment) <SH2>
                                                                                                                                                                                                                                                                                                                                            82.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.9%;
77.8%;
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190 QLIDMAAQV 198
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Best Local Similarity
Matches 7; Conserv
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A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S09609
                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
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A;Cross-references: UNIPARC:UP1000016ABFC; EMBL:X06369; NID:g34288; PIDN:CAA29667.1; PID Biochim. Biophys. Acra 888, 286-295, 1986
A;Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56 (LSTRA). A;Reference number: S07143; MUID:87000726; PMID:3489486
A;Rocession: S07143
A;Molecule type: mRNA
A;Residues: 'A',376-509 <TRE>
A;Cross-references: UNIPARC:UP1000016AF39; EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PID R;Takadera, T; Leung, S.; Gernone, A.; Roga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W Mol. Cell. Biol. 9, 2173-2180, 1989
A;Tile: Structure of the two promoters of the human lck gene: differential accumulation A;Recession: A32797; MUID:89313764; PMID:2787474
A;Recession: A32797; MUID:89313764; PMID:2787474
A;Residues: L35 <TRAC
A;Gross-references: UNIPARC:UP1000016ABFF; GB:M26692; NID:g341523; PIDN:AA59503.1; PID: R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
A;Reidues: L35 <TRAC
A;Cross-references: UNIPARC:UP1000016ABFF; GB:M26692; NID:g341523; PIDN:AA59503.1; PID: A;Reference number: 157636; MUID:89096891; PMID:2850479
A;Reference number: 157636; MUID:87636
A;Accession: 157636; MUID:87606891; PMID:2850479
A;Accession: 157636
A;Accession: 15763
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N.Alternate names: src-type tyrosine kinase 2
C;Species: Spongilla lacustris
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPROT:P42688; UNIPARC:UPI0000135F48; EMBL:X61602; NID:g10151; PIDN
C;Genetics:
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C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; tyrosine-speci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPARC:UPI000016ABFD; GB:M21510; NID:g187031; PIDN:AAA59501.1; PID:
C;Comment: Protein tyrosine Kinases play important roles in the control of cell growth a
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3,5/Binding site: palmitate (Cys) (covalent) #status predicted
273/Active site: Lys #status predicted
394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status
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424-501/Domain: protein kinase homology <KIN>
;251-259/Region: protein kinase ATP-binding motif
;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-35,'VR' <RES>
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A;Accession: S24551
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and

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F;273-281/Region: protein kinase ATP-binding motif
F;27/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experime
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A; Cross-references: UNIPROT:064994; UNIPROT:092806; UNIPROT:060567; UNIPROT:007461; UNIP
B; Cxoss-references: UNIPROT:064994; UNIPROT:092806; UNIPROT:060567; UNIPROT:007461; UNIP
B; Experimental source: strain Prague A
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989
A; Note: only a list of differences from sequence S09665 is given; however, the list is i
B; Fincham, V.J.; Wyke, J.A.
A; Fincham, V.J.; Wyke, J.A.
A; Title: Localization of temperature-sensitive transformation mutations and back mutatio
A; Reference number: S09665; MUID:86200422; PMID:3009882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C.Superfamily: Tyrosine-protein kinase homology C.Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc C.Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc F; 88-137/Domain: SH3 homology <SH3>
F; 148-245/Domain: SH3 homology <SH3>
F; 255-523/Domain: protein kinase homology <KIN>
F; 255-523/Domain: protein kinase ATP-binding motif F; 270-281/Region: protein kinase ATP-binding motif F; 270-dified site: myristylated amino end (Gly) (in mature form) #status predicted F; 295/Active site: Lys #status predicted F; 416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague A)
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R;Liu, Z; Hackett, P.B.
Nucleic Acids Res. 17, 3986, 1989  
A;Title: Sequence variation of the Rous sarcoma virus PrA src gene. A;Reference number: $15582; MUID:89282411; PMID:2543959  
A;Accession: $15582  
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A;Residues: 231-241,'TH',244-287,'G',289-463,'P',465-501,'N',503-526
A;Cross-references: UNIPARC:UP100001755F1
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
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Pred. No. 20;
2; Mismatches
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Pred. No. 20;
2; Mismatches
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77.8%;
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Best Local Similarity 77.0.
Best Local 7; Conservative
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Best Local Similarity 77.0.
Best Local 7; Conservative
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362 QLVDMAAQI 370
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OLVDMAAQI 370
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protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague C)
C; Species: Rous sarcoma virus
C; Accession: A00632
R; Schwartz, D.; Tizard, R.; Gilbert, W.
submitted to the Nucleic Acid Sequence Database, September 1982
A; Reference number: A00632
A; Reference number: A00632
A; Residues: 1-526 < SCH-
A; Resi
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A; Contents: amotation; phosphorylation site
C; Coment: The sequence from the Schmidt-Ruppin strain is shown.
C; Genetics:
A; Gene: src
C; Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C; Keywords: AFP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc C; Superfamin: SH3 homology <SH3>
F; 148-245, Domain: SH3 homology <SH3>
F; 148-245, Domain: SH3 homology <SH2>
F; 265-523/Domain: protein kinase homology <KIN>
F; 273-281/Region: protein kinase ATP-binding motif F; 27/Modified site: myristylated amino end (Gly) (in mature form) #status predicted F; 25/Active site: Lys #status predicted
F; 2416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experime
                                                                                                                                                                                                                                                                        A;Title: Nucleotide sequence of the src gene of the Schmidt-Ruppin strain of Rous Sarcom A;Acession: S02726, MUID:89160256; PMID:2537953
A;Accession: S02726
A;Accession: S02726
A;Molecule type: DNA
A;Residues: 1-9, 'G',11-62,'D',64-123,'V',125-319,'K',321-495,'S',497-526 <BAR>A;Residues: 1-9, 'G',11-62,'D',64-123,'V',125-319,'K',321-495,'S',497-526 <BAR>A;Cross-references: UNIPARC:UP10000135P2C; EMBL:X13745; NID:g61908; PIDN:CAA32012.1; PID B;Takey, T.; Feldman, R.A.; Hanafusa, H.
J. Virol. 44, 1-11, 1982
A;Title: DNA sequence of the viral and cellular src gene of chickens: I. Complete nuclec A;Reference number: A38018; MUID:83059858; PMID:6292477
A;Accession: A38018
A;Molecule type: DNA
A;Accession: A38018
A;Molecule type: DNA
A;Residues: 1-15, 'C', 17-94, 'RT', 97-116, 'D', 118-337, 'T', 339-526 <TA2>A;Cross-references: UNIPARC:UP10000135P24; GB:K00928; NID:g210187; PIDN:AAA42565.1; PID:
                                                                                                   A, Experimental source: strain Schmidt-Ruppin
R; Barnier, J.V.; Dezelee, P.; Marx, M.; Calothy, G.
Nucleic Acids Res. 17, 1252, 1989
A;Title: Nucleotide sequence of the src gene of the Schmidt-Ruppin strain of Rous Sarcom A; Reference number: $02726; MUID:89160256; PMID:2537953
A;Accession: $02726
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0
Residues: 1-62,'D',64-95,'T',97-123,'V',125-300,'N',302-526 <TAK>;Cross-references: UNIPARC:UP10000172582
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Length 526; 0; Indels

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Score 34; DB Pred. No. 20; 2; Mismatches

82.9**%**; 77.8**%**;

Query Match Best Local Similarity

7; Conservative

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1 KLLDMAAQI

A; Experimental source: strain rASV1441
R;Neil, J.C.; Ghysdael, J.; Vogt, P.K.; Smart, J.E.
Nature 291, 675-677, 1981
A;Title: Homologous tyrosine phosphorylation sites in transformal A;Reference number: A38019; MUID:81220979; PMID:6264320
A;Contents: annotation; phosphorylation site
C;Comment: The sequence from the Schmidt-Ruppin strain is shown.

Query Match

Best Loc Matches

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A,Title: Avian sarcoma virus Y73 genome sequence and structural similarity of its transf
A,Reference number: A00633; MUID:82195528; PMID:6281656
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C,Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C,Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; tran
F,88-137/Domain: SH3 homology <SH3>
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F;265-523/Domain: protein kinaee homology <KIN>
F;232-321/Region: protein kinaee ATP-binding motif
F;205/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
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| Cross_references: UNIPROT:P13116; UNIPARC:UPI000017159F; GB:M23422; GB:J04822; NID:g21
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A; Introns: 464/1
C; Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C; Superfamily: Tyrosine-protein, kinase, proto-oncogene SRC type; protein, myristylation; pho C; Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho F; 87-136/Domain: SH2 homology <SH2>
F; 87-136/Domain: SH2 homology <SH2>
F; 244-522/Domain: protein kinase homology <KIN>
F; 252-280/Region: protein kinase ATP-binding motif
F; 272-280/Region: protein kinase ATP-binding motif
F; 294/Active site: myristylated amino end (Gly) (in mature form) #status predicted
F; 294/Active site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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A;Cross-references: UNIPARC:UPI00001715A0; GB:M30858; NID:g214799; PIDN:AAA51644.1; PID:
A;Note: host Gallus gallus (chicken)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 05-Oct-2004
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A,Reference number: I51563; MUID:85215578; PMID:2987836
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C;Comment: This protein is synthesized as a gag-yes polyprotein.
C;Genetics:
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                                                                                 C;Accession: A00633
R;Kitamura, N.; Kitamura, A.; Toyoshima, K.; Hirayama, Y.;
Nature 297, 205-208, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.9%; Score 34; DB 1; 77.8%; Pred. No. 20;
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Best Local Similarity 77.85
Conservative
                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: genomic RNA A; Residues: 1-528 <KIT>
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362 QLVDMAAQI
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                               A; Molecule type: DNA
A; Residues: 1-526 <BOD>
A; Residues: 1-526 <BOD>
A; Residues: 1-526 <BOD>
A; Cross-references: UNIPROT:060567; UNIPARC:UPI00001068B2; EMBL:X52822; NID:g49656; PIDN A; Cross-references: Wesocricetus auratus (golden hamster) provirus
C; Genetics: C; Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                  F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;265-521/Region: protein kinase ATP-binding motif
F;275/Active site: Lys #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-526 <KAS>
A;Cross-references: UNIPROT:Q07461; UNIPARC:UPI000010512B; EMBL:X68524; NID:g61903; PIDN
R;Kashuba, V.I.; Serge, Z.V.; Rynditch, A.V.; Kavsan, V.M.; Hlozanek, I.
submitted to the EMBL Data Library, March 1990
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-526 <KA2>
A,Cross-references: UNIPARC:UPI000010512B; EMBL:X51861; NID:g61896; PIDN:CAA36154.1; PID
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F; 148-245/Domain: SH3 homology calls.

F; 255-523/Domain: protein kinase homology ckIN>
F; 255-523/Domain: protein kinase ATP-binding motif
F; 273-281/Region: protein kinase ATP-binding motif
F; 273-281/Region: protein kinase ATP-binding motif
F; 2595/Active site: myristylated amino end (Gly) (in mature form) #status predicted
F; 295/Active site: pys #status predicted
F; 416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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C;Species: avian sarcoma virus Y73
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Conservative
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362 QLVDMAAQI 370
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QLVDMAAQI 370
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les 7; Conserv
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Matches 7; Conser
A;Accession: S20808
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Query Match

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361 QLVDMAAQI 369

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1 KLLDMAAQI

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Mol. Cell. Biol. 11, 4165-4176, 1991
A)Title: Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5' exons and po A)Tetle: Analysis of CDNAs of the Proto-oncogene c-src: heterogeneity in 5' exons and po A)Accession: A41256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 484-533 < LONL>
A; Cross-references: UNIPARC: UPI0000171468; GB:S43579; NID:g1679964; PIDN:AAB19353.1; PID
A; Cross-references: UNIPARC: UPI0000171468; GB:S43579; NID:g1679964; PIDN:AAB19353.1; PID
A; Note: the authors translated the codon CAG for residue 527 as Glu
R; Dorai, T.; Mang, L.H.
A; Dorai, T.; Mang, L.H.
A; Title: An alternative non-tyrosine protein kinase product of the c-src gene in chicken
A; Reference number: A35650; MUID:90318371; PMID:2115117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-182, DECIPLESCLC' <DOR2>
A;Cross-references: UNIPARC:UPI00000FD3A4; GB:M57290; NID:g212703; PIDN:AAA49078.1; PID:A;Cross-references: UNIPARC:UPI00000FD3A4; GB:M57290; NID:g212703; PIDN:AAA49078.1; PID:A;Note: alternatively spliced mRNA exclusively replaces the long form in skeletal muscle A;Note: this ORF appears not to be translated
B;Shenoy, S.; Choi, J.K.; Bagrodia, S.; Copeland, T.D.; Maller, J.L.; Shalloway, D. Coll 57, 763-774, 1989
A;Title: Purified maturation promoting factor phosphorylates pp60(c-src) at the sites pha;A;Reference number: A32432; MUID:89249341; PMID:2470512
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C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Superfamily: Tyrosine-protein kinase homology cSH3>
F;Reyards: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
F;Reyards: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
F;148-245/Domain: SH3 homology cSH2>
F;148-245/Domain: protein kinase homology cKIN>
F;273-281/Region: protein kinase ATP-binding motif
F;12,48/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;12,48/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F;34,46/Binding site: phosphate (Ser) (covalent) #status experimental
F;25/Active site: Lys #status predicted
F;125/Active site: Lys #status predicted
F;416,527/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: (08-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: S33569; S29626
R;Sudol, M.; Greulich, H.; Newman, L.; Sarkar, A.; Sukegawa, J.; Yamamoto, T.
A;Title: A novel Yes-related kinase, Yrk, is expressed at elevated levels in neural and ba;Reference number: S33568; MUID:93205395; PMID:8455940
                                          of chickens: II comparison of
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A,Note: 34-Thr, 46-Thr, and 72-Ser are phosphorylated during mitosis
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                                          gene
A; Reference number: I50217; MUID:83059861; PMID:6292480
                                                                                                                                                                           A;Status: preliminary; translated from G3/EMBL/DDBJ
A;Molecule type: DNA
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Pred. No. 20;
2; Mismatches
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77.8%;
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A;Residues: 2-88 <SHE>
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A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                             Allerante names: Kinase-related transforming protein (src); kinase-related transforming protein-tyrosine kinase related transforming protein (src); kinase-related transforming C,Species: Xenopus laevis (African clawed frog)
C,Decies: Xenopus laevis (African clawed frog)
C,Date: 16-Uun-2000 #sequence revision 16-Uun-2000 #text_change 31-Dec-2004
C,Accession: A34104; ISIS64
J. Biol. Chem. 264, 10649-10653, 1989
J. Biol. Chem. 264, 10649-10653, 1989
J. Biol. Chem. 264, 10649-10653, 1989
J. Biol. Chem. 24104; MUID: 89278134; PMID: 2499582
A,Racession: A34104
A,Recession: A34104; MUID: 89278134; PMID: 2499582
A,Recession: Domograd with conceptual translation
A,Wolecule type: mRNA
A,Residues: 1-512 <STE
A,Cross-references: UNIPARC: UDIO000172581; GB:M24704; GB:J04822; NID: 221
R,Steele, R. E.; Chosn, R.; Ral, B.B.A.; Winokur, S.T.; Unger, T.F.
A,Cross-references: UNIPARC: UDIO000F97A; GB:M33646; NID: 214808; PIDN: AAA49963.1; PID: A,Residues: 1-13 <STE
A,Accession: 151564
A,Accession: 151564
A,Accession: 151564
A,Accession: Lated from GB/EMBL/DDBJ
A,Accession: 151564
A,Accession: SEGE
A,Accession: A,MulD: 93064714; PMID: 1437158
A,Accession: SEGE
A,Accession: SEGE
A,Accession: SA, MulD: 93064714; PMID: 910000797; SH3 homology; SH3 homology C,Keywords: MP; homology C,Keywords: MP; homology C,Keywords: MP; homology C,Reynords: SH3 homology; SH3: homology C,Keywords: MP; homology C,Reynords: SH3 ho
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N;Alternate names: kinase-related transforming protein src
C;Species: Gallus gallus (chicken)
C;Date: 19-Feb-1984 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C;Accession: A00630; 150217; Ā41256; C35650; A32432
R;Takeya, T.; Hanafusa, H.
C;Accession: A010530; ISO217; Ā41256; C35650; A32432
A;Title: Structure and sequence of the cellular gene homologous to the RSV sec gene and A;Reference number: A00630; MUID:83155664; PMID:6299580
A;Accession: A00630
A;Accession: A00630
A;Mosidues: 1-500, R, 502-533 <TAK>
A;Cross-references: UMIPROT:P00523; UNIPROT:Q90993; UNIPARC:UPI000017257F; GB:J00844; NI Cell 34, 319, 1983
A;Reference number: A90838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147-244/Domain: SH2 homology <SH2>
;264-522/Domain: protein kinase homology <KIN>
;272-280/Region: protein kinase ArP-binding motif
;272-280/Region: protein kinase ArP-binding motif
;273-280/Active site: myristylated and (Gly) (in mature form) #status predicted
;294/Active site: Lys #status predicted
;415,526/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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Score 34; DB 1; Pred. No. 20; 2; Mismatches (

82.9%; 77.8%;

Query Match 82.9 Best Local Similarity 77.8 Matches 7; Conservative

361 QĽVĎMAAQÍ 369

ò g A,Contents: annotation; erratum, correct translation of residue 526 R,Takeya, T.; Hanafusa, H. J. Virol. 44, 12-18, 1982

us-10-062-257a-14.rpr

Mon

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Gaps

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A;Residues: 1-539 <8WO>
A;Cross-references: UNIPROT:Q7LZHO; UNIPARC:UP100001755F6; GB:U01350
C;Superfamily: Tyrosine-protein Kinase, proto-oncogene SRC type; protein kinase homology C;Superfamily: Tyrosine-protein; kinase homology C;Reywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phr F;91-140/Domain: SH2 homology <8H2>
F;21-248/Domain: SH2 homology <8H2>
F;21-229/Domain: protein kinase homology <KIN>
F;279-287/Region: protein kinase ATP-binding motif
F;279-287/Region: protein kinase ATP-binding motif
F;279-287/Region: protein kinase ATP-binding motif
F;301/Active site: Lys #status predicted
F;301/Active site: Lys #status predicted
F;322,533/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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A; Residues: 1-66, IHPLR', 72-81, 'Q', 83-541 <KAP>
A; Residues: 1-66, IHPLR', 72-81, 'Q', 83-541 <KAP>
A; Cross-references: UNIPARC:UP10000171303; EMBL:X13207; NID:g63362; PIDN:CAA31595.1; PIDR; Sudol, M.; Kieswetter. C.; Zhao, Y.H.; Dorai, T.; Wang, L.H.; Hanafusa, H.
Nucleic Acids Res. 16, 9876, 1988
A; Title: Nucleotide sequence of a cDNA for the chick yes proto-oncogene: comparison with A; Reference number: S01689; MUID:89041591; PMID:3054816
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P; 2-541/Product: protein-tyrosine kinase yes #status predicted <MAT>
F; 96-145/Domain: SH3 homology <SH3>
F; 156-253/Domain: SH3 homology <SH2>
F; 213-531/Domain: protein kinase homology <KIN>
F; 281-289/Region: protein kinase ATP-binding motif R; 281-289/Region: protein kinase ATP-bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P09324; UNIPARC:UPI0000047A82; EMBL:X13207 R;Kaplan, P.L. submitted to the EMBL Data Library, October 1988
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         A; Reference number: A49114; MUID: 94043386; PMID: 8227079
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A;Residues: 1-237,'S',239-541 <SUD>
A;Cross-references: UNIPARC:UP1000017258C; EMBL:X12461
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Pred. No. 21;
2; Mismatches
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Pred. No. 21;
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77.8%;
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ilarity 77.8%;
Conservative
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nes 7; Conserv
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Best Local Similarity
Matches 7; Conserv
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A; Residues: 1-541 <ZHE>
                                                                                                      A; Status: preliminary A; Molecule type: mRNA
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A/Recession: A45501
A/Recession: A45501
A/Recession: A45501
A/Residues: 1-237 <STR
A/Residues: 1-237 <STR
B/Steele, R.E.; Irwin, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B.
R/Steele, R.E.; Irwin, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B.
R/Steele, R.E.; Irwin, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B.
A/Residues: 1-250, S./. 252-537 <ST2>
A/Residues: 1-250, S./. 252-537 <ST2>
A/Residues: 1-250, S./. 252-537 <ST2>
A/Cross-references: UNIPARC:UP1000013ACB9; EMBL:X14377; NID:g65272; PIDN:CAA32551.1; PIC
C/Genetics:
A/Gene: yes
C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C/Reywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming profounces: SST SST Region: STE homology <SH2>
F/32-249/Domain: SH2 homology <SH2>
F/32-249/Domain: protein kinase homology <KIN>
F/32-248/Region: protein kinase homology <KIN>
F/32-24/Domain: myristylated amino end (Gly) (in mature form) #status predicted
F/299/Active site: Lys #status predicted
F/299/Active site: Lys #status predicted
F/420,531/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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                                                 A;Cross-references: UNIPROT:Q02977; UNIPARC:UPI0000151F15; EMBL:X67786; NID:g63895; PIDN C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho C;Reywords: ATP; autophosphorylation; blocked amino end; lipoprotein, myristylation; pho F;Re-137/Domain: SH3 homology <SH3>
F;Re-137/Domain: SH2 homology <SH2>
F;268-526/Domain: protein kinase homology <KIN>
F;276-228/Region: protein kinase homology ocity
F;276-228/Region: protein kinase ATP-binding motif
F;276-284/Region: protein minase ATP-binding motif
F;248-848/Region: protein kinase ATP-binding motif
F;288/Active site: Lys #status predicted
F;298/Active site: Lys #status predicted
F;419,530/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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B49114
C. Specien-tyrosine kinase (EC 2.7.1.112) fyk - Pacific electric ray
C. Species: Torpedo californica (Pacific electric ray)
C. Species: Torpedo californica (Pacific electric ray)
C. Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 05-Oct-2004
C. Accession: B49114
R. Swope, S. L.; Huganir, R. L.
J. Biol. Chem. 268, 25152-25161, 1993
A: Title: Molecular cloning of two abundant protein tyrosine kinases in Torpedo electric
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Pred. No. 21;
2; Mismatches
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Pred. No. 20;
2; Mismatches
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Matches 7; Conservative
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QLVDMAAQI 373
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A;Residues: 1-536 <SUD>
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A)Residues: 192-542 <AND>
A)Residues: 192-542 <AND>
A)Cross-references: UNIPARC:UPI000016B068; GB:X02647; NID:g36588; PIDN:CAA26485.1; PID:g
A)Cross-references: UNIPARC:UPI000016B068; GB:X02647; NID:g36588; PIDN:CAA26485.1; PID:g
A)Barch, R.C.; Mardon, G.; Lebo, R.V.; Varmus, H.E.; Bishop, J.M.
Mol. Cell. Biol. 5, 831-838, 1985
A)Title: Isolation of duplicated human c-src genes located on chromosomes 1 and 20.
A)Reference number: A28832; MUID:85187981; PMID:2581127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP C, Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C, Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho F;1-542/Product: protein-tyrosine kinase src, neuronal #status predicted <MAT> F;1-117,124-542/Product: protein-tyrosine kinase src, short form #status predicted <MAZ> F;1-147,00main: SH3 homology <SH3> F;21-146/Domain: SH2 homology <SH3> F;274-532/Domain: protein kinase homology <KIN> F;280-290/Region: protein kinase ATP-binding motif F;280-290/Region: protein kinase ATP-binding motif F;280-290/Region: protein kinase ATP-binding motif F;380-40/Active site: Lys #status predicted F;380/Active site: Lys #status predicted F;380/Active site: Lys #status predicted F;425,536/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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A;Residues: 1-543 <SUK>
A;Cross-references: UNIPROT:P07947; UNIPARC:UPI000062316; GB:M15990; NID:9181267; PIDN:
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C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:120750; OMIM:190090
A;Map position: 20q11.2-20q11.2
A;Introns: 84/1; 117/2; 123/2; 156/2; 191/1; 241/1; 293/1; 353/1; 378/3; 430/1; 474/1
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                                                                                                                                                                                                                                                                                                                                                                                        RiPyper, J.M.; Bolen, J.B.
Mol. Cell. Biol. 10, 2035-2040, 1990
A;Title: Identification of a novel neurcnal C-SRC exon expressed in human brain.
A;Reference number: A34704; MUID:90220588; PMID:1691439
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Oct-2004
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Pred. No. 21;
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A;Map position: 18p11.31-18p11.22
                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 382-542 <PAR>
A;Cross-references: UNIPARC:UP1000017257D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 118-123 <PY3>
A;Cross-references: UNIPARC:UP1000017257E
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77.8%;
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371 QLVDMAAQI 379
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Best Local Similarity
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A, Accession: A. 20091
A, Accession: A. 20091
A, Accession: A. 20091
A, Accession: Bolen, J.B.
A, Cross-references: UNIPROT: P12931; UNIPARC: UPI0000172579; UNIPARC: UPI0000172579; GB:M16
B, Pyper, J.M.; Bolen, J.B.
J. Neurosci. Res. 24, 89-96, 1989
A, Title: Neuron-specific splicing of C-SRC RNA in human brain.
A, Reference number: A61083; MUID: 90040822; PMID: 2681803
A, Accession: A61083
A, Accession: A61083
A, Accession: B61083
A, Accession: B61083
A, Accession: B61083
A, Accession: B61083
A, Accession: B1083
A, Accession: A23287; MUID: 85213483; PMID: 2582238
A, Accession: A23287
                                                                                                                                                                   RESULT 19
31645
protein-tyrosine kinase (EC 2.7.1.112) yes - mouse
N;Alternate names: gene c-yes protein
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1994 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: 148318; S31645
R;Klages, S.; Adam, D.; Eiseman, E.; Fargnoli, J.; Dymecki, S.M.; Desiderio, S.V.; Bolen
A;Title: Molecular cloning and analysis of CDNA encoding the murine c-yes tyrosine prote
A;Reference number: 148318; MUID:93173515; PMID:8437854
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-541 cRES>
A;Kesidues: 1-541 cRES>
C;Genetics:
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Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
96-145/Domain: SH3 homology <SH3>
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 Hsequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C;Accession: A26891; A61083; B61083; A22387; A28832; B34704
R;Tanaka, A, Gibbs, C.P.; Arthur, R.R.; Anderson, S.K.; Kung, H.J.; Fujita, D.J.
Mol. Cell. Biol. 7, 1978-1983, 1987
A;Title: DNA sequence encoding the amino-terminal region of the human c-src protein:
A;Reference number: A26891; MUID:87257903; PMID:3299057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;281-289/Region: protein kinase ATP-binding motif F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted F;303/Active site: Lys #status predicted
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Pred. No. 21;
2; Mismatches
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F;273-531/Domain: protein kinase homology <KIN>
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77.8%;
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Matches 7, Conservative
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370 OLVDMAAQI 378
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KLLDMAAQI
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F;436/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
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(S.Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F;88-137/Domain: SH3 homology <SH3>
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F;265-523/Domain: protein kinase homology <KIN>
F;255-523/Domain: protein kinase ATP-binding motif
F;273-281/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
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F,148-1245/Domain: BH2 homology <SH3.>
F,245-523/Domain: protein kinase homology <KIN.>
F,205-521/Region: protein kinase ATP-binding motif F;273-281/Region: protein kinase ATP-binding motif F;273-281/Region: protein kinase ATP-binding motif F;295/Active site: Lys #status predicted E;325/Active site: Lys #status predicted F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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C;Species: avian sarcoma virus S2
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
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C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C;Accession: A25375
R;Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, K.
Mol. cell. Biol. 6, 2420-2428, 1986
A;Title: Activation of the cellular src gene by transducing retrovirus.
A;Reference number: A25375, WUID:87064539; PMID:3097513
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R;Kawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, Mol. Cell. Biol. 6, 2420-2428, 1986
A;Title: Activation of the cellular src gene by transducing retrovirus. A;Reference number: A25375; MUID:87064539; PMID:3097513
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                                                                                  Length 546;
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A;Residues: 1-557 <1KA>
A;Cross-references: UNIPROT:P14085; UNIPARC:UP10000135F26
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A;Cross-references: UNIPROT:P14084; UNIPARC:UP10000135F25
                                                                              Score 34; DB 2;
Pred. No. 21;
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Pred. No. 21;
2; Mismatches
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Matches 7; Conservative
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QLVDMAAQI 370
                                         Query Match
Best Local Similarity
7; Conserv?
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A;Batus: preliminary
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-546 <4Tx>
A;Cross-references: UNIPROT:Q86363; UNIPARC:UPI0000106213; EMBL:X84073; NID:g663085; PID
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP: autophosphorylation; blocked amino end; lipoprotein; myristylation; phd
C;Keywords: ATP: autophosphorylation; blocked amino end; lipoprotein; myristylation; phd
F;108-157/Domain: SHZ homology <SHZ>
F;168-265/Domain: protein kinase homology <KIN>
F;285-543/Domain: protein kinase ATP-binding motif
F;295-301/Region: protein kinase ATP-binding motif
F;295-301/Region: protein kinase ATP-binding motif
F;315/Active site: Lys #status predicted
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A;Battus: preliminary
A;Molecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-545 cTRT>
A;Cross-references: UNIPROT:Q86362; UNIPARC:UPI0000105D06; EMBL:X84074; NID:g663083; PID
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phd
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phf
C;Reywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phf
F;108-157/Domain: SH3 homology <SH2>
F;885-543/Domain: protein kinase homology <KIN>
F;293-301/Region: protein kinase homology oxif
F;293-301/Region: protein kinase ATP-binding motif
F;293-301/Region: protein kinase ATP-binding motif
F;215/Active site: myristylated amino end (Gly) (in mature form) #status predicte
F;315/Active site: Lys #status predicted
F;315/Active site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
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R;Tatosyan, A.; Yatsula, B.; Shtutman, M.; Moinova, E.; Kaverina, I.; Musatkina, E.; Les submitted to the EMBL Data Library, January 1995
A;Description: Two new isoforms of v-src oncogene isolated from low and high metastatic A;Reference number: $52313
                                                               F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted F;3/Binding site: palmitate (Cys) (covalent) #status predicted F;305/Active site: Lys #status predicted F;305/Active site: Lys #status predicted F;426/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
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A;Description: Two new isoforms of v-src oncogene isolated from low and high metastatic A;Reference number: S52313
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Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Oct-2004
Accession: $52313
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C;Species: Rous sarcoma virus
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                                     'Region: protein kinase ATP-binding motif
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275-533/Domain: protein kinase homology <KIN>
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Best Local Similarity 77.8
Matches 7; Conservative
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372 QLVDMAAQI 380
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382 QLVDMAAQI 390
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Matches 7; Conser
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C,Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Oct-2004
C;Accession: I37206; S51647
C;Accession: I37206; S51647
C;Accession: I37206; S51647
C;Accession: I37206; S51647
J:Immunol. 154, 1265-1272, 1995
A;Title: Molecular cloning, characterization, and chromosomal localization of a human ly A;Reference number: 137206; MUID:95123078; PMID:7822795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-505 <RES>
A;Cross-references: UNIPROT:P51451; UNIPARC:UPI0000163B22; EMBL:Z33998; NID:g601951; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 8p23-8p22
S.Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; tyro
F;65-113/Domain: SH3 homology <SH3>
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R;Bosch, T.C.G.; Unger, T.F.; Fisher, D.A.; Steele, R.E.
A)Ol. Cell. Biol. 9, 4141-4151, 1989
A;Title: Structure and expression of STK, a src-related gene in the simple metazoan Hydr. A;Reference number: A34094; MUID:90066418; PMID:2479820
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A;Residues: 1-509 <BOS>
A;Cross-references: UNIPROT:P1713; UNIPARC:UPI000013610D; GB:M25245; NID:g159273; PIDN:
C;Genetics:
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F;238-497/Domain: protein kinase homology <KIN>
F;238-497/Domain: protein kinase homology <KIN>
F;246-254/Region: protein kinase ATP-binding motif
F;246-254/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;2/Modified site: palmitate (Cys) (covalent) #status predicted
F;268/Active site: Lys #status predicted
F;390/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pre
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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Oct-2004
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F;239-497/Domain: protein kinase homology <KIN>
F;247-255/Region: protein kinase ATP-binding motif
F;2/Modified slite: myristylated amino end (GLy) (in
F;269/Active site: Lys #status predicted
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7
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66.7%; Pred. No. 32;
iive 3; Mismatches
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Matches 6; Conserv
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Matches 6; Conserv
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C;Species: avian sarcoma virus PR2257
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C;Accession: A30174
J. Virol. 63, 481-492, 1989
A;Title: Transduction of the cellular src gene and 3' adjacent sequences in avian sarcom
A;Reference number: A30174; MUID:89094972; PMID:2463376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; ond
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S0420: #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S0420: #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S0420: #sexione number: S0420: #sexione sarcoma virus encodes a fgr-related oncogene lacking A;Accession: S0420: #sexione number: S0420: #sexione s0420: #sexione number: S0420: #sexione num
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C,Superfamily: feline sarcoma virus protein-tyrosine kinase fgr; protein kinase homology
C,Keywords: ATP; autophosphorylation; myristylation; oncogene; phosphoprotein; phosphot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:P15054; UNIPARC:UP10000135F23; GB:M21526; NID:g210264; PIDN:
C,Genetics:
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Species: feline sarcoma virus
Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
                                            Gaps
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66.7%; Pred. No. 24;
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N,Alternate names: qaq-onc fusion nrote
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7; Conservative
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362 OLVDMAAOI 370
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362 QLVDMAAQI 370
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A; Residues: 1-587 <GER>
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358 QLVDMAAQV 366
                                                                                                                                                protein-tyrosine kinase (EC 2.7.1.112) fgr - human
N;Alternate names: kinase-related transforming protein (fgr)
S;Species aspiens (man)
C;Date: 31-Dec-1988 #sequence revision 30-Sep-1989 #text_change 05-Oct-2004
C;Accession: A27676; A28353; A24842; A45930; S24306
K;Atamine, S.; Notario, V.; Rao, C.D.; Mikl, T.; Cheah, M.S.C.; Tronick, S.R.; Robbins, Mol. Call. Biol. 8, 259-266, 1988
A;Title: Primary structure of the human fgr proto-oncogene product p55(c-fgr).
A;Reference number: A27676; MUID:88094395; PMID:3275868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-529 <REA>
A;Cross-references: UNIPROT:P09769; UNIPARC:UPI000012A72F; GB:M19722; GB:U03429; NID:g18
R;Inoue, K.; Ikawa, S.; Semba, K.; Sukegawa, J.; Yamamoto, T.; Toyoshima, K.
Oncogene 1, 301-304, 1987
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A;Molecule type: DNA
A;Rosidues: 111-416 - REB->
A;Cross-references: UNIPARC:UPI000016A8FC; GB:M12724; NID:g182581; PIDN:AAA52762.1; PID:
Br. J. Cancer 58, 704-709, 1988
A;Title: Structure and expression of c-fgr protooncogene mRNA in Epstein-Barr virus conv
A;Reference number: A45930; MUD:89134667; PMID:2852026
A;Accession: A45930
A;Accession: A45930
A;Residues: 1-177;524-529 <BRI>
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R, Patel, M.; Leevers, S.J.; Brickell, P.M.
Orocgene 5, 201-206, 1990
A;Title: Structure of the complete human c-fgr proto-oncogene and identification of mult A, Reference number: S24306; MUID:90206622; PMID:1690869
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F;84-241/Domain: SH2 homology <SH3>
F;144-241/Domain: SH2 homology <SH2>
F;144-241/Domain: SH2 homology <SH2>
F;269-277/Region: protein kinase homology <KIN>
F;269-277/Region: protein kinase ATP-binding motif
F;269-277/Region: protein kinase ATP-binding motif
F;26/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;21/Active site: palmitate (Cys) (covalent) #status predicted
F;231/Active site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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C;Genetics:
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C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Isolation and sequencing of cDNA clones homologous to the v-fgr oncogene from A;Reference number: A28353; MUID:88262220; PMID:3330776
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A; Cross-references: UNIPARC: UPI000017258D
R; Nishizawa, M.; Semba, K.; Yoshida, M.C.; Yamamoto, T.; Sasaki, M.; Toyoshima, K. Mol. Cell. Biol. 6, 51-517, 1986
A; Title: Structure, expression, and chromosomal location of the human c-fgr gene.
A; Reference number: A24842; MUID: 87064334; PMID: 3023853
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iive 3; Mismatches
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A;Map position: 1p36.2-1p36.1
C;Function:
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A;Status: translation not shown
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A; Molecule type: mRNA
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A; Molecule type: mRNA
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P626zi8
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Q7RTZ3_HUMAN
Q95M32_9PRIM
Q95M32_9PRIM
Q95M95_BORNA
Q2KW85_BORNA
DAPB_BORPA
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8RC AVISR
SRC RSVH
SRC 007461_9RETR 066567_9RETR 066567_9RETR 06693_RRUA SRCJ_XENLA SRCJ_XENLA SRCJ_XENLA SRCZ_XENLA QZTĀRI_XENLA QZDĀRI_XENLA QZDĀRI_XENLA QZBĀRI_XENLA YES HUMAN Q76P87 HUMAN Q86362 9RETR 9RETR BRARE THIDA ORYSA GIALA 9BRAD LACAC LACJO MONBE MAIZE 9RETR Q28414_FLV AVIS2 Q2R196_C 064817 Q6EWH1 086363 Q74HP0 Q6JAC8 07YZH8 DAPB

sapien

ALIGNMENTS

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Pubmedial 11126/8018nce 1112014;

Ray Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Gyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V. B., Branter S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidnis V., Allen J.E., Born H., Chalk A.M., Rahasi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Rad ansal M., Batter L., Belsel K.W., Bersano T., Bono H., Chalk A.M., R. Allen J.E., Crowe M.L., Dalla E., Dalrymple B.P., Ge Bono B., Della Gatta G., Allerther C.F., Fukushima T., Engstrom P., Regiolini M., Fauthner G., Allerber G.F., Fukushima T., Engstrom P., Ragiolini M., Farlando D., Harbers M., Haybesh Y., Krishnan S.P., Kruger A., Ishikawa T., Alli D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Alli D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Alli D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Krishnan S., Mcurini J., Lazarevic D., Lipovich L., Liu J., Allin S., Madan Babu M., Madera M., Marchionni L., Allin S., Mchiliam S., Madan Babu M., Madera M., Marchionni L., Allisson R., Nishikawa S., Miki H., Mignon F., Miyake S., Morris K., Misson R., Nishikawa S., Nori F., Ohara O., Sestiguchi S., Nishikawa S., Nori F., Ohara O., Sestiguchi K., Semple C.A., Senos L., Yachenaka Y., Shimada H., Shimada K., Salva D., Sinclair B., Stonbacta Y., Shimada H., Shimada K., Sulva D., Sinclair B., Stonbacta Y., Shimada H., Shimada K., Sulva D., Sinclair B., Takenaka Y., Rammishi H., Zabarovsky E., Zhu S., Tegner J., Tachman S., Mahleredt C., Mattick J.S., Ramer A., Hide W., Bult C., Matheredt C., Mattick J., Malone A., Kai C., Sasaki D., Tammishi H., Zabarovsky E., Zhu M., Andersaya H., Kai C., Wattick J., Sasaki D., Tammishi H., Tasadayama M., Tammishi H.,
                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea, Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Mammary gland;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                    11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 7.
Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched
library, clone:G830026006 product:lymphocyte protein tyrosine kinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Mammary gland;
bubbacl=1641073; DoI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005).
                                                11-OCT-2005, integrated into UniProtKB/TrEMBL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Mammary gland;
PubMed=16141072; DOI=10.1126/science.1112014;
     368 AA.
                                                                                                                                                                        insert sequence. (Fragment)
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                     [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
Q3TLX4_MOUSE
Q3TLX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki
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R. Vartisense Transcription in the Nammalian Transcriptome.',
Science 209:1564-1565(2005).
R. MICLEGUIDS SEQUENCE.
R. MICLEGUI

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NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                          Arakawa T. Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Shibata K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.,
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Samamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J. Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Ryikan integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                      MGI; MGI:96756; Lck.
GO; GO:0004664; F:protein serine/threonine kinase activity; RCA.
InterPro; IPR00019; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001980; SH2.
InterPro; IPR001945; Tyr_pkinase.
InterPro; IPR001846; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase_AS.
Pfam; PP07714; Pkinase_Tyr; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 41; DB 2; Length 368; 100.0%; Pred. No. 2.1; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 AA; 42018 MW; 7AB6AE53AF1A5059 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding; Kinase; Nucleotide-binding; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-AUG-2005, integrated into UniProtKB/TrEMBL. 30-AUG-2005, sequence version 1. 07-FBB-2006, entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                379 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Proc. kinase; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS500107; PROTEIN KINASE ATP; 1.
PROSITE; PS500109; PROTEIN KINASE DOM; 1.
PROSITE; PS500109; PROTEIN KINASE DOM; 1.
PROSITE; PS500109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                           EMBL; AK166263; BAE38668.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY; PRT;
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Name=Lck_mapped;
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les 9, Conservative
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                                                                                                                                                                                                                                                              tyrosine phosphate.
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                                                                                                                                NUCLEOTIDE SEQUENCE
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Q4FZR6;
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SEQUENCE
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04FZR6 RAT
10 Q4FZR6
D0 Q4FZR6
D1 30-AUG
D1 30-AUG
D2 07-FEB
D8 LCK maj
GN Name=LC
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MEDLINE-22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausberg R.L., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Biapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Marmson R.D., Mullahy S.J.,
A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahas S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Mind M., Madan A., Schein J.E., Jones S.J.M., Marra M.N.;
Rohnerstion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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TIM MGC Project;

Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
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GO; GO:000166; F:Rucleotide binding; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:000740; F:transferase activity; IEA.

GO; GO:000742; P:Intracellular signaling cascade; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR00219; Prot kinase.

R InterPro; IPR0019; Prot kinase.

R InterPro; IPR0019; Prot kinase.

R InterPro; IPR0019; Tyr_pkinase.

R InterPro; IPR001645; Tyr_pkinase.

R InterPro; IPR001645; Tyr_pkinase.

R InterPro; IPR001675; Tyr_pkinase.

R Pfam; PF00171; SH2; 1...
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SWART; SM00219; TYKC: 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS50010; PROTEIN KINASE TYR; 1.
ATP-binding; Kinase; Nucleotide-binding; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PRO0109; TYRKINASE.
PRODOM; PD000001; Prot_Kinase; 1.
ProDom; PD000093; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.
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LIPID
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DOR NOOR CON CONTRACT CONTRACT
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                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [MRNA] OF 1-88.
MEDILTRE-92186854; PubMed=1545804;
Chow L., Ratcliffe M., Vallette A.;
"tkl is the avian homolog of the mammalian lck tyrosine protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: Phosphorylated on Tyr-503. This phosphorylation downregulates catalytic activity. Phosphorylated on Tyr-392 either by itself or another kinase, leading to increased enzymatic activity. SIMILARITY: Belongs to the Tyr protein kinase family. SRC
                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine phosphate.
SUBUNIT: Binds to the cytoplasmic domain of cell surface
receptors, such as CD4, CD8 (By similarity).
SUBCELLULAR LOCATION: Bound to the cytoplasmic domain of either
CD4 or CD8 (By similarity).
                                                                                                                     Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (Protein-
tyrosine kinase C-TKL) (p56tkl).
                                                                                                                                                                                                                                                                                                                   TISSUE=Spleen;
Gaertner T., Khnel H., Strebhardt K., Ruebsamen-Waigmann H.;
Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases.
                             LCK CHICK STANDARD; PKT; 50, Am. P4268; Q53M88; Q10-NOV-1995, integrated into UniProtKB/Swiss-Prot. 01-NOV-1995, sequence version 1. 07-MAR-2006, entry version 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X60380; CAA42930.1; -; mRNA.
EMBL; M85043; AAA49003.1; -; mRNA.
EMBL; J03579; AAA49081.1; ALT_INIT; mRNA.
HSSP; P06529; 3LCK.
SMR; P42683; 63-507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000719; Prot kinase.
InterPro; IPR0002209; Ser thr pkinase.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001455; Tyr pkinase.
InterPro; IPR008266; Tyr pkinase AS.
Pfam; PF07714; Pkinase Tyr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Cell. Biol. 12:1226-1233(1992).
                                                                                                                                                                                                                                                                                 Pfam; PF00018; SH3 1; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subfamily
                                                                                                                                                                                                                                            Gallus
             LCK_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---
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PUCLEOTIDE SEQUENCE [MRNA].

A PUTCLEOTIDE SEQUENCE [MRNA].

A PREST-Quintero L.A., Vernot J.P.;

Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.

Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.

C --- FUNCTION: Tyrosine kinase that plays an essential role for the mature in a maturation of developing T-cell in the thymus and in mature T-cell function. Is constitutively associated with the cytoplasmic portions of the CD4 and CD8 sufface receptors and plays a key role in T-cell antigen receptor(TCR)-linked signal transduction pathways. Association of the TCR with a peptide antigen-bound MHC complex facilitates the interaction of CD4 and thereby recruits the associated LCK to the vicinity of the TCR/CD3 complex. LCK then phosphorylates tyrosines residues within the immunoreceptor tyrosines-based activation motifs (ITAMs) in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aotus nancymaae (Ma's night monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                         Proto-oncogene tyrosine-protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proton acceptor (By similarity).
ATP (By similarity).
Phosphotyrosine (by autocatalysis) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphotyrosine (negative regulation) similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-2005, sequence version 3.
07-MAR-2006, entry version 13.
Proto-oncogene tyrosine-protein kinase LCK (BC 2.7.1.112) (p56-LCK) (Lymphocyte cell-specific protein-tyrosine kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-myristoyl glycine (By similarity).
S-palmitoyl cysteine (By similarity).
S-palmitoyl cysteine (By similarity).
BCB3C4FA891B6170 CRC64;
                                                                                                                                                                                                                                                                        ATP-binding, Kinase; Lipoprotein, Membrane; Myristate;
Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 41; DB 1; Length 507; 100.0%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                             LCK.
/FTId=PRO_0000088128.
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Protein kinase
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
                                      Prodom; PD000065; SH3; 1.
Prodom; PD000066; SH3; 1.
SWART; SW00252; SH2; 1.
SWART; SW00216; SH3; 1.
SWART; SW00219; TYPKC; 1.
SWART; SW00107; PYPKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00001; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                 Probable.
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                 PD000001; Prot kinase; 1.
PD000093; SH2; 1.
PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58009 MW;
PR00109; TYRKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
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362
271
392
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NCBI_TaxID=37293;
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125
243
249
362
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392
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ACT SITE
BINDING
MOD RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
                          ProDom;
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cytoplasmic tails of the TCRgamma chains and CD3 subunits, initiating the TCR/CD3 signaling pathway. In addition, contributes to signaling by other receptor molecules. Associates directly with the cytoplasmic tail of CD2, and upon engagement of the CD2 plays a role in the IL2 receptor-linked signaling pathway that controls T-cell proliferative response. Binding of IL2 to its receptor results in increased activity of LCK. Is expressed at receptor results in increased activity of LCK. Is expressed at all stages of thymocyte development and is required for the regulation of maturation events that are governed by both pre-TCR and mature alpha beta TCR (By similarity).

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                     Uprosine phosphate.

SUBUNIT: Binds to the cytoplasmic domain of cell surface receptors, such as CD2, CD4, CD5, CD8, CD4, CD5, and CD122. Also binds to effector molecules, such as P14K, VAVI, RASAI, FYB and to other proteins kinases including CDC2, RAFI, ZAP70 and SYK. Binds to phosphatidylinositol 3'-kinase (P13K) from T lymphocytes through its SH3 domain and to the tyrosine phosphorylated form of RHDRBSI/P70 through its SH2 domain. Interacts with SQSTM1.
                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane. Present in lipid rafts in an unactive form (By similarity). DOMAIN: The SH2 domain mediates interaction with SQSTM1. Interaction is regulated by Ser-58 phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proto-oncogene tyrosine-protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding, Kinase, Lipoprotein, Membrane, Myristate,
Nucleotide-binding, Palmitate, Phosphorylation, Proto-oncogene,
SH2 domain, SH3 domain, Transferase, Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein kinase.
ATP (By similarity).
Interactions with CD4 and CD8 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the Tyr protein kinase family. SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTId=PRO_0000088123
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Probom; PD000006; SH2; 1.
SWART; SM00252; SH2; 1.
SWART; SM00252; SH3; 1.
SWART; SW00219; TYRC; 1.
SWART; SW00119; TYRC; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AY821852; AAV70114.2; -; mRNA. SNR; QSPXS1; 64-508.
INTERPRO; IPR000719; Prot kinase.
INTERPRO; IPR000719; Prot kinase.
INTERPRO; IPR000290; Ser_thr_pkinase.
INTERPRO; IPR001452; SH3.
INTERPRO; IPR001452; TYr_pkinase.
INTERPRO; IPR001245; TYr_pkinase.
INTERPRO; IPR001245; TYr_pkinase_AS. Pfam; PP00714; Pkinase_Tyr; 1.
Pfam; PP00101; SH2; 1.
PRINTS; PR00401; SH2; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00401; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 1 SH2 domain. SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probable.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHZ domain; SH3 domain; INT MET 0 0 CHAIN
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223
497
258
71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
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126
244
250
250
                                                                                                                                                                                                                                                                                                                                                                                            similarity)
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NP BIND
REGION
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similarity)

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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure of the human lck gene: differences in genomic organisation within src-related genes affect only N-terminal exons."; Gene 84:105-113(1989).
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLECTIDE SEQUENCE [MRNA] (ISOFORM SHORT), AND ALTERNATIVE SPLICING.
TISSUE=Leukemic T-cell;
MEDLINE=96085119; PubMed=7495859; DOI=10.1016/0167-4781(95)00162-A;
                                   (By
                              Phosphotyrosine (by autocatalysis) (By similarity).
Phosphotyrosine (negative regulation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=90108697; PubMed=2558056; DOI=10.1016/0378-1119(89)90144-3;
Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
Benarous R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK) (Lymphocyte cell-specific protein-tyrosine kinase) (LSK) (T cell-specific protein-tyrosine kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wright D.D., Sefton B.M., Kamps M.P.; "Oncogenic activation of the Lck protein accompanies translocation the LCK gene in the human HSB2 T-cell leukemia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE (MRNA), VARIANTS LEU-27; GLN-LYS-PRO-231 INS; VAL-352 AND LEU-446, AND PHOSPHORYLATION SITES TYR-393 AND TYR-504.
TISSUE-Leukemia;
                                                                               similarity).

N-myristoyl glycine (By similarity).

S-palmitoyl cysteine (By similarity).

S-palmitoyl cysteine (By similarity).

8B61951BC192A3A4 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A human'T cell-specific cDNA clone (YT16) encodes a protein with extensive homology to a family of protein-tyrosine kinases."; Eur. J. Immunol. 16:1643-1646(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87133831; Pubmed=3493153;
Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai
Mak T.W.;
                                                                                                                                                                                                                                                                                                                                                     PO6239; PO7100; Q12850; Q13152; Q5TDH8; Q5TDH9; Q9GDW4; Q9NYT8; Q1-JAN-1988, integrated into UniProtKB/Swiss-Prot. O1-FEB-1994, sequence version 5. O7-MAR-2006, entry version 87. Proto-process.
                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F., Wilson C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure and expression of 1ck transcripts in human lymphoid
   Proton acceptor (By similarity)
                                                                                                                                                                                100.0%; Score 41; DB 1; Length 508; 100.0%; Pred. No. 3;
                                                                                                                                                                                                                  0; Indels
                  ATP (By similarity)
                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Cell. Biol. 14:2429-2437(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell. Biochem. 38:117-126(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89123626; PubMed=3265417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94187714; PubMed=8139546;
                                                                                                                                                 58041 MW;
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                                                                                                                                                                                                                9; Conservative
 363
272
393
                                                                  504
                                                                                                                                                                                                                                                                                 339 KLLDMAAQI 347
                                                                                                                                                                                                                                                 1 KLLDMAAQI 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                508 AA;
                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
 363
272
393
                                                                  504
ACT SITE
BINDING
                                                                                                                                                SEQUENCE
                                                                                                                                                                                Query Match
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                                MOD_RES
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LIPID
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ID LCK H
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us-10-062-257a-14.rup

PHOSPHORYLATION SITE TYR-504 TISSUE=Lymph;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WA Strausberg R.L., Feligodd B.A., Grouse L.H., Derge J.G.,

Rausberg R.L., Feligodd B.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Lapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergien B.J., Lu X., Glibbs R.N.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rochriguez A.C., Schwutz J.M., Marra M.A.;

Rochriguez A.C., Schwutz J.M., Marra M.A.;

Rochriguez A.C., Schwutz J.M., Marra M.A.; MEDLINE=88217332; PubMed=2835736; Veillette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.; Expression of the lck tyrosine kinase gene in human colon carcinoma and other non-lymphoid human tumor cell lines."; Oncogene Res. 1:357-374 (1987). Human T lymphocytes express a protein-tyrosine kinase homologous to TISSUB=Peripheral blood lymphocyte;
MEDLINE=20462621; PubMed=11009097;
DOI=10.1002/1521-411(200009)30:9<2632::AID-IMMU2632>3.0.CO;2-C;
Boncristiano M., Majolini M.B., D'Elios M.M., Pacini S., Valensin S. Ulivieri C., Amedei A., Falini B., Del Prete G., Telford J.L., Takadera T., Leung S., Gernone A., Koga Y., Takihara Y., Miyamoto N.G., Mak T.W.;
"Structure of the two promoters of the human lck gene: differential accumulation of two classes of lck transcripts in T cells.";
Mol. Cell. Biol. 9:2173-2180(1989). a murine MEDLINE-87000726; PubMed-3489486; DOI=10.1016/0167-4889(86)90228-4; Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C., "Defective recruitment and activation of ZAP-70 in common variable immunodeficiency patients with T cell defects."; Eur. J. Immunol. 30:2632-2638(2000). Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.; "Structure of the murine lck gene and its rearrangement in lymphoma cell line."; Human chromosome 1 international sequencing consortium; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. "An aberrant lck mRNA in two human T-cell lines."; Biochim. Biophys. Acta 1264:168-172(1995). NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3) Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]. [8] NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34. [9] NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34. ps6LSTRA."; Biochim. Biophys. Acta 888:286-295(1986) [13] NUCLEOTIDE SEQUENCE [MRNA] OF 374-508 NUCLEOTIDE SEQUENCE [MRNA] OF 367-508 NUCLEOTIDE SEQUENCE [MRNA] OF 13-508. L.B., Arthur R., Fujita D.J.; Mol. Cell. Biol. 8:3058-3064(1988) MEDLINE=89096891; PubMed=2850479; MEDLINE=89313764; PubMed=2787474; cDNA sequences. Ulivieri C., A Baldari C.T.; Linna T

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MEDLINE=94067101; PubMed=7504174;
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Muroidea; Muridae; Murinae; Mus.
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                                                             100.0%; Score 41; DB 1; 100.0%; Pred. No. 3;
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PubMed=16141072; DOI=10.1126/science.1112014;
                                                                                          0; Mismatches
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Mus musculus (Mouse).
                              INTERACTION WITH LIME!
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PubMed=10646608; DOI=10.1038/35003228;
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3. Virol. 75:925-9261(2001).

4. J. Virol. 75:925-9261(2001).

5. Selection and maturation of developing T-cell in the thymus and in mature T-cell function. Is constitutively associated with the cytoplasmic portrions of the CD4 and CD8 surface receptors and plays a key role in T-cell antigen receptor (TCR) linked signal transduction pathways. Association of the TCR with a peptide antigen-bound MHC complex facilitates the interaction of CD4 and CD8 with MHC class II and class I molecules, respectively, and thereby recruits the associated LCK to the vicinity of the TCR/CD3 complex. LCK then phosphorylates tyrosines residues within the complex. LCK then phosphorylates tyrosines residues within the cytoplasmic tails of the TCR/CD3 signaling pathway. In addition, contributes to signaling by other receptor molecules. Associates directly with the CYtoplasmic tail of CD2, and upon engagement of the CD2 molecule, LCK undergoes hyperphosphorylation and activation. Also plays a role in the LI2 receptor molecules. Secondared at 11 receptor results in increased activity of LCK. Is expressed at all stages of thymogenes the required for the regulation of the required for the regulation and is required for the regulation and section of the regulation and section and section of the regulation of the regulation and section of the regulation of the regulation and section of the regulation of the regulation of the regulati
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1. SUBUNIT. Binds to the cytoplasmic domain of cell surface
1. SUBUNIT. Binds to the cytoplasmic domain of cell surface
1. SUBUNIT. Binds to the cytoplasmic domain of cell surface
1. SUBUNIT. Binds to the cytoplasmic domain of course to binds to effector molecules, such as PI4K, VAVI, RASAI, FYB and to binds to effector molecules, such as PI4K, VAVI, RASAI, FYB and to other proteins kinases including CDC2. RAFI, ZAP70 and SYK. Binds to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
1. Chrough its SH3 domain and to the tyrosine phosphorylated form of KHDRBSI/p70 through its SH2 domain. Interacts with SQSTM1.

1. Chromatic and the phosphorylated LIMEI. Interacts with SQSTM1.

2. SUBCELDULAR LOCATION: Cytoplasmic and attached to the membrane.
2. Present in lipid rafts in an unactive form (By similarity).
2. Interacts with Sapersed specificaly in lymphoid cells.
3. Chromatic and attached to the membrane.
3. Chromatic and attached to t
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CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOI=10.1128/JVI.75.19.9252-9261.2001;
Greve T., Tamgueney G., Fleischer B., Fickenscher H., Broeker B.M.;
"Downregulation of p56Lck tyrosine kinase activity in T cells of
squirrel monkeys (Saimiri sciureus) correlates with the non-
transforming and apathogenic properties of herpesvirus saimiri in its
natural host.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] -
NUCLEOTIDE SEQUENCE [MRNA], ENZYME REGULATION, AND INTERACTION WITH
SAIMIRINE HERPESVIRUS 2 TIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK) (Lymphocyte cell-specific protein-tyrosine kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                  508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saimiri sciureus (Common squirrel monkey).
                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21424508; PubMed=11533187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-2005, sequence version 07-MAR-2006, entry version 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          integrated into
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                  339 KLLDMAAQI 347
     σ
1 KLLDMAAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cebinae; Saimiri.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-2005,
                                                                                                                                                                                                                                                                                                                                                                       SAISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=LCK;
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                                                                                                                                                                                                                                                                                                                                                                                                                   THE HERE WAS COOCCUPANTE THE THE TRANSPORT OF COOCCUPANTE TO COOCC
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                         -!- PTM: Phosphorylated on Tyr-504 presumably by CSK. This phosphorylation downregulates catalytic activity. Phosphorylated on Tyr-393 atther by itself or another kinase, leading to increased enzymatic activity.
-!- SIMILARITY: Belongs to the Tyr protein kinase family.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
-!- GAUTION: LCK seems to be active in all vertebrates, except in squirrel monkey T-cells, in which it is inactivated. The reason seems to be that squirrel monkey are the natural host for Saimirine herpesvirus 2, which is able to efficiently transform F-cells through a mecanism involving viral Tip/ host LCK interaction. Its inactivation may a mecanism that specificaly counteracts the transformation effects of viral Tip.
                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphotyrosine (negative regulation) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proto-oncogene tyrosine-protein kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
N-myristoyl glycine (By similarity).
S-palmitoyl cysteine (By similarity).
S-palmitoyl cysteine (By similarity).
5088C64061853819 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding, Kinase, Lipoprotein, Membrane, Myristate,
Nucleotide-binding, Palmitate, Phosphorylation, Proto-oncogene,
SH2 domain, SH3 domain, Transferase, Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein kinase.
ATP (By similarity).
Interactions with CD4 and CD8 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proton acceptor (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 41; DB 1; Length 508; 100.0%; Pred. No. 3; tive 0; Mismatches 0; Indels
Interaction is regulated by Ser-58 phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTId=PRO_0000088127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (By similarity
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002290; Ser_Ehr_pkinase.
InterPro; IPR002290; Ser_Ehr_pkinase.
InterPro; IPR00290; Ser_Ehr_pkinase.
InterPro; IPR001452; SH3.
InterPro; IPR001452; SH3.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Ffam; PF001714; Pkinase_Tyr; 1.
Pfam; PF001714; Pkinase_Tyr; 1.
Pfam; PF0018; SH3 1; 1.
PRINTS; PR001401; SH3-DOMAIN.
PRINTS; PR001401; SH3-DOMAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000009; TYRKINASE.
ProDom; PD000009; SH2; 1.
ProDom; PD000066; SH3; 1.
SWART; SM00225; SH3; 1.
SWART; SM00225; SH3; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
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HSSP; P06239; 1LKK.
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Best Local Similarity
Matches 9; Conserva
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BINDING
MOD_RES
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REGION
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DOMAIN
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Gaps

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Streambl; ENSG00000182866; Homo sapiens.

R GO; GO:00045121; C:lipid raft; ISS.
R GO; GO:0004722; F:protein retiriolar material; ISS.
R GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
R GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
R GO; GO:0004713; F:RHZ domain binding; ISS.
R GO; GO:00042169; F:RHZ domain binding; ISS.
R GO; GO:00042169; F:RHZ domain binding; ISS.
R GO; GO:0006919; P:reapase activation; ISS.
R GO; GO:0006917; P:induction of apoptosis; ISS.
R GO; GO:0006917; P:protein amino acid phosphorylation; ISS.
R GO; GO:0001249; P:respulation of lymphocyte activation; ISS.
R GO; GO:000149; P:respulation of lymphocyte activation; ISS.
R GO; GO:00014; P:respulation of progression through cell cycle; ISS.
R GO; GO:00017; P:respulation of progression through cell cycle; ISS.
R GO; GO:000044; P:respulation of progression through cell cycle; ISS.
R GO; GO:000044; P:respulation of progression through cell cycle; ISS.
R GO; GO:000044; P:respulation of progression through cell cycle; ISS.
R GO; GO:0000044; P:respulation; ISS.
R GO; GO:0000044; P:respulation of progression through cell cycle; ISS.
R GO; GO:0000044; P:respulation of progression through cell cycle; ISS.
R GO; GO:0000044; P:respulation of progression through cell cycle; ISS.
R GO; GO:0000044; P:respulation of progression through cell cycle; ISS.
R GO; GO:0000004; P:respulation of progression through cell cycle; ISS.
R GO; GO:0000004; P:respulation cycle; ISS.
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                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diabetes 51:3326-3330(2002).
-!- MISCELLANEOUS: The sequence shown here is derived from an
EMBL/GenBank/DDBJ third party annotation (TPA) entry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nervi S., Nicodeme S., Gartioux C., Atlan C., Lathrop M., Reviron D., Naquet P., Matsuda F., Imbert J., Vialettes B.; "No association between 1ck gene polymorphisms and protein level in
                                                                                                                                                                                                          15-DEC-2003, integrated into UniProtKB/TrEMBL 15-DEC-2003, sequence version 1.
17-EBE-2006, entry version 13.
Protein tyrosine kinase.
                                                                                                                                                                   509 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BN000073; CAD55807.1; -; Genomic_DNA.
HSSP; P06239; 1BHF.
SMR; Q7RTZ3; 65-509.
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Interpro, IPR002290; Ser thr pkinase.
Interpro, IPR000980; SH2.
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InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001265; Tyr_pkinase_AS.
Pfam; PF00714; Pkinase_Tyr; 1.
Pfam; PF00017; SH2; 1.
                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22289034; PubMed=12401726;
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PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00450; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Proc. Kinase; 1.
ProDom; PD0000063; SH2; 1.
ProDom; PD0000065; SH3; 1.
SMART; SM00252; SH3; 1.
                                                                                                                                                      Q7RTZ3_HUMAN PRELIMINARY;
Q7RTZ3;
                                          339 KLLDMAAQI 347
σ
                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
1 KLLDMAAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type 1 diabetes."
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                               Name=LCK;
                                                                                                                                       HUMAN
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GO; GO: 00045121; C: lipid raft; ISS.

GO; GO: 0004722; F: protein serine/threonine phosphatase activity; ISS.

GO; GO: 0004713; F: protein-tyroaine kinase activity; ISS.

GO; GO: 0006919; P: caspase activityino; ISS.

GO; GO: 0006919; P: hemopoiesis; ISS.

GO; GO: 0006919; P: hemopoiesis; ISS.

GO; GO: 0006919; P: protein amino acid phosphorylation; ISS.

GO; GO: 0006468; P: protein amino acid phosphorylation; ISS.

GO; GO: 0007265; P: Ras protein amino acid phosphorylation; ISS.

GO; GO: 0007265; P: Pregulation of Iymphocyte activation; ISS.

GO; GO: 0007265; P: Pregulation of Iymphocyte activation; ISS.

GO; GO: 0007263; P: response to drug; ISS.

RO; GO: 00042493; P: response to drug; ISS.

RO; GO: 0000682; P: print of progression through cell cycle; ISS.

RO; GO: 0000682; P: print control cand; ISS.

RO; GO: 0000682; P: print cand cand; ISS.

RO; GO: 0000692; P: print c
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                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
Hylobatidae, Hylobates.
NCBI_TaxID=9581;
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                                                                                                                                                                                                                                                                                                                 Length 509;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            509 AA
                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                      PROSITE; PSO0107; PROTEIN KINASE ATP; 1.
PROSITE; PSC0011; PROTEIN KINASE DOW; 1.
PROSITE; PSC0001; PROTEIN KINASE TYR; 1.
PROSITE; PSC0001; SH2; 1.
PROSITE; PSC0002; SH3; 1.
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Q95M32;
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Virology 295:320-327(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLLDMAAQI
                                                                                                                                                                                                                                                                                                                                               Local Similarity
   SM00219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lck protein.
                                                                                                                                                                                                                Kinase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Picard C.
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=1ck
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SMR; C
                                                                                                                                                                                                                                                                                                                                                                                        Matches
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REMBL; BC102046; AA102047.1; -; mRNA.

R GO; GO:00045121; C:lipid raft; ISS.
R GO; GO:0004722; C:pericentriolar material; ISS.
R GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
R GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
R GO; GO:0004719; F:SH2 domain binding; ISS.
R GO; GO:0006919; P:caspase activation; ISS.
R GO; GO:0006919; P:caspase activation; ISS.
R GO; GO:0006919; P:nemopolesis; ISS.
R GO; GO:0007242; P:intracellular signaling cascade; ISS.
R GO; GO:0007842; P:intracellular signaling cascade; ISS.
R GO; GO:0050870; P:positive regulation of T cell activation; ISS.
R GO; GO:0006862; P:positive regulation of T cell activation; ISS.
R GO; GO:0007265; P:Ras protein signal transduction; ISS.
R GO; GO:0007265; P:Ras protein signal transduction; ISS.
R GO; GO:0007265; P:Ras protein signal transduction; ISS.
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Crossbred x Angus; TISSUE=Ileum;
Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
Matsuc C., Mayo M., Santos R.R., Stort J., Teai M., Wong D.,
Siddiqui A., Holt R., Jones S.J., Marra M.A.;
Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57947 MW; FIBFESC237C8DB7E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      509 AA.
                                                                                                                                                             PRINTS; PRO0401; SHZDOWAIN.
PRINTS; PRO0401; SHZDOWAIN.
PRINTS; PRO04019; TYRKINASE.
ProDom; PD0000001; Proct kinase; 1.
ProDom; PD0000065; SH3; 1.
ProDom; P0000065; SH3; 1.
SMART; SM00226; SH3; 1.
SMART; SM00226; SH3; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase_AS.
Pfam; PF07714; Pkinase_Tyr; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2005, sequence version 1.
07-WAR-2006, entry version 6.
Hypothetical protein MGC126900.
Name=MGC126900;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 KLLDMAAQI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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InterPro; IPR002290; Ser_thr_pkinase.
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ID Q4RR72 TETNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A rare mRNA variant of the human lymphocyte-specific protein tyrosine kinaseLCK gene with intron B retention and exon 7 skipping encodes a putativeprotein with altered SH3-dependent molecular interactions."; Gene 359:18-25(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
GO; GO:0000074; P:regulation of progression through cell cycle; ISS. GO; GO:0042493; P:response to drug; ISS. GO; GO:0030217; P:T cell differentiation; ISS. GO; GO:0006882; P:zinc ion homeostasis; ISS.
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Nervi S., Guinamard R., Delaval B., Lecine P., Vialettes B.,
Naquet P., Imbert J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 509,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ865079; CAI23831.1; -; mRNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      il protein.
509 AA; 58116 MW; CEOE80DCD6D0F2F8 CRC64;
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100.0%; Pred. No. 3;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-WAY-2005, integrated into UniProtKB/TrEMBL 10-WAY-2005, sequence version 1. 07-FEB-2006, entry version 5.
                                                                                      UnterPro; IPR00119; Prot kinase.
InterPro; IPR002290; Ser_th_pkinase.
InterPro; IPR002290; Ser_th_pkinase.
InterPro; IPR002290; Ser_th_pkinase.
InterPro; IPR001452; SH3:
InterPro; IPR001245; TYr_pkinase.
InterPro; IPR001019; SH3: 1:
IPRNTS; PR00109; TYRKINASE.
IPR0Dom; PD0000093; SH2; I.
IPR0Dom; PD0000093; SH2; I.
IPR0Dom; PD00000245; SH3; I.
IPR0SITE; PS00107; PROTEIN KINASE_ATP; I.
IPROSITE; PS00107; PROTEIN KINASE_TYR; I.
IPROSITE; PS00107; PROTEIN KINASE_TYR; I.
IPROSITE; PS00107; PROTEIN KINASE_TYR; I.
IPROSITE; PS00109; PROTEIN KINASE_TYR; I.
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Q573B4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 KLLDMAAQI 348
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NUCLEOTIDE SEQUENCE.
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SEQUENCE 50
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Matches
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0573B4 HUM
1D 05773B
AC 0573B
DT 10-MA
DT 10-MA
DT 07-FE
DE PROTO
CC BUKAR
OC HOMOO
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PubMed=15496914; DOI=10.1038/nature03025;

PubMed=15496914; DOI=10.1038/nature03025;

PubMed=15496914; DOI=10.1038/nature03025;

Jaillon O., Aury J.-M., Brunet F., Ozouf-Costaz C., Bernot A.,

Mauceli E., Bouneau L., Fischer S., Lutfalla G., Dossat C., Segurens B.,

Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

Cruud C., Duprat S., Brottier P., Coutaneau J.-P., Gouzy J.,

Cruud C., Lardier G., Chapple C., McKernan K.J., McGwan P., Bosak S.,

Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

"The early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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-!- FUNCTION: Plays a key role in the control of the eukaryotic cell cycle. It is required in higher cells for entry into S-phase and mitosis. Component of the kinase complex that phosphorylates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2005, sequence version 1.
O-FEBL-2006, entry version 6.
Chromosome 14 SCAF15003, whole genome shotgun sequence. (Fragment)
ORFNames-GSTENG00030294001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetración nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neoteleostei;
Actinopterygii; Neopterygii; Percomorpha; Tetraciontoidea; Tetraciontoidea; Tetraciontoidea; Tetraciontoidea; Tetraciontoidea; MCBI_TaxID=99883;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 41; DB 2; Length 516; 100.0%; Pred. No. 3.1;
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InterPro; IPR001969; SH2.
InterPro; IPR00145; SH3.
InterPro; IPR00145; SH3.
InterPro; IPR00145; SH3.
InterPro; IPR00146; Tyr_pkinase_AS.
Pfam; PF07114; Pkinase_Tyr; 1.
Pfam; PF00017; SH3. 1.
Pfam; PF00018; SH3 1; 1.
PRINTS; PR00401; SH3DOMAIN.
PRINTS; PR00452; SH3; 1.
SMART; SM00252; SH2; 1.
SMART; SM00252; SH2; 1.
PR051TE; PS00199; TYRK; INASE_DOM; 1.
PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Best Local Similarity luv...
9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS50001; SH2; 1.
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PROSITE; PS50002; SH3; 1.
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                       STANDARD;
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                                                                                  131 KLLDMAARI 139
                            σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIRSF; PIRSF000161;
                      1 KLLDMAAQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase
                                                                                                                                                                                                                                       DAPB BORBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                           RESULT 14
DAPB_BORBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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repetitive C-terminus of RNA polymerase II. Catalytic component of MPF (By similarity)
                                                                                                               tyrosine phosphate.
SUBUNIT: Forms a stable but non-covalent complex with cyclin B in mature oocytes (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                     MPF (By similarity).
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sebaihia M.; "The genome sequence of the poultry pathogen Bordetella avium, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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07-MAR-2006, entry version 1.
Dihydrodipicolinate reductase (EC 1.3.1.26).
Name-dapB; ORFNames=BAV2726;
Bordetella avium 197N.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                         SMA; VARKA(2): 2-24.

GO; GO:00015524; F:ATP binding; IEA.

GO; GO:000413; F:nucleotide binding; IEA.

GO; GO:000413; F:protein-tyrosine kinase activity; IEA.

GO; GO:0006468; F:protein-tyrosine kinase activity; IEA.

GO; GO:0006468; F:protein amino acid phosphorylation; IEA.

InterPro; IPR00129; F: protein amino acid phosphorylation; IEA.

R PRIOSITE; PR00109; TYRKINASE.

R PROSITE; PR00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00107; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R ATP-binding; Kinase; Nucleotide-binding; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic comparisons with related species infecting mammals.";
Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.2%; Score 37; DB 2; Length 263; 88.9%; Pred. No. 13; 0; Indels tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 2; Length 322;
Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 AA; 36768 MW; EC0ED0B6DB1CBB2F CRC64;
                                                                                                                                                                                                                                                                                                          CAAE01015003; CAG09110.1; -; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-2006, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QZKW85 BORAV PRELIMINARY;
Q2KW85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85..
8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                Q4RR72; 2-322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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C2KW85 BOR
1D C2KW8
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AC Q2KW8
DT 07-MA

                         SO THE SECOND DESCRIPTION OF THE SECOND DESC
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STRAINERESO / ATCC BAA-588;

MEDLINEE-2287954; PubMed=12910271; DOI=10.1038/Ng1227;

MEDLINEE-2287954; PubMed=12910271; DOI=10.1038/Ng1227;

Martis D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A chroman M. Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chilingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Chilingworth T., Gollen M., Hauser H., Holroyd S., Jagels K.,

Reltwall T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Sanders D., Seger K.,

Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

"More Constant S. S. Anders M. Scholes M. Sch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: 2,3,4,5-tetrahydrodipicolinate + NAD(P)(+) = 2,3-dihydrodipicolinate + NAD(P)H.
-!- PATHWAY: Amino-acid biosynthesis; L-lysine biosynthesis via DAP pathway; tetrahydrodipicolinate from L-aspartate: step 4.
-!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
-!- SIMILARITY: Belongs to the dihydrodipicolinate reductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                 Name-dapB; OrderedLocusNames=BB1944;
Bordeella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dihydrodipicolinate reductase.
/FTId=PRO 0000141413.
68D79CFD3AD76ADF CRC64;
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Pred. No. 13;
1; Mismatches 0; Indels
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Amino-acid biosynthesis; Complete proteome;
Diaminopimelate biosynthesis; Lysine biosynthesis; NADP;
                                                                                                                                                                                                                                                                                     Dihydrodipicolinate reductase (BC 1.3.1.26) (DHPR).
                                                                                                            15-DEC-2003, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BX640449; CAE34307.1; -; Genomic_DNA.
GenomeReviews; BX470250 GR; BB3944.
BioCyc; BBRO518:BB3944-MONOMER; -.
                                                                                                                                                                              01-OCT-2003, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP, MF_00102, -, 1.
InterPro, IPR000846, DapB.
InterPro, IPR011770, DapB_bac.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dapB; 1.
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88.9%;
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REPLINE-22827954; PubMed=12910211; DOI=10.1038/ng1227;
REPLINE-22827954; PubMed=12910211; DOI=10.1038/ng1227;
REPLINE-22827954; PubMed=12910211; DOI=10.1038/ng1227;
REPLINE-22827954; PubMed=12910211; DOI=10.1038/ng1227;
RA Harris D.E., Holden M.T.G., Churcher C.M., Bencley S.D., Mungall K.L.,
RA Achtman M., Akin R., Baker S., Basham D., Harris B., Quail M.A.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Chillingworth E., Norberczak H., O'Nell S., Ormond D., Price C.,
Rabbinowitsch E., Rutter S., Sanders R., Saunders D., Seeger K.,
Rabbinowitsch E., Rutter S., Sanders R., Squares S., Stevens K.,
Rabbinowitsch E., Rutter S., Barrell B.G., Maskell D.J.;
Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
Rutter S., Sanders M., Saunders D.J.;
Rat "Comparative analysis of the genome sequences of Bordetella pertussis,
R. "Comparative analysis of the genome sequences of Bordetella pertussis,
R. Genet. 35:32-40(2003).
C. "CATALYTIC ACTIVITY: 2,3,4,5-tetrahydrodipicolinate + NAD(P)(+) =
2,3-dihydrodipicolinate + NAD(P)H.
C. "SUBCELLULAR LOCATION: Cytoplasm (By similarity).
C. "SUBCELLULAR LOCATION: Cytoplasm (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                    Name=dapB; OrderedLocusNames=BP2509;
Borderella pertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 269 Dihydrodipicolinate reductase.
/FTId=PRO 0000141415.
269 AA; 28328 MW; 68DF3E7158BDAA31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 1; Length 269; Pred. No. 13;
                                                                                                                                                                                                                                                                                 Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino-acid biosynthesis; Complete proteome;
Diaminopimelate biosynthesis; Lysine biosynthesis; NADP;
                        07-MAR-2006, entry version 37.
Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR).
                                                                                                                                                                                                                                                                                                         [2] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN-TOhama I / ATCC BAA-589 / NCTC 13251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ238308; CAB41012.1; -; Genomic_DNA.
EMBL; BX640418; CAE42781.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenomeReviews; BX470248 GR; BP25
BioCyc; BPER520:BP2509-MONOMER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF05173; DapB_C; 1.
Pfam; PF01113; DapB_N; 1.
PIRSF; PIRSF000161; DHPR; 1.
ProDom; PD004105; DapB; 1.
TIGREAMS; TIGR0036; dapB; 1.
PROSITE; PS01298; DAPB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR010846; DapB.
InterPro; IPR011770; DapB bac.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 88.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 KLLDMAARI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P04036; 1DRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase
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ID DAPB_CHRVO
                                                                                                                                                                                                                                                         Pradel E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                      TRAIN=12822 / ATCC BAA-587;

WEDLINE=22822/ ATCC BAA-587;

WEDLINE=22822 / ATCC BAA-587;

WEDLINE=22822 / ATCC BAA-587;

WEDLINE=22822 / ATCC BAA-587;

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Achtman M., Atkin R., Salder S., Basham D., Bason N., Cherevach I.,

RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

RA Rabbinowitsch E., Rutter S., Sanders D., Seager K.,

RA Rabbinowitsch E., Rutter S., Sanders D., Seager K.,

RA Nary S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

RT "Comparative analysis of the genome sequences of Bordetella pertussis,

RT "Comparative analysis of the genome sequences of Bordetella pertussis,

R. Mat. Genet. 35:32-40(2003).

C. - CATALYITC ACTIVITY: 2,3,4,5-tetrahydrodipicolinate + NAD(P) (+) =

C. 2,3-diphydrodipicolinate + NAD(P) H.

C. - PATHWAY: Amino-acid biosynthesis, L-lysine biosynthesis via DAP

C. - SUBCELLULAR LOCATION: Cytoplasm (By similarity).

C. - SUBLELLULAR LOCATION: Cytoplasm (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                        Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR).
Name-dapB; OrderedLocusNames-BPP3496;
Bordetella parapertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
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/FTId=PRO 0000141414.
68D79CFD3AD76ADF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.2%; Score 37; DB 1; Length 269; 88.9%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino-acid biosynthesis; Complete proteome;
Diaminopimelate biosynthesis; Lysine biosynthesis; NADP;
Oxidoreductase.
                                                            Q7W5I0;
15-DEC-2003, integrated into UniProtKB/Swiss-Prot.
01-OCT-2003, sequence version 1.
07-MAR-2006, entry version 17.
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                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=12822 / ATCC BAA-587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BX640433; CAE38780.1; -; Genomic_DNA. GenomeReviews; BX470249 GR; BPP3496.
BioCyc, BPARS19:BPP3496-MONOMER; -. HAMAP; MF 00102; -; 1.
InterPro; IPR010846; DapB.
InterPro; IPR011770; DapB bac.
Pfam; PF05173; DapB_C; 1.
Pfam; PF05173; DapB_N; 1.
PIRSF; PIRSF000161; DHPR; 1.
                                         269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 AA; 28329 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD004105; DapB; 1.
TIGRFAMS; TIGR00036; dapB; 1.
PROSITE; PS01298; DAPB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 88.9
                                         STANDARD;
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                                         BORPA
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DAPB_BORPE
ID_DAPB_BC
AC_Q9X6\folday9;
DT_30-MAY-
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                                         DAPB
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Gaps

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267

Gaps

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Indels

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Mismatches

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7; Conservative

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Matches
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                                                                                                                                                                                                                                                                                                                       REC STRAIN=ATCC 12472 / DSM 30191.

REC STRAIN=ATCC 12472 / DSM 30191.

RED MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;

RA VASCONCEJOS A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,

RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.Y.,

RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Araujo M.F.F.,

RA Ascolfi-Filho S., Azevedo V., Baptista A.J., Barans L.A.M.,

RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,

RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,

RA Carvalho C.M.B., Cascardo J.C.M., Cardada B.S., Chueire L.M.O.,

RA Carvalho C.M.B., Cascardo J.C.M., Cardada B.S., Chueire L.M.O.,

RA Carvalho C.M.B., Cascardo J.C.M., Cardada B.S., Chueire L.M.O.,

RA Ferro M.I.T., Franco G.R., Felipe M.S.S., Ferraro D.M.,

RA Ferro M.I.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,

RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,

RA Gaztapadia D., Grisard B.C., Hanna B.S., Jardim S.N., Laurino J.,

RA Gaztapadia D., Grisard B.C., Hanna B.S., Jardim S.N., Laurino J.,

RA Gaztapadia D., Garisard B.C., Hanna B.S., Jardim S.N., Laurino J.,

RA Gaztanelli R.F., Nanfio G.P., Maranhao A.Q., Martins W.S.,

Al Mauro S.M.Z., de Medelaros S.R.B., Meissner R.V., Morsira M.A.M.,

RA Bamalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,

Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Seuanez H.N.,

Saltva A.M.R., da Silva A.M.M., Silva B.W., Solva R., Simoes I.C.,

RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seuanez H.N.,

Solva R.C., Steffens M.B.R., Schipson A., Silva B.W., Solva R., Urmenyi I.,

RA Vertore A., Wassem R., Zaha A., Silmpson A.G., Urmeryi I.,

RA Vertore A., Wassem R., Zaha A., Silmohali R., Silva A.M., Sholva R., Silmon D., Soares C.M.A., Solva R., Silmon D., Soares C.M.A., Solva R., Silmon A., G., Chrimpharterium violacemm represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: Amino-acid biosynthesis; L-lysine biosynthesis via DAP pathway; tetrahydrodipicolinate from L-aspartate: step 4.
-!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
-!- SIMILARITY: Belongs to the dihydrodipicolinate reductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Chromobacterium violaceum reveals remarkable and exploitable bacterial adaptability."; Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
-!- CATALYTIC ACTIVITY: 2,3,4,5-terrahydrodipicolinate + NAD(P)(+) 2,3-dihydrodipicolinate + NAD(P)H.
                                                                                                                                                                                           Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Chromobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dihydrodipicolinate reductase.
/FIId=PRO_0000141430.
AB3EA3EFAE3E27ED CRC64;
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                                                                                                          Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR) Name=dapB; OrderedLocusNames=CV1795;
                       15-DEC-2003, integrated into UniProtKB/Swiss-Prot.
15-DEC-2003, sequence version 1.
07-MAR-2006, entry version 17.
                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE016825; AAQ59469.1; -; Genomic_DNA.
GenomeReviews; AE016825 GR; CV1795.
BioCyc; CVIO243365:CV1795-MONOMER; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MP_00102; ; 1.
InterPro; IPR000046; DapB.
InterPro; IPR011770; DapB.bac.
Pfam; PF05173; DapB.C; 1.
Pfam; PF01113; DapB.N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dapB; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIRSF; PIRSF000161; DHPR; 1.
                                                                                                                                                                    Chromobacterium violaceum.
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TIGRFAMS; TIGR00036; dapB
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                                                                                                                                                                                                                                                  NCBI_TaxID=536;
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ACTIVE SOLUTION OF THE PROPERTY OF THE PROPERT
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DB 1; Length 267; 22;

Score 36; Pred. No.

87.8%;

Local Similarity

Query Match

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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLIRE=22423060; PubMed=12534463;

DOI=10.1046/j.1462-2920.2002.00366.x;

DOI=10.1046/j.1462-2920.2002.00366.x;

DOI=10.1046/j.1462-2920.2002.00366.x;

DOI=10.1046/j.1462-2920.2002.00366.x;

DOI=10.1046/j.1462-2920.2002.00366.x;

Marting dos Santos V.A.P. Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F., Rainkac L.M., Beanan M.J., Marting D., Khouri H.M., Hance I., Chris Lee P., Hollzapple E.K., Scanlan D., Tran K., Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808 (2002).

-!- CATALYTIC ACTIVITY: 2,3,4,5-terrahydrodipicolinate + NAD(P)(+) = 2,3-dihydrodipicolinate + NAD(?)H.
-!- PATHWAY: Amino-acid biosynthesis; L-lysine biosynthesis via DAP pathway; tetrahydrodipicolinate from L-aspartate: step 4.
-!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
-!- SIMILARITY: Belongs to the dihydrodipicolinate reductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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/FTId=PRO_000141470.
267 AA; 28424 MW; 2F5BE5545D754C7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.8%; Score 36; DB 1; Length 267; 77.8%; Pred. No. 22; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino-acid biosynthesis; Complete proteome;
Diaminopimelate biosynthesis; Lysine biosynthesis; NADP;
                                                                                                                                                                                                                                                                                                                                                                         Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR)
Name-dapB; OrderedLocusNames=PP4725;
                                                                                                                                                                                                                                                                                 24-OCT-2003, integrated into UniProtKB/Swiss-Prot. 01-JUN-2003, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                     267 AA.
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                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas putida (strain KT2440)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR; PP4725; -. 1.
HAMAP; MF 00102; -; 1.
InterPro; IPR000046; DapB.
InterPro; IPR011770; DapB bac.
Pfam; PF05173; DapB C; 1.
Pfam; PF01113; DapB C; 1.
PIRSF; PIRSF000161; DHPR; 1.
ProDom; PD004105; DapB; 1.
                                                                                                                                                                                                                                                                                                                                                  entry version 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS01298; DAPB; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                     STANDARD;
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                                                       134 KLLDMAARV 142
1 KLLDMAAQI 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P04036; 1DRW
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les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=160488;
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                                                                                                                                                                                                                     DAPB PSEPK
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                                                                                                                                                                                                                                                      Q88D<u>U</u>4;
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Matches
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Gaps

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BMBL; CP000076; AAY96229.1; -; Genomic_DNA.
GO; GO:000839; F: Crytoplasm; IEA.
GO; GO:000889; F: Crytoplasm; Collinate reductase activity; IEA.
GO; GO:0009089; F: Plysine biosynthesis via diaminopimelate; IEA.
InterPro; IPR011770; DapB.
Pfam; PF05173; DapB.C.
Pfam; PF05173; DapB.C.
Pfam; PF05173; DapB.C.
Pfam; PF01113; DapB.C.
Pfam; PF01113; DapB.N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=15980861; DOI=10.1038/nbt1110;
Paulsen I.T., Press C.M., Ravel J., Kobayashi D.Y., Myers G.S.A.,
Mavrodi D.V., DeBoy R.T., Seshadri R., Ren O., Madupu R., Dodson R.J.,
Durkin A.S., Brinkac L.M., Daugherty S.C., Sullivan S.A.,
Rosovitz M.J., Gwinn M.L., Zhou L., Schneider D.J., Cartinhour S.W.,
Nelson W.C., Weidman J., Watkins K., Tran K., Khouri H., Pierson E.A.,
Pierson L.S. III., Thomashow L.S., Loper J.B.;
"Complete genome sequence of the plant commensal Pseudomonas
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                         R GO; GO:00094; ABA72568.1; -; Genomic_DNA.

R GO; GO:000833; C:cytoplasm; IEA.

GO; GO:0008839; F:dihydrodipicolinate reductase activity; IEA.

R GO; GO:0008899; F:dihydrodipicolinate reductase activity; IEA.

R GO; GO:0009089; P:lysine biosynthesis via diaminopimelate; IEA.

R InterPro; IPR011770; DapB.bac.

R Pfam; PF01113; DapB.c. 1.

R Pfam; PF01113; DapB.l. 1.

R ProDom; PD004105; DapB; 1.

R ProDom; PD004105; DapB; 1.

R PROSTIE; PS01298; DAPB; 1.

Complete proteome.

O SEQUENCE 268 AA; 28499 MW; B6D702E0339A7ADI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=dapB; OrderedLocusNames=PFL 0829;
Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                  Score 36; DB 2; Length, 268; Pred. No. 22;
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22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2005, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                     2; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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SEQUENCE 268 AA; 28486 MW; F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-2005, sequence version 1. 07-FEB-2006, entry version 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD004105; DapB; 1.
TIGRFAMS; TIGR00036; dapB; 1.
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77.8%;
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Best Local Similarity 77...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   135 KLLDMAARV 143
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Best Local Similarity
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Q4KIG9;
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                                                                                                                                                                                                                                                                                                                Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=F1;
US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.
Annotation of the draft genome assembly of Pseudomonas putida F1.";
Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US DOE Joint Genome Institute;

Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina Hammon N., Israni S., Pitluck S., Saunders B.H., Schmutz J.,
Larimer F., Land M., Kyripides N., Anderson I., Richardson P.;

"Complete sequence of Pseudomonas fluorescens Pfo-1.";
Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                           10-JAN-2006, integrated into UniProtKB/TrEMBL.
10-JAN-2006, sequence version 1.
07-FEB-2006, entry version 3.
Dihydrodipicolinate reductase, bacterial.
ORFNames=PputDRAFT_2379;
Pseudomonas putida F1.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AALMO1000117, EAPS0349-11; -; Genomic DNA.
SEQUENCE 267 AA; 28414 MW; DFSBESCD79670417 CRC64;
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                                                                 267 AA
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2; Mismatches
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                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-NOV-2005, sequence version 1.
21-FBB-2006, entry version 4.
Dihydrodipicolinate reductase.
OrderedLocusNames=Pfl_0765;
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Q3K198;
                                                                 PRELIMINARY;
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Best Local Similarity 77.55,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary data.
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                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                               NCBI_TaxID=351746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=205922;
                                                               QZXEZ8_PSEPU
Q2XEZ8;
                                                                                                                                                                                                                                                                                                                   Copeland A.,
                                                                                                                                                                                                                                                                                 STRAIN=F1;
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                              RESULT 19
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FIGR; PG1366; -.
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PubMed=15466707; DOI=10.1073/pnas.0404172101;
Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=15746427; DOI=10.1126/science.1107008;
Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A.,
Barron A., Lordk L., Orcton C., Doggett J., Holden M.T.G., Larke N.,
Line A., Lord A., Norbertczak H., Ormond D., Price C.,
Rabbinowitsch E., Woodward J., Barrell B.G., Parkhill J.;
"Extensive DNA inversions in the B. fragilis genome control variable
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    Gaps
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                                                                                                                                                                                                                                                                                                                                             Bacteria, Bacteroidetes, Bacteroidetes (class), Bacteroidales, Bacteroidaceae, Bacteroides.
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Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
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GO; GO:0016740; F:transferase activity; IEA.
GO; GO:001927; P:UDP-N-acetylgalactosamine biosynthesis; IEA.
InterPro; IPR05750; AcGlu_Tran MurA.
InterPro; IPR001986; EBSP Synth.
ProDom; PD001867; EPSP Synth; 1.
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Pred. No. 62;
    0; Indels
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                                                                                                                                                                                                                                           21-JUN-2005, sequence version 1.
07-FEB-2006, entry version 6.
Putative peptidoglycan biosynthesis related protein.
OrderedLocusNames=BF3495;
                                                                                                                                                                                                                                                                                                                            Bacteroides fragilis (strain ATCC 25285 / NCTC 9343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UDP-N-acetylglucosamine 1-carboxyvinyltransferase
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                                                                                                                                                                                    434 AA.
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  Mismatches
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07-FEB-2006, entry version 8.
5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 307:1463-1465(2005).
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7; Conservative
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135 KLLDMAARV 143
                                        1 KLLDMAAQI 9
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=272559;
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                                                                                                                                                                                  Q5L9P3_BACFN
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NUCLEOTIDE
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Matches
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OSC1993 BAC
OSC1991
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Distributed under the Creative Commons Attribution-NoDerivs License
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DOI=10.1128/JB.185.18.5591-5601.2003;
Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
Dewhirst F.E., Fraser C.M.;
"Complete genome sequence of the oral pathogenic bacterium
Porphyromonas gingivalis strain W82.";
J. Bacteriol. 185:5591-5601(2003).
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Kuhara S., Hattori M., Hayashi T., Ohnishi Y.; "Genomic analysis of Bacteroides fragilis reveals extensive DNA inversions regulating cell surface adaptation."; Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924 (2004).
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Name=murA; OrderedLocusNames=PG1366; ORNames=PG 1366;
Porphyromonas gingivalis (Bacteroides gingivalis):
Bacteria; Bacteroidetes; Bacteroidetes (Class); Bacteroidales;
                                                                                                                                                                                                                                                        EMBL; AP006841; BAD50445.1; -; Genomic_DNA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:001927; F:UDP-N-acetylgalactosamine biosynthesis; IEA.
InterPro; IPR005750; AcGlu_Tran MurA.
InterPro; IPR001986; EPSP_Synth.
Pfam; PF00275; ESPSP_Synth.
ProDom; PD001867; EPSP_Synth, 1.
TIGRFAMS; TIGR01072; murA; 1.
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BioCyc; PGIN242619:PG1366-MONOMER; -.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:001927; P:UDP-N-acetylgalactosamine biosynthesis; IEA.
InterPro; IPR005756; Acdlu Tran MurA.
InterPro; IPR001986; EPSP_synth.
ProDom; PD00187; EPSP_synth, 1.
IIGRFAMS; TIGR01072; murA; 1.
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62;
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HSSP; P33038; 1DLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.4%; Score 35;
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SEQUENCE 434 AA; 47298 MW;
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Matches 7; Conservative
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
                                                                                          EMBL; BX842684; CAH69080.1; -; Genomic_DNA.

BRR; OSTYU7; 42-485.

BRR; OSTYU7; 42-485.

BRSABARGO000007783; Danio rerio.

CO; GO:0004713; F:ATP binding; IEA.

GO; GO:0004713; F:Protein-tyrosine kinase activity; IEA.

GO; GO:0007242; P:Intracellular signaling cascade; IEA.

GO; GO:0007424; P:Protein-tyrosine kinase activity; IEA.

GO; GO:0007425; P:Intracellular signaling cascade; IEA.

GO; GO:0007429; P:Intracellular signaling cascade; IEA.

RO; GO:0007429; P:Intracellular signaling cascade; IEA.

GO; GO:0007468; P:Protein amino acid phosphorylation; IEA.

InterPro; IPR000390; SET_CHT_pkinase.

InterPro; IPR00145; SH3.

InterPro; IPR00145; Tyr_pkinase.

InterPro; IPR00145; Tyr_pkinase.

InterPro; IPR00145; Tyr_pkinase.

InterPro; IPR00145; Tyr_pkinase.

R Pfam; PF0017; SH3; 1.

Pfam; PF0017; SH3; 1.

PRINTS; PR00401; SH2; 1.

PRODOM; PD000001; Prote kinase; 1.

R PRINTS; PR00109; TYRKINASE.

R ProDOM; PD000001; TyrKINASE.

R PRODOM; PD000001; TyrKINASE.

R PROSTIE; SR00107; PROTEIN KINASE ATP; 1.

R PROSTIE; PS00107; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 485;
        Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Anopheles gambiae Sequence Committee; "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-2003, integrated into UniProtKB/TrEMBL.
15-DEC-2003, sequence version 1.
07-FBB-2006, entry version 15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORFNames=ENSANGG00000004562;
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PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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nes 7; Conserv
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Q7PPB4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIR=VEI-SHSZ / ATCC 29148;
MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
                          Gaps
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07-DEC-2004, sequence version 1.
07-FEB-2006, entry version 8.
07-FEB-2006, entry version 8.
Novel protein tyrosine kinase.
Name=si-dkey-33122.2; Synonyms=OTTDARP0000004623;
ORFNames=DKEY-33122.2-001;
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                  Bacteroides thetaiotaomicron.
Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
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BioCyc; BTHE226186:BT2005-MONOMER; -.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0019277; P:UDP-N-acetylgalactosamine biosynthesis; IEA.
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                          Indels
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                                                                                                                                                                                                                                 01-JUN-2003, integrated into UniProtKB/TrEMBL.
01-JUN-2003, sequence version 1.
07-FEB-2006, entry version 12.
UDP-N-acetylglucosamine 1-carboxyvinyltransferase.
OrderedLocusNames-BT2005, ORFNames-BT_2005,
                          1;
                                                                                                                                                                                                 434 AA
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      Pred. No. 62;
1; Mismatches
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    77.8%; Pred. No.
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InterPro; IPR001986; BPSP_synth.
Pfam; PF00275; BPSP_synthase; 1.
ProDom; PD001867; BFSP_synth; 1.
TIGRFAMS; TIGR01072; murA; 1.
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SEQUENCE 434 AA; 47416 MW;
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QSTYU7;
                      7; Conservative
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                                                                                  351 KLIDMGAQI 359
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Best Local Similarity
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                                                            1 KLLDMAAQI
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                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
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RESULT 26
05TYUT BRA
1D Q5TYU
AC Q5TYU
DT 07-DE
DT 07-DE
DF NOvel
GN Name=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Berkeley;
Stableton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Erachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Figure 1000011, Anguston 1, Marker 1
Larimer F., Land M.;
"Annotation of the draft genome assembly of Syntrophobacter funaroxidans MPOB.";
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                  82.9%; Score 34; DB 2; Length 183; 77.8%; Pred. No. 42; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide-binding; Receptor; Transferase; Transmembrane;
                                                                                                                                                                                                                                                                                                                                EMBL; AAJF01000042; EA020012.1; -; Genomic_DNA.
SEQUENCE 183 AA; 20001 MW; 1065FDF64EE9B32D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 AA; 27038 MW; 8B9F65DB2EE15B9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-DEC-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 AA
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Pred. No. 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-2004, sequence version 1.
21-FEB-2006, entry version 13.
RE19378p.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
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SEOUENCE 235 AA; 270
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4 KLLDIAAEI 12
                                                                                                                                                                                 preliminary data.
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Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
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ID QSU175_DROME
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                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Syntrophobacteraceae, Syntrophobacter.
NCBI_TaxID=315543;
                                    EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
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0
                                                                                                                                                                                                                                                             GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:Protein-tyrosine kinase activity; IEA.
GO; GO:000713; F:protein-tyrosine kinase activity; IEA.
GO; GO:000742; P:intracellular signaling cascade; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot kinase.
InterPro; IPR001290; Ser thr pkinase.
InterPro; IPR001245; SH3.
InterPro; IPR001245; Tyr pkinase.
Ffam; PF00714; Pkinase Tyr; 1.
Ffam; PF00714; Pkinase Tyr; 1.
Ffam; PF00017; SH3. 1.
FFam; PF00018; SH3. 1.
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      CAUTION: The sequence shown here is derived from an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          508 AA; 57965 MW; DC6B6B65201B12F8 CRC64;
                                                                                                                                                                                                               EMBL; AAAB01008960; EAA10750.2; -; Genomic_DNA
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PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKITASE.
ProDom; PD0000091; TYRKITASE.
ProDom; PD0000091; Prot_kinase; 1.
ProDom; PD0000091; PR12; 1.
SWART; SW00252; SH2; 1.
SWART; SW00219; TYRK; 1.
PROSITE; PS00109; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
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US DOE Joint Genome Institute (JGI_ORNL);
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US DOE Joint Genome Institute (JGI-PGF);
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Q3MYH2;
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Length 235;

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RESULT 28
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         Gaps
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MEDILINE=20020130; PubWed=10552041;
Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
"Protein tyrosine kinase CDNAs from amphioxus, hagfish, and lamprey:
isoform duplications around the divergence of cyclostomes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gnathostomes.";
J. Mol. Bvol. 49:601-608(1999).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.
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GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein-tyrosine kinase activity; IEA.
InterPro; IPR001299; Prot kinase.
R InterPro; IPR001299; Ser_th_Dkinase.
R InterPro; IPR001245; Tyr_pkinase.
R InterPro; IPR00109; TyrKINASE.
R PRODM: PROMO109; TYRKINASE.
R PROMOTE; PS0011; PROTEIN_KINASE_DOM; 1.
R PROSITE; PS0011; PROTEIN_KINASE_TYR; 1.
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      0; Indels
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   1; Mismatches
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HSSP; P12931; 1FMK.
SMR; Q9PVU9; 1-245.
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7; Conservative
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LIDMAAQI 72
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DD Q9PWU9
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DT 07-FER
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Search completed: June 29, 2006, 09:29:39 Job time : 107.942 secs

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re version 5.1.9 33 - 2006 Biocceleration Ltd. sw model	Βĸ	08:59:14; Search time 87.8313 Seconds (without alignments) 46.851 Million cell updates/sec		tt 0.5	457216429 residues	chosen parameters: 2589679		* summaries	*	**	* *	* *	. *.	oguilte avendiated by change to base a	umber of results predicted by chance to have a or equal to the score of the result being printed, analysis of the total score distribution.	CINTANANTOC	SUMMARIES	ID Description		Abg22262 Novel h	Ady52570 Human		Aay43955 Human	Adr88385 2hr56203	Abr56204 Muta	Adr88384 HCK tyz	ADBII88 Ady85449	ADY85468 Ady85468 Catalytic	Ady85448 Aav76750	Aae06208 Human		Human			
GenCore Copyright (c) 1993	OM protein - protein search, using s	Run on: June 29, 2006, 08:	Title: US-10-062-257A-15 Perfect score: 43 Sequence: 1 QIAEGWAFI 9	Scoring table: BLOSUM62 Gapop 10.0 , Gapext	Searched: 2589679 seqs, 4572	Total number of hits satisfying cha	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 100% Maximum Match 100% Listing first 100 %	Database : A Geneseq 8:*		4: geneseqp2001s: 5: geneseqp2002s:				greater than sering a	•		kesuit No. Score Match Length DB II	43 100 0 4	43 100.0 85 4	43 100.0 250 9	43 100.0 259 2	43 100.0 259 2	43 100.0 263 8 43 100:0 265 7	43 100.0 271 7	43 100.0 271 8 43 100 0 272 E	43 100.0 279 9	43 100.0 300 9	43 100.0 346 3	43 100.0 346 4	43 100.0 346 5 43 100.0 355 8	43 100.0 383 7	43 100.0 417 2 43 100.0 436 8	22 43 100.0 437 5 AE 23 43 100.0 438 9 AE	

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WO200175067-A2.
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                                                                                                                                                                                                                                                                             Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and polynucleotides encoding them for treatment of cancer.
                                                                                                                                                                                                                                                                                                                 The present invention relates to peptides which are partial sequences of sto/lck family proteins. The present sequence is one such peptide. The peptides are useful for producing vaccines for the treatment of cancer, including colon cancer and small-cell lung cancer.
                                                                                                                                          Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
Human
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       Ady16487 PRO p
Ady16487 PRO p
Ady19685 PRO p
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                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #22253.
ADS88430
ADP23372
ADY16487
ADY19685
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                                                                                AAB73131 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                   Claim 1; Page 70; 75pp; Japanese.
                                                                                                                                                                                                      03-AUG-2000; 2000WO-JP005220
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                                                                                                                            Tumour antigen peptide #15
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                      Sequence 9 AA;
                                                                                                             09-MAY-2001
                                                                                                                                                           Homo sapiens
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 0444
                                                                                               AAB73131;
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                                                                                                                                                                                                                                                 Itoh K;
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consists of (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is ouseful for generating antibodies against it, detecting or quantitating a colypoptide in tissue, as molecular weight markers and as a food cusplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders convolving aberrant protein expression or biological activity. The diagnostics, forensics, gene mapping, identification of mutations of capportice and polymucleotide sequences have applications in diagnostic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this captent did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human oncogene screening method-related HCK kinase domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 52621; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADY52570 standard; protein; 250 AA.
30-MAR-2001; 2001WO-US008631
                                                                    31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                       Tang YT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAY-2005 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
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                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS86449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 85 AA;
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AAY43957 standard; protein; 259 AA.
    07-AUG-2003; 2003JP-00206534.
              07-AUG-2003; 2003JP-00206534.
                        (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                            92US-00857224
                                                                                                                                                                                                                                                                                                                                     92US-00857224
                                                                                                                                                                                                                                                     21-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                Human protein kinase #16.
                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                        103 QIAEGMAFI 111
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                                   WPI; 2005-187380/20.
                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-570766/48
                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                              1 QIAEGMAFI
                                                                                                                                                                Sequence 250 AA;
                                                                                                                                                                                                                                                                                                                                               (BENN/) BENNER
                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                            25-MAR-1992;
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predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure, active sites, and parsing segments. Secondary structural units are assigned by identifying periodicity in the assignments, and assembled into globular form using distance constraints imposed by disulfide bridges, active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein molecule, as guides for site directed mutagenesis studies, and for understanding the
                                                                                                                                   Sequences AAY43902-Y44015 represent proteins used in a novel method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 43; DB 2; Length 259; 100.0%; Pred. No. 1.5; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interaction of a protein with other molecules
Predicting the folded structure of proteins.
                                                               Disclosure; Col 257-260; 113pp; English.
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse protein kinase #6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 QIAEGMAFI 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 259 AA;
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AAY43956
ID AAY4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel method for screening an oncogene. The method comprises producing a cDNA library for a fusion DNA, comprising a cDNA region of TEL connected downstream of a vector promoter, introducing the PVT region of TEL connected downstream of a vector promoter, introducing the produced cDNA library into a host cell, expressing the fusion DNA, selecting the transformed cells and analyzing the base sequence of the fusion DNA in the transformed cells and analyzing the base sequence of the fusion DNA in the transformed cells, and thus identifying the fusion DNA as an oncogene. TEL is a transcription factor which belongs to the Ets family and is known to form various genes and fusion genes via a chromosomal translocation in cancer cells, such as cocurs in some cases of leukemia. The method of the invention may be useful for screening a substance which suppresses the proliferative property of a cancer cell, screening a substance which inhibits the activity of a kinase gene introduced into the cell and screening a substance for the treatment of cancer. The current sequence is that of the human HCK kinase domain protein of the invention.
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                                                                                                                                                                                                                                                                                            Screening oncogene, by producing cDNA library having fusion DNA comprising cDNA encoding PNT region of TEL connected to downstream of promoter, introducing library into host cell, expressing fusion DNA and selecting transformed cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; SEQ ID NO 2; 216pp; Japanese.
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Gaps

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Sequences AAY43902-Y44015 represent proteins used in a novel method of predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure, active sites, and parsing segments. Secondary structural units are assigned by identifying periodicity in the assignments, and assembled into globular form using distance constraints imposed by disulfide bridges, active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein molecule, as guides for site directed mutagenesis studies, and for understanding the
                                                                                                                        Prediction, secondary structure, alignment, evolutionary conservation, homology, periodicity, co-variation analysis, antigenic site, site directed mutagenesis, interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Predicting the folded structure of proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Col 255-258; 113pp; English.
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AAY43955;

AAY43955

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The present invention relates to a method of designing a ligand binding to a target molecule. The method involves identifying as molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesising ligand. The invention is useful for designing drug products and for designing ligand binding to target molecules such as nuclear hormone receptors, TNF receptors, G-protein coupled receptors, methyl transferases, ligases, etc. The present sequence is the LCK tyrosine kinase protein. This sequence is used to illustrate the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Designing a ligand binding to a target molecule, comprises identifying amplecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
Src-family protein tyrosine kinase; T-cell; immune response; mutein;
mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant Lymphocyte Cell Kinase, Lck, fragment (237-501, D364N).
                                                                                                                                               Molecular scaffold; nuclear hormone receptor; TNF receptor; G-protein coupled receptor; methyl transferase; ligase; LCK tyrosine kinase; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 43; DB 8; Length 263; 100.0%; Pred. No. 1.5;
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ADR88385 standard; protein; 263 AA.
                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2002; 2002US-0360651P.
16-SEP-2002; 2002US-0411398P.
20-SEP-2002; 2002US-043731P.
02-JAN-2003; 2003US-0437929P.
                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003; 2003US-00377268.
                                                                                                                 LCK tyrosine kinase protein
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                                                                           (first entry)
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nes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PLEX-) PLEXXIKON INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Milburn MV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthesizing ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 263 AA;
                                                                                                                                                                                                                                                                     US2004171062-A1
                                                                                                                                                                                                                                 Unidentified
                                                                         18-NOV-2004
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                                     ADR88385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAY43902-Y44015 represent proteins used in a novel method of predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure, active sites, and parsing segments. Secondary structural units are assigned by identifying periodicity in the assignments, and assembled into globular form using distance constraints imposed by disulfide bridges, active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein molecule, as interaction of a protein with other molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                             Prediction; secondary structure, alignment; evolutionary conservation; homology; periodicity; co-variation analysis; antigenic site; site directed mutagenesis; interaction.
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                                                                           2; Length 259;
                                                                                                                 0; Indels
   interaction of a protein with other molecules
                                                                           100.0%; Score 43; DB 2
100.0%; Pred. No. 1.5;
iive 0; Mismatches
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Best Local Similarity luv.
9, Conservative
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105 QIAEGMAFI 113
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Best Local Similarity
Matches 9; Conserv
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                                       Sequence 259 AA
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                                                                                                                                                                                                                                                 New crystalline polypeptide comprising ligand binding domain or catalytic domain of Lck protein, for determining three-dimensional structure of catalytic domain of Lck, has predetermined unit cell parameters.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Wild-type D substituted with N. This position is 364 in the full-length sequence (see ABR56202 for the
                                                      with N. This position (see ABR56202 for the
                                                                                                                                                                                                       Loew A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
Src-family protein tyrosine kinase; T-cell; immune response; mutein;
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                                                                                                                                                                                                      Hrnciar P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutant Lymphocyte Cell Kinase, Lck, fragment (231-501, D364N)
                                                                                                                                                                                                                                                                                                                                                                                                   Length 265;
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                                                                                                                                                                                                      Hirst GC,
                                                     /note= "Wild-type D substituted 364 in the full-length sequence wild-type full length sequence"
                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 43; DB 7;
100.0%; Pred. No. 1.5;
cive 0; Mismatches 0;
                                                                                         /note= "Phosphorylation site"
                                                                                                                                                                                                      Dixon RW,
                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR56204 standard; protein; 271 AA
                                                                                                                                                                                                                                                                                      Claim 12; Fig 2; 994pp; English.
                                                                                                                                               02-AUG-2002; 2002WO-US024546
                                                                                                                                                                 03-AUG-2001; 2001US-0310051P
                                                                                                                                                                                                     Calderwood D,
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                                                                                                                                                                                                             Ritter K;
                                                                                                                                                                                  (ABBO ) ABBOTT LAB
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 265 AA;
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Misc-difference
                                            Misc-difference
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                                                                                 Modified-site
         sapiens
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                                                                                                                                                                                                     Borhani DW,
                   Synthetic
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New crystalline polypeptide comprising ligand binding domain or catalytic domain of Lck protein, for determining three-dimensional structure of catalytic domain of Lck, has predetermined unit cell parameters.
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                                                                                                                                                                                                                                                                                                                                                                                                     Dixon RW, Hirst GC,
wild-type full length sequence"
                                                     /note= "Phosphorylation site"
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16-SEP-2002; 2002US-041139BP.
20-SEP-2002; 2002US-0412341P.
02-JAN-2003; 2003US-0437829P.
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Borhani DW, Calderwood
Leung A, Ritter K;
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                                                                                                                 WO2003020880-A2
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                          Modified-site
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Receptor tyrosine kinase; RTK; kinase domain; cytostatic; antiarthritic; antiinflammatory; immunosuppressive; antirheumatic; virucide; nootropic; neuroprotective; cerebroprotective; antiparkinsonian; dermatological; nephrotropic; tranquilizer; vulnerary; anticonvulsant; human; KIT.
                                                                                                                                                          The present invention relates to a method of designing a ligand binding to a target molecule. The method involves identifying as molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesising ligand. The invention is useful for designing drug products and for designing ligand binding to target molecules such as nuclear hormone receptors, TNF receptors, G-protein coupled receptors, methyl transferases, ligases, etc. The present sequence is the HCK tyrosine kinase protein. This sequence is used to illustrate the method of
                                                      Designing a ligand binding to a target molecule, comprises identifying molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and
                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 43; DB 8; Length 271; 100.0%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                   Disclosure; SEQ ID NO 23; 186pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB81188 standard; protein; 272 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2002; 2002WO-CA000114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human KIT protein sequence.
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1es 9; Conservative
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K, Milburn MV;
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                            WPI; 2004-642017/62
                                                                                                       synthesizing ligand
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                                                                                                                                                                                                                                                                                                                                   Sequence 271 AA;
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                                                                                                                                                                                                                                                                                                       invention.
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Novel isolated binding pocket of receptor tyrosine kinase that regulates the kinase domain of the receptor, useful for identifying modulator of the receptor for treating lymphoproliferative conditions.

WPI; 2002-643365/69

The invention relates to an isolated binding pocket (I) of a receptor tyrosine kinase (RTK) that regulates the kinase domain of RTK. A crystal (II) comprising a binding pocket of an RTK that regulates the kinase

Disclosure; Fig 1; 116pp; English.

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Gaps

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cc domain of the RTK, or comprising a juxtamembrane region and/or kinase comain of an RTK or its part, or formed by a juxtamembrane region and a cc domain of an RTK in an autoinhibited state and a model (III) of (I) made using (I); are useful for determining the secondary and/or tertiary structure of a polypeptide, or for screening for a ligand capable of binding to a binding pocket and/or inhibiting or enhancing the atomic contacts of interactions in a binding pocket. (I) is useful for identifying a modulator of an RTK. (II) is useful for designing, identifying, evaluating and/or synthesizing mimeries of binding pocket, or ligands that associate with the binding pocket, to binding pocket, or ligands that associate with the binding pocket, to pulpaptides with unknown structures. Pharmaceutical compositions comprising the ligand or modulator is useful for treating polypeptides with unknown structures. Pharmaceutical compositions (such as cancer), arthritis, inflammation, autoimmune disorder (such as cancer), arthritis, inflammation, graft versus host disease, atthritis), viral infection, inflammation, graft versus host disease, contendegenerative diseases and conditions involving traum and injury to the nervous system (e.g., Altheimer's disease, Parkinson's disease. Huntington's disease and multiple sclerosis). The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a new kinase scaffold library comprises at least 1 set of compounds, each set comprising at least 1 N-heterocyclic compound of formulae (I)-(VII) given in the specification. Also included
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kinase; protein co-ordinate data; protein structure; cancer; cytostatic; neoplasm; inflammation; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catalytic domain of PIM kinase-like protein LCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 43; DB 5
100.0%; Pred. No. 1.6;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADY85449 standard; protein; 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-SEP-2003; 2003US-0503277P
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es 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 272 AA;
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che electronic representations of the compounds can be selectively
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cettieved and functionally connected with computer software adapted to
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binding to a protein kinase with greater affinity and/or specificity
cof [1]-(VII) binds to the kinase with greater affinity and/or specificity
than [1]-(VII) binds to the kinase with greater affinity and/or specificity
cof [1]-(VII) binds to the kinase with greater affinity and/or specificity
comprises determining if a derivative of [1]-(VII) that binds
corresses has greater for specificity for the particular kinase than [1](VII), developing ligands binding to a kinase (which comprises
cofferentining the orientation of at least 1 molecular scaffold of [1]-(VII)
in co-crystals with the kinase, identifying affinity and/or
specificity between the scaffold and kinase and synthesizing allique in
which at least 1 chemical structure of the scaffold is modified).

comprises testing a derivative of a kinase binding compound (I)-(VII) for
increased specificity on the kinase binding compound (I)-(VII) preparation of co-crystals of pin-1 with (I)-(VII)
identifying potential kinase binding compound including a
core structure (I)-(VII) preparation of co-crystals of pin-1 with (I)-(VII)
identifying potential kinase binding compounds (omprises fitting
affinity and/or specificity), a co-crystal of a kinase binding site), and according a kinase binding compound (I)-(VII) binds
core structure (I)-(VII) preparation of co-crystals of pin-1 with (I)-(VII)
identifying potential kinase binding compounds (C)-(VII) in and attachment component (which comprises ficting
compound (I)-(VII) and attachment component (which comprises ficting
compound (I)-(VII) in a contracting a kinase binding site), a at least kinases, for modulating kinase activity and for treating disease condition associated with abnormal kinase activity e.g. cancer, inflammatory disease. The method identifies improved ligands binding to a kinase resulting in ligands having high affinity and specificity towards kinase. The co-crystals of kinase and the binding compound are of sufficient size and quality to allow structural determination of at least PIM-like a system for fitting compounds in binding sites of protein kinases (comprising an electronic kinase scaffold, and a scaffold library comprising at least 1 collection of electronic representations of (1)-2 Angstroms. The present sequence is a catalytic domain from a kinase. NOTE: It is not clear whether the sequence as presented represents a continuous amino acid sequence.

Sequence 279 AA;

Gaps . 0 100.0%; Score 43; DB 9; Length 279; 100.0%; Pred. No. 1.6; 0; Indels 0; Mismatches Best Local Similarity 100. Matches 9; Conservative Query Match

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ADY85468 standard; protein; 300 AA. ADY85468;

(first entry)

16-JUN-2005

Catalytic domain of PIM kinase-like protein Src-2.

Kinase; protein co-ordinate data; protein structure; cancer; cytostatic; neoplasm; inflammation; antiinflammatory.

The invention relates to a new kinase scaffold library comprises at least compounds, each set comprising at least 1 N-heterocyclic compound of formulae (1) - (VII) given in the specification. Also included are a system for fitting compounds in binding sites of protein kinases (comprising an electronic kinase scaffold, and a scaffold library is comprising at least 1 collection of electronic representations of (I) - (VII), where the scaffold library is embedded in a computer device and the electronic representations of the compounds can be selectively certieved and functionally connected with computer software adapted to fit electronic representations of compounds in an electronic representations of compounds in an electronic representation of a binding site of a kinase, obtaining improved ligands binding to a protein kinase (which comprises determining if a derivative of (I) - (VII) binds to the kinase with greater affinity and/or specificity than (I) - (VII), developing ligands specific for a particular kinase than (I) - (VIII), developing ligands binding to a kinase (which comprises than (I) - (VIII), developing ligands binding to a kinase (which comprises than (I) - (VIII) that binds to a kinase (which comprises). developing ligands with increased specificity on a kinase (which comprises testing a derivative of a kinase binding compound (1)-(VII) for increased specificity on the kinase), identifying a ligand binding to a kinase (which comprises determining if a derivative compound (1)-(VII) for specificity, a co-crystal of a kinase and a binding compound (1)-(VII) preparation of co-crystals of a kinase and a binding compound (1)-(VII), preparation of co-crystals of a kinase and a binding compound (1)-(VII), preparation of co-crystals of pin-1 with (1)-(VII), identifying potential kinase binding compounds (which comprises fitting compound (1)-(VII) in an electronic representation of co-crystals of a kinase binding site), attaching a kinase binding compound (1)-(VII) and attachment of the component on a kinase binding compound (1)-(VIII) and attachment of the component on a kinase binding compound (1)-(VIII) and attachment of the component on a kinase binding compound (1)-(VIII) and attachment of the component on a kinase binding compound (1)-(VIII) and attachment at the allowed site), modified compounds (comprising (1)-(VIII) binds comprising conserved residues matching at least on of pin-1 residues 49, 52, 67, 121, 128 and 186 which comprises determining if (1)-(VIII) binds conserved residues matching at least on of pin-1 residues 49, 52, 67, 121, 128 and 186 which comprises determining if (1)-(VIII) binds conserved residues matching at least on of pin-1 residues 49, 52, 67, 121, 128 and 186 which comprises determining if (1)-(VIII) binds conserved residues at order receptor, endethelial growth factor endethelial growth factor endet kinases, for modulating kinase activity and for treating disease condition associated with abnormal kinase activity e.g. cancer, inflammatory disease. The method identifies improved ligands binding to a kinase resulting in ligands having high affinity and specificity towards kinase. The co-crystals of kinase and the binding compound are of sufficient size and quality to allow structural determination of at least in co-crystals with the kinase, identifying chemical structures of the scaffolds, that, when modified, change the binding affinity and/or specificity between the scaffold and kinase and synthesizing a ligand in which at least I chemical structure of the scaffold is modified), New scaffold library used for identifying and developing ligands for protein kinases and treating kinase associated disorders e.g. cancer, comprises set of compounds comprising N-heterocyclic compounds. Bremer RE, Gillette SJ, Hurt CR, Ibrahim PL; Disclosure; Page 170-174; 236pp; English 15-SEP-2004; 2004WO-US030360. 15-SEP-2003; 2003US-0503277P (PLEX-) PLEXXIKON INC. WPI; 2005-273155/28. WO2005028624-A2. Unidentified. Zuckerman RL; 31-MAR-2005. Artis DR,

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The inversion regards to a new Annaes beathcoid.

In the inversion regards to a new Annaes beathcoid.

In the inversion regards and the profit of the compound of formulae (I)-(VII) given in the specification. Also included are a system for fitting compounds in binding sites of protein kinases (comprising at least 1 collection of electronic representations of (I)-(VII) where the scaffold library is embedded in a computer device and the electronic representations of the compounds can be selectively retrieved and functionally connected with computer software adapted to it electronic representations of compounds in an electronic adapted to retrieved and functionally connected with computer software adapted to it electronic representations of compounds in an electronic profit of a binding site of a kinase), obtaining if a derivative binding to a protein kinase (which comprises determining if a derivative of (I)-(VII) binds to the kinase with greater affinity and/or specificity to than (I)-(VII)), developing ligands specific for a particular kinase than (I)-(VII), developing ligands specific of (I)-(VII) that binds to kinase (which comprises determining if a derivative of (I)-(VII) caterior in co-crystals with the kinase, identifying chemical structures of the coefficiaty between the scaffold and kinase and synthesizing a ligand in modified), which at least 1 chemical structure of the scaffold is modified),
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a new kinase scaffold library comprises at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kinase; protein co-ordinate data; protein structure; cancer; cytostatic; neoplasm; inflammation; antiinflammatory.
2 Angstroms. The present sequence is a catalytic domain from a PIM-like
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New scaffold library used for identifying and developing ligands for protein kinases and treating kinase associated disorders e.g. cancer, comprises set of compounds comprising N-heterocyclic compounds.
                  kinase. NOTE: It is not clear whether the sequence as presented represents a continuous amino acid sequence.
                                                                                                                                                                ö
                                                                                                                      100.0%; Score 43; DB 9; Length 300; 100.0%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gillette SJ, Hurt CR, Ibrahim PL;
                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catalytic domain of PIM kinase-like protein HCK.
                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 170-174; 236pp; English
                                                                                                                                                                                                                                                                                                                                                 ADY85448 standard; protein; 316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-SEP-2004; 2004WO-US030360.
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                                                                                                 Query Match
Best Local Similarity 10v.v.
Pos 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             16-JUN-2005 (first entry)
                                                                                                                                                                                                                                            138 QIAEGMAFI 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PLEX-) PLEXXIKON INC.
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                                                                                                                                                                                                    1 QIAEGMAFI
                                                                                Sequence 300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2005028624-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Artis DR,
                                                                                                                                                                                                                                                                                                                                                                                       ADY85448;
                                                                                                                                                                                                                                                                                                         RESULT 14
ADY85448
88888
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developing ligands with increased specificity on a kinase (which comprises testing a derivative of a kinase binding compound (I)-(VII) for increased specificity on the kinase), identifying a ligand binding to a kinase (which comprises determining if a derivative compound including a core structure (I)-(VII) binds to the kinase with changed binding a finity and/or specificity), a co-crystal of a kinase and a binding compound (I)-(VII), preparation of co-crystals of pim-1 with (I)-(VII), identifying potential kinase binding compounds (which comprises fitting colectronic representations of (I)-(VII) in an electronic representation of a kinase binding site), attaching a kinase binding compound to an attachment component (which component on a kinase binding compound (I)-(VII) and attaching the compound or derivative to the attachment of the compound or derivative to the attachment at the allowed site), modified compounds (comprising conserved residues matching at least on of Pim-1 residues 49, (VII) and attached linker group, and developing a ligand for a kinase comprising conserved residues matching at least on of Pim-1 residues 49, (CC optic kinase comprises determining if (I)-(VII) binds comprising conserved residues matching at least on of Pim-1 residues 49, (CC optic kinase comprises pim-1, PykZ, c-Abl, HerZ, CME, vascular endothelial growth factor receptor, endothelial growth factor receptor, endothelial growth factor receptor, endothelial growth factor receptor, endothelial growth factor receptor, endothelial growth factor seceptor, endothelial growth factor seceptor, endothelial growth factor condition associated with abnormal kinase activity e.g. cancer, cancer, inflammatory disease. The method identifying and developing ligands binding to a kinase. The co-crystals of kinase activity e.g. cancer, condition associated with abnormal kinase activity e.g. cancer, condition associated with abnormal kinase activity e.g. cancer, condition associated with abnormal kinase activity e.g. cancer, condition associated w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein kinase homologue; human; PKH; diagnosis; therapy; cancer; AIDS; autoimmune disorder; inflammatory disorder; reproductive defect; asthma; diabetes mellitus; infertility; ovulatory defect; endometriosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 43; DB 9; Length 316; 100.0%; Pred. No. 1.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein kinase homologue, PKH-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY76750 standard; protein; 346 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00173581.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 100
Matches 9; Conservative
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154 QIAEGMAFI 162
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Bandman O,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-1998;
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24-JUL-2001.

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expression such as cancers (e.g. Imphoma, melanoma and cancers of the breast lung and prostate), autoimmune/inflammatory disorders (e.g. AIDS, asthma and diabetes mellitus), and reproductive defects (e.g. AIDS, asthma and diabetes mellitus), and reproductive defects (e.g. AIDS, antatility, ovulatory defects, endometriosis and polycystic ovary syndrome). The DNA may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of FKH by expressing inactive proteins or to supplement the patients own production of PKH polypeptides. Additionally, the DNA may be used to produce PKH, according to standard recombinant DNA methodology, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. Conversely, antisense nucleic acid molecules may be administered to down regulate PKH expression. The DNA, and antisense and quantitate the presence of similar nucleic acid assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and ence which patients may be in need of restorative therapy. They may also be used as DNA probes in diagnostic acid sequences in samples, and ence which patients may be in need of restorative therapy. They may also be used to study the expression and function of PKH polypeptides and their production of antibodies against PKH and in assays to identify modulators (agonists and antagonists) of PKH expression and activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-PKH antibodies and PKH antagonists may also be used to down regulate PKH expression and activity. The anti-PKH antibodies may also be used as diagnostic agents for detecting the presence of PKH polypeptides in
                                                                                                                                                                                                                                                     This sequence represents a human protein kinase homolog (PKH) of the invention. The PKH sequences may be used in the prevention, treatment an diagnosis of diseases associated with inappropriate PKH expression such
                                                                                                                                                                                                                                                                                                                                                  as cancers, autoimmune/inflammatory disorders and reproductive defects.
They may be used to treat disorders associated with decreased PKH
                                                             Nucleic acids encoding a human protein kinase homolog useful for preventing, diagnosing and treating cancer, autoimmune/inflammatory disorders and reproductive defects.
                                                                                                                                                                                    Claim 1; Col 47-50; 38pp; English
   N-PSDB; AAZ86794.
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Sequence 346 AA;

Gaps ö 100.0%; Score 43; DB 3; Length 346; 100.0%; Pred. No. 2; 0; Indels Mismatches 0; 9; Conservative Best Local Similarity Query Match Matches

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AAE06208 standard; protein; 346 AA

25-SEP-2001 (first entry)

AAE06208;

Human protein kinase homolog-3 (PKH-3).

Human; protein kináse homolog-3; PKH-3; cytostatic; protein therapy; vaccine; immunosuppressive; antisclerotic; antiabortive; adenocarcinoma; Acquired immune deficiency Syndrome; AlDS; melanoma; cancer; bone; liver; breast; autoimmune disorder; multiple sclerosis; drug screening; anaemia; Crohn's disease; ectopic pregnancy; tubal disease; inflammatory disorder; reproductive disorder; polycystic ovary syndrome; asthma RESULT 16
AARO6208
XX
AC AARO6
XX
XY
DT 25-SE
XX
DD Human
XX
KW Vaccii
KW Vaccii
KW Crohn
XW Crohn
XW FR CPIO
XX
KW FR CPIO
XX
XY
FT REGIO

Homo sapiens

125. .333 /note= "Signature sequence" Location/Qualifiers

Region

US6264947-B1

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prevention, diagnosis and treatment of diseases associated with increased or decreased expression of PKH. Examples of such disorders include, cancer (e.g. adenocarcinoma, melanoma and bone, breast and liver cancer), syndrome (AIDS), anaemia, asthma, Crohn's disease and multiple sclerosis) and reproductive disorders (e.g. tubal disease, ectopic pregnancy and polycystic ovary syndrome). PKH, its catallytic or immunosenic fragment screening techniques. PKH nucleic acids are used to generate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hybridisation probes useful in mapping the naturally occurring genomic sequences. PKH are also used as antigens in the production of antibodies against protein kinases (PK) and in assays to identify modulators of PK expression and activity. PKH is also used in protein therapy
                                                                                                                                                                                                                                                                                   Human protein kinase proteins and homologs, useful for preventing, diagnosing and treating cancers, autoimmune/inflammatory disorders and
                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is human protein kinase homolog-3 (PKH-3). Human protein kinase homologs (PKH) and their cDNA molecules are used in the
                                                                                                                                                                     Corley NC;
                                                                                                                                                                    Yue H, Guegler KJ,
                                                                                                                                                                                                                                                                               Human protein kinase proteins and homologs,
                                                                                                                                                                    Hillman JL,
                                                                                                                                                                                                                                                                                                                                                             Claim 1; Col 47-50; 38pp; English.
                                                                                                                                                                  Tang YT, Hillman JL,
Azimzai Y, Lu DAM;
                                                                                           98US-00173581.
                                                      99US-00420915.
                                                                                                                              (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                      reproductive disorders.
                                                                                                                                                                                                                            WPI; 2001-450728/48.
                                                                                                                                                                                                                                              N-PSDB; AAD11845
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                                                      20-0CT-1999;
                                                                                           15-0CT-1998;
                                                                                                                                                                    Bandman O,
Gorgone GA,
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100.0%; Score 43; DB 4; Length 346; 100.0%; Pred. No. 2; 0; Indels ive 0; Mismatches 0; Indels Conservative 1 QIAEGMAFI 9 Local Similarity les 9; Conserv Query Match Matches ò

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184 QIAEGMAFI 192

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Gaps

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Human protein kinase homologue from clone 507669. ABB84435 standard; protein; 346 AA. (first entry) 08-NOV-2002 ABB84435; RESULT 17 ABB84435

Protein kinase homologue, PKH, cytostatic; immunosuppressive, antifungal, antiinflammatory; antiallergic; antiasthmatic; antianaemic; antidiabetic; antiarteriosclerotic; antithyroid; dermatological; nephrotropic; human; antigout; thyromimetic; nootropic; osteopathic; antiarthritic; allergy; antirheumatic; ophthalmological; antiulcer; antiviral; antibacterial; antiprotozoal; antiparasitic; antihelmintic; ankylosing spondylitis; acquired immunodeficiency syndrome; AIDS; Addison's disease; amyloidosis; dermatomyositis, diabetes mellitus, emphysema, atrophic gastritis, gout, glomerulonephritis, Goodpasture's syndrome; Graves' disease, psoriasis, Hashimoto's Lhyroiditis, hypereosinophilia; irritable bowel syndrome; multiple sclerosis; myasthenia gravis; myocardial inflammation; uveitis; pericardial inflammation; osteoarthritis; osteoporosis; pancreatitis; adult respiratory distress syndrome; anaemia; asthma; atherosclerosis; autoimmune haemolytic anaemia; autoimmune thyroiditis; bronchitis; cholecystitis; contact dermatitis; Crohn's disease; atopic dermatitis;

(INCY-) INCYTE PHARM INC Bandman O, Gorgone GA, cancer.

Sjogren's syndrome; systemic lupus erythematosus; systemic sclerosis; thrombocytopenic purpurs; ulcerative colitis; Werner syndrome; infection; haemodialysis; extracorporeal circulation; infertility; tubal disease; ovulatory defect; endometriosis; oestrous; menstrual cycle; gene therapy; uterine fibroid; autoimmune disorder; polycystic ovary syndrome; enzyme; ovarian hyperstimulation syndrome; ectopic pregnancy; teratogenesis; polymyositis; Reiter's syndrome; rheumatoid arthritis; scleroderma; SLE; 30-MAY-2001; 2001US-00870962. 98US-00173581. 99US-00420915. US2002081290-A1. Homo sapiens. 15-OCT-1998; 20-OCT-1999; 27-JUN-2002

Nucleic acids encoding a human protein kinase homolog useful for preventing, diagnosing and treating cancer, autoimmune/inflammatory preventing, diagnosing and treating disorders and reproductive defects. Hillman JL, Y, Lu DAM; Tang YT, Azimzai 2002-655433/70 N-PSDB; ABQ76288.

Corley NC;

Guegler KJ,

Yue H,

Claim 47; Page 27; 43pp; English.

This invention describes a novel protein kinase homologue (PKH)

contiallergic, antiasthmatic, antianeamic, antiarterisoslerotic,
antiallergic, antiasthmatic, antianeamic, antiarterisoslerotic,
antiallergic, antiasthmatic, antianeamic, antiarterisoslerotic,
antiallergic, antiasthmatic, antianeamic, antiantentic,
contributoric, dermatological, antidabetic, nephrotropic, antipuloct,
thyromimetic, nootropic, osteopathic, antiarthritic, antirheumatic,
thyromimetic, nootropic, osteopathic, antibacterial, antifungal,
antiprotozoal, antiparasitic and antihelmintic activity. The polypeptide
control control propertied and polypeptide is used to screen for
agonists and antagonists of PKH which can also be used in disease
creamen. The polypeptide and polymetheotide are used for treating
caquired immunodeficiency syndrome (AIDS), Addison's disease, adult
respiratory distress syndrome, allergies, ankylosing spondylitis,
amyloidosis, anaemia, asthma, atherosclerosis, autoimmune haemolytic
contact dermatitis, Crohn's disease, allergies, ankylosing spondylitis,
contact dermatitis, crohn's disease, atopic dermaticis, dermatomyositis,
diabbetes mellitus, emphysema, atrophic gastritis, glomerulonephritis,
contact dermatitis, myocardial or pericardial inflammation,
hypereosinophilia, irritable bowel syndrome, multiple sclerosis,
hypereosinophilia, irritable bowel syndrome, solymopsitis,
creaner, haemodalalysis, and extraoorporasis, plymyositis, psoriasis,
cancer, haemodalalysis, and extraoorporasic collections, viral, bacterial,
cancer, haemodalalysis, and extraoorporasis, plymyositis, infertility,
cancer, haemodalalysis, and extraoorporasis, and endometriosis,
cancer, haemodalalysis, and extraoorporasis, and endometriosis,
cancer, haemodalalysis, and extraoorporasis, and endometriosis,
cancer, haemodalalysis, and extraoorporasis,
cancer, haemodalalysis, and extraoorporasis,
cancer, haemodalalysis, and extraoorporasis,
conlocated the menstrinal polymore propreserion produces of the poestrous cycle, disruptions of hemography in par polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian tumours, uterine fibroids, autoimmune disorders, ectopic pregnancies, and teratogenesis. The polypeptides of the invention can be used for gene therapy. This sequence represents a PKH from clone ID 507669 isolated from TML3DTO2, a library constructed using RNA isolated from non-adherent peripheral blood monounclear cells collected from a pool of male and female donors

Sequence 346 'AA;

Query Match

DB 5; Length 346; 100.0%; Score 43;

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           Gaps
                                                                                                                                                               gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
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TA, Suchorolaki MT, Altus CM, Pitts SJ, Elder LV,
Delegeane AM, Panear IS, Barville SC, Reddy TP;
Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Anderson SB, Rioux P, Shen EJ, Wu C, Stuve LL;
Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietze
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           Indels
                                                                                                                                             Human diagnostic and therapeutic pprotein SEQ ID NO:3229
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           Mismatches
  Pred. No.
                                                                                        ABM82980 standard; protein; 355 AA.
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                                                                                                                                                                                                                                                                                                                                                     Kwong M, Policky ..., S. Shi X, Suarez CJ;
100.08;
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                                                                                                                           18-NOV-2004 (first entry)
           Conservative
                                            184 QIAEGMAFI 192
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 Best Local Similarity
                            1 QIAEGMAFI
                                                                                                                                                                                                  WO2004023973-A2
                                                                                                                                                                                                                                                                                                                            Stevens KA,
                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                  Peralta CH,
                                                                                                                                                                                                                                                                                                           Harthshorne
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                                                                                                         ABM82980;
           Matches
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnost a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine avtoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, dastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp collections caused by virus, bacteria, fungi or parasite. The dithp collections also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as equence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

N-PSDB; ACN41632

Claim 27; Page; 190pp; English.

in gene mapping.

Sequence 355 AA;

DB 8; Length 355; Score 43; DB 8 Pred. No. 2.1; 100.0%; Best Local Similarity Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leber's hereditary optic neuropathy; LHON, mitochondrial encephalopathy lactic acidosis and stroke; MELAS; myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroparotective; nootropic; antidiabetic; anticonvulsant; antiarthritic; osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human heat mitochondrial protein as a therapeutic target SegID784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gibson BW, Taylor SW, Glenn GM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitochondrial; human; screening assay; diabetes mellitus;
      0; Indels
   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huntington's disease; osteoarthritis;
                                                                                                                                                                                                                                                                                                     ADJ68978 standard; protein; 383 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-APR-2003; 2003WO-US010870
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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(BUCK-) BUCK INST AGE RES.
9; Conservative
                                                                                                                                    193 ÇİAEGMAFİ 201
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                                                                  1 QIAEGMAFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-2003.
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Warnock DE;
                                                                                                                                                                                                                                                                                                                                                                           ADJ68978;
Matches
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ADJOR 8978

ADJOR 8978

ADJOR 8978

ADJOR 9078

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                      (Beta-galactosidase N-terminal) - (lck gene prod.) fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 43; DB 2; Length 417; llarity 100.0%; Pred. No. 2.4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                    'note= "beta-galactosidase fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; kinase; phosphatase; enzyme; KPP; cytostatic;
                                                                                                                                                                                                                                                                            /note= "lck gene polypeptide"
                                                                                                                                                                                                                               Location/Qualifiers
                                                                                 AAR14201 standard; protein; 417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  derived polypeptides in human cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADN61468 standard; protein; 436 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 4,2; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                    89JP-00338268.
                                                                                                                                13-DEC-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                      221 ÇIAEGMAFI 229
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QIAEGMAFI
                                                                                                                                                                              Multi-cloning site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ14201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 417 AA;
                                                                                                                                                                                                                                                                                                     JP03201994-A
                                                                                                                                                                                                                                                                                                                                                   28-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                           28-DEC-1989;
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                                                                                                                                                                                                                                                                                                                           03-SEP-1991
                                                                                                                                                                                                       Synthetic.
Η.
                                                                                                        AAR14201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADN61468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                  Region
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                                                          RESULT 20
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                                                                     AAR1420
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Gaps

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100.0%; Score 43; DB 7; Length 383; 100.0%; Pred. No. 2.2; cive 0; Mismatches 0; Indels

Query Match 100. Best Local Similarity 100. Matches 9; Conservative Tumour involved gene (TIG) splice variant protein, NV-3.

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Hafalia AJA, Lee S, Murage J, Swarnakar A, Chawla NK, Khare R; Biltott VS, Tran UK, Rankumar J, Gurarjan R, Baughn MR, Gietzen KJ; Yang YG, Chien D, Wang JT, Favero KD, Becha SD, Richardson TW; Jin P, Hawkins PR, Yue H, Lee BA, Marquis JP;
                                                                                                                                                                                                                                                                                                                                                                                                                            New human kinases and phosphatases (KPP), useful for diagnosing, treating
antiarteriosclerotic, anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; thyromimetic; gene therapy; cell proliferative disorder; cancer; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; inflammatory disorder; AIDS; allergy; developmental disorder; Hypothyroidism; Cushing's syndrome; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                       and preventing diseases or conditions associated with the aberrant KPP expression e.g. cancer, AIDS, epilepsy, or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 34; 320pp; English.
                                                                                                                                                                                                                            15-NOV-2002; 2002US-0426713P. 26-NOV-2002; 2002US-0429766P.
                                                                                                                                                                                   30-OCT-2003; 2003WO-US034809
                                                                                                                                                                                                              01-NOV-2002; 2002US-0423226P
                                                                                                                                                                                                                                                         11-FEB-2003; 2003US-0447043P
                                                                                                                                                                                                                                                                                   (INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-390608/36.
                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADN61524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 436 AA;
                                                                                                                             WO2004042022-A2.
                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide.
                                                                                                                                                        21-MAY-2004.
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The present sequence represents a human kinase and phosphatase protein designated KPP-34. Human KPP sequences have cytostatic, anticonvulsant, nootropic, neuroprotective, carticonvulsant, nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic, antinflammatory and thyromannetic activities, and can be used in gene therapy. The human KPP polypeptides and polymucleotides of the invention are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of KPP, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. proliferative (e.g. cancer, atherosclerosis), neurological (e.g. proliferative (e.g. disease, stroke), immune/inflammatory (e.g. AIDS, epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome) disorders, or infections. They are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of KPP. The KPP sequences or their fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polymptides, or in altering the expression of the target polymucleotide and compounds that specifically bind to or modulate the activity of the
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100.0%; Pred. No. 2.6;
iive 0; Mismatches
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274 OIAEGMAFI 282 RESULT 22 셤

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Gaps

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100.0%; Score 43; DB 5; Length 437; 100.0%; Pred. No. 2.6; ive 0; Mismatches 0; Indels

Local Similarity 100. nes 9; Conservative

Best Loc Matches

Sequence 437 AA;

Query Match

disclosed

347 QIAEGMAFI 355

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> (first entry) 15-NOV-2002

ABG79672 ID ABG XX AC ABG XX DT 15-

ABG79672 standard; protein; 437 AA. ABG79672;

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The invention discloses isolated human nucleic acid alternative splicing variants that are all tumour-involved genes (TIGS). The nucleic acids and polypeptides are useful for determining the level of a nucleic acid or polypeptide are useful for determining the level of a nucleic acid or polypeptide sequence in a biological sample, for determining the level or or polypeptide sequence in a biological sample, for determining the level of variant sequence in a first biological sample and the level of the original sequence in a first biological sample and for raising antibodies. A pharmaceutical composition comprising a carrier and the nucleic acid, is useful for treating diseases (e.g. cancer) that can be ameliorated or cured by increasing or decreasing the level of the encoded protein. The nucleic carding acids are also useful for diagnostic purposes, especially for detecting cancer or a predisposition to cancer, for evaluating the state or carding pharmaceuticals, for distinguishing various stages in the life cycle of the same type of cells which may be helpful for the development of physiological function of the original TiG, in targeting or development for determining mutations in tumour-involved genes and in gene therapy. The polypeptides are useful for identifying compounds capable of binding to the variant produce and modulating its activity and for modulating endothelial differentiation and proliferation, as well as to modulating employed either avivo or in vivo. The sequences presented in condulating employed either avivo or in vivo. The sequences presented in the proprosis either avivo or in vivo. The sequences presented in the proprosis either avivo or in vivo. The sequences presented in the proprosis either avivo or in vivo. The sequences presented in the proprosis either avivo or in vivo. The sequences presented in the proprosis either avivo or in vivo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modulate apoptosis either ex vivo or in vivo. The sequences presented i
ABG796700-ABG79705 are the new variants (NV) 1-36 proteins of the TIGs
                                                           Human; splice variant; tumour-involved gene; TIG;
pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
endothelial cell; cell differentiation; cell proliferation; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid sequence, which is an alternative splicing variant tumor involved genes, useful for detecting cancer, predisposition to cancer, for evaluating cancer state and in gene therapy for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 68-69; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Romano C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid sequence,
tumor involved genes, useful
                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2000; 2000IL-00135402.
16-MAY-2000; 2000IL-00136154.
                                                                                                                                                                                                                                                                                                                      13-MAR-2001; 2001US-00805020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Levine Z, David A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROMANO C.
BERNSTEIN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-635679/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                   LEVINE Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAVID A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABS65202
                                                                                                                                                                                                                             JS2002086384-A1
                                                                                                                                     gene therapy
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                        04-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ROMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                   (LEVI/)
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The invention relates to a novel method for screening an oncogene. The method comprises producing a cDNA library for a fusion DNA, comprising a cDNA encoding the PNT region of TEL connected downstream of a vector promoter, introducing the produced cDNA library into a host cell.

Expressing the fusion DNA, selecting the transformed cells and analyzing the bease sequence of the fusion DNA in the transformed cells and analyzing dentifying the fusion DNA as an oncogene. TEL is a transcription factor which belongs to the Ets family and is known to form various genes and custon bear and chromosomal translocation in cancer cells, such as coccurs in some cases of leukemia. The method of the invention may be useful for screening a substance which suppresses the proliferative cuseful for screening a substance which suppresses the proliferative activity of a kinase gene introduced into the cell and screening a substance for the treatment of cancer. The current sequence is that of the human transcription factor TEL-ECO-RI adapter-HCK kinase (residues 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening oncogene, by producing cDNA library having fusion DNA comprising cDNA encoding PNT region of TEL connected to downstream of promoter, introducing library into host cell, expressing fusion DNA and selecting transformed cells.
                                                                                                                                                                                                oncogene; cancer; cytostatic; neoplasm; TEL; transcription factor; fusion protein; hck tyrosine kinase; enzyme.
                                                                                                                                                         Human transcription factor TEL-Eco-RI-HCK kinase fusion protein 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227) fusion protein of the invention.
                                    ADY52642 standard; protein; 438 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page; 216pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                07-AUG-2003; 2003JP-00206534.
                                                                                                                                                                                                                                                                                                                                                                                                                                         07-AUG-2003; 2003JP-00206534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-187380/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 438 AA;
                                                                                                                                                                                                                                                                                                                  JP2005052018-A.
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                19-MAY-2005
                                                                                                                                                                                                                                                                                                                                                           03-MAR-2005.
                                                                                                                                                                                                                                                                               Synthetic.
                                                                           ADY52642;
RESULT 23
                ADY52642
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ö Gaps ; 0 100.0%; Score 43; DB 9; Length 438; 100.0%; Pred. No. 2.6; ive 0; Mismatches 0; Indels 9; Conservative Sest Local Similarity Query Match Matches

276 QIAEGMAFI 284 1 QIAEGMAFI 9 ò В ADC99048 standard; protein; 458 AA. ADC99048;

01-JAN-2004 (first entry)

immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological; antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective; osteopathic; antiarthritic, antiparasitic; antihelminthic; antipacoriatic; urropathic; ophthalmological; antiparasitic; haemostatic; antibacterial; virucide; protozoacide; fungicide; kinase; phosphatase; KPP; call proliferative disorder; atherosclerosis; cirrhosis; hepatitis; cancer; developmental; mental retardation; neurological; phosphater; Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's; diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan; helminthic infection; transgenic; gene therapy; human; enzyme. antiparkinsonian; nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic; antianaemic; anti-HIV; antiallergic; antiinflammatory; Human KPP protein - SEQ ID 1. 17-OCT-2002; 2002WO-US033723. 2001US-0343910P. 2001US-0333098P. 2001US-0332424P. 2001US-0345474P 30-NOV-2001; 2001US-0334288P (INCY-) INCYTE GENOMICS INC WO2003033680-A2. Homo sapiens. 19-OCT-2001; 13-NOV-2001; 16-NOV-2001; 02-NOV-2001; 24-APR-2003.

Tang YT; Yao MG, Yue H; Lee SY; Arvizu CS; Duggan BM; Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Grif Guruzajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Ramkumar J, Rec Thornton MB, Tr Zebarjadian Y;

WPI; 2003-403214/38. N-PSDB; ADC99100 New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.

Claim 1; SEQ ID NO 1; 424pp; English.

The invention relates to a novel isolated polypeptide which is a human kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides, agonists and antegonists are useful for dagnosing, treating or preventing cell proliferative disorders such as atherosclerosis, cirrhosis, hepatitis and cancer, developmental disorders e.g. mental retardation, neurological disorders including Alzheimer's disease and Parkinson's disease and inflammatory disorders such as Crohn's disease and diabetee mellitus and finally, viral, bacterial, fungal, parasitic, protozoan or helminthic infections. Furthermore, the polymucleotides encoding KPP may be useful for creating transgenic animals to model human disease, as well as during gene therapy procedures. The current sequence is that of the human KPP protein of the

Sequence 458 AA;

Gaps .; 0 100.0%; Score 43; DB 7; Length 458; 100.0%; Pred. No. 2.7; 0; Indels ive 0; Mismatches 0; Indels 0; Indels 9; Conservative 1 QIAEGMAFI 9 Local Similarity Query Match Matches

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296 OIAEGMAFI 304 ઠે 셤 Human transcription factor TEL-Eco-RI-HCK kinase fusion protein 5. oncogene; cancer; cytostatic; neoplasm; TEL; transcription factor; fusion protein; hck tyrosine kinase; enzyme.

ADY52641 standard; protein; 465 AA.

19-MAY-2005 (first entry)

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0XCCCCCCCCCCCCCX8X4444XX8XX4X4X4XX8XXXXX8XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel isolated NOVX polypeptide. A polypeptide of the invention has cytostatic, antidiabetic, anorectic, CNS-gen., cardiovascular-gen., and antiinflammatory activity. A polymucleotide encoding a polypeptide of the invention may have a use in gene therapy, and antisense therapy. The methods and compositions of the present invention are ugeful for the diagnosis and treatment of disorders associated with aberrant expression or activity of the NOVX polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS, cardiovascular and inflammatory disorders. They can also be used in various detection and screening assays, chromosome mapping, tissue typing and predictive medicine. The present sequence represents a NOVX polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polypeptides (NOVX) and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                           Guo X;
                                                                                                                                human; cytostatic; antidiabetic; anorectic; CNS; cardiovascular; antiinflammatory; gene therapy; antisense therapy; cancer; diabetes; obesity; endocrine disorder; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                           Gorman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 43; DB 8; Length 458; 100.0%; Pred. No. 2.7; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Catterton E, Edinger SR, Li L, Rieger DK, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; SEQ ID NO 58; 267pp; English.
                                 ADJ71657 standard; protein; 458 AA.
                                                                                                         Human NOV5a protein SEQ ID NO:58.
                                                                                                                                                                                                                                                                           07-AUG-2002; 2002US-0401597P.
09-AUG-2002; 2002US-0402848P.
12-AUG-2002; 2002US-0402815P.
13-AUG-2002; 2002US-0403485P.
14-AUG-2002; 2002US-0403574P.
15-AUG-2002; 2002US-040822P.
20-AUG-2002; 2002US-040822P.
27-AUG-2002; 2002US-0406822P.
                                                                                                                                                                                                                                                       07-AUG-2003; 2003WO-US024788
                                                                                                                                                                                                                                                                                                                                                                            2003US-00406392
                                                                                 (first entry)
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Kekuda 1
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N-PSDB; ADJ71656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 458 AA;
                                                                                                                                                                                                        WO2004015076-A2
                                                                                                                                                                                                                                                                                                                                                                            06-AUG-2003;
                                                                                 06-MAY-2004
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Herrmann JL,
                                                                                                                                                                                                                                19-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention.
                                                           ADJ71657;
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Screening oncogene, by producing cDNA library having fusion DNA comprising cDNA encoding PNT region of TEL connected to downstream of promoter, introducing library into host cell, expressing fusion DNA and selecting transformed cells.

07-AUG-2003; 2003JP-00206534. 07-AUG-2003; 2003JP-00206534 (KYOW) KYOWA HAKKO KOGYO KK

JP2005052018-A.

03-MAR-2005

Homo sapiens

Synthetic.

WPI; 2005-187380/20

N-PSDB; ADYS2599

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The invention relates to a novel method for screening an oncogene. The method comprises producing a cDNA library for a fusion DNA, comprising a cDNA encoding the PWT region of TEL connected downstream of a vector promoter, introducing the produced cDNA library into a host cell, cxpressing the fusion DNA selecting the transformed cells and analyzing the base sequence of the fusion DNA in the transformed cell, and thus cidentifying the fusion DNA in the transformed cell, and thus the base sequence of the fusion DNA in the transformed cell, and thus confirmed to the Ets family and is known to form various genes and fusion genes via a chromosomal translocation in cancer cells, such as coccurs in some cases of lenkemia. The method of the invention may be useful for screening a substance which suppresses the proliferative property of a kinase gene introduced into the cell and screening a cubstance for the treatment of cancer. The current sequence is that of the human transcription fearcor Tells. Eco-RI adapter-HCK kinase (residues 1-200) fusion protein of the invention.
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Disclosure; Page; 216pp; Japanese.
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9; Conserve
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9; Conservative

Local Similarity

Query Match

296 QIAEGMAFI 304

26 RESULT

1 QIAEGMAFI 9

ઠે g 02-MAY-2005; 2005WO-US014965.

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                                                                                                                                                                                                                                                                                                         The invention relates to a novel method for screening an oncogene. The method comprises producing a CDNA library for a fusion DNA, comprising a CDNA region of TEL connected downstream of a vector connected downstream of a vector promoter, introducing the produced CDNA library into a host cell, cap a sequence of the fusion DNA, selecting the transformed cells and analyzing the base sequence of the fusion DNA in the transformed cell, and thus identifying the fusion DNA as an oncogene. TEL is a transcription factor which belongs to the Ets family and is known to form various genes and fusion genes via a chromosomal translocation in cancer cells, such as cocurs in some cases of leukemia. The method of the invention may be useful for screening a substance which inhibits the property of a cancer cell, screening a substance which inhibits the activity of a kinase gene introduced into the cell and screening a cubstance for the treatment of cancer. The current sequence is that of the human transcription factor TEL-Eco-RI adapter-HCK kinase (residues 1-6194) fusion protein of the invention.
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                                                                                                                                                                                                                             Screening oncogene, by producing cDNA library having fusion DNA comprising cDNA encoding PNT region of TEL connected to downstream of promoter, introducing library into host cell, expressing fusion DNA and selecting transformed cells.
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 oncogene; cancer; cytostatic; neoplasm; TEL; transcription factor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; microarray; hybridoma; monoclonal antibody; screening;
RNA interference; diagnosis; cytostatic; neoplasm; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 43; DB 9; Length 471; 100.0%; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
             fusion protein; hck tyrosine kinase; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEE05159 standard; protein; 504 AA
                                                                                                                                                                                                                                                                                    Disclosure, Page, 216pp, Japanese.
                                                                                                                     07-AUG-2003; 2003JP-00206534.
                                                                                                                                            07-AUG-2003; 2003JP-00206534.
                                                                                                                                                                 (KYOW ) KYOWA HAKKO KOGYO KK
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                                                                                                                                                                                        WPI; 2005-187380/20.
N-PSDB; ADY52598.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 471 AA;
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                                                                      JP2005052018-A.
                                    Homo sapiens
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                                                  Synthetic.
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The invention relates to new isolated cancer-associated nucleic acid and polypeptide sequences. Also included are the following: a host cell comprising the recombinant nucleic acid or expression vector; an expendinant nucleic acid or expression vector; an expendinant nucleic acid comprising at least 10 contiguous nucleotides of the sequence given in the specification; an isolated polypeptide encoded within an open reading frame of a CA sequence; an isolated antibody or its antigen is binding frame of a CA sequence; an isolated antibody or its antigen control antibody; a kit for detecting cancer cells comprising the attribody; a kit for disposing the presence of cancer in a test sample, comprising at least one polynucleotide that selectively hybridizes to a CA polynucleotide sequence; a method for detecting a presence or an absence of cancer cells in an individual; an electronic library comprising the polynucleotide or polypeptide sequence; or its fragment comprising the polynucleotide or polypeptide sequence; or its complement; a method of screening for anticancer activity; a method for accenting for a bloactive agent capable of modularing the cativity of a CA protein (CAP), where the CAP is encoded by the nucleic actid sequence given in the specification; a method for diagnosing cancer; and a method for inhibiting expression of a cancer associated (CA) gene in a cell comprises contacting a cancer casociated (CA) gene in a cell comprises contacting a sequence cancer associated (CA) gene in a cell comprises contacting a cell expression of a cancer associated (CA) gene in a cell comprises contacting a sequence cancer associated (CA) gene in a cell comprises contacting a sequence cancer associated (CA) gene in a cell comprises contacting a sequence cancer cancer associated (CA) gene in a cell comprises contacting a sequence cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer canc
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                                                                                                                                                                                                                                                                                                                                                                                                       New cancer-associated (CA) polynucleotide comprising at least 10 contiguous nucleotides, useful in preparing a composition for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                 Fattaey A;
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30-APR-2004; 2004US-00836956
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                                                                                                                                                                       Malandro
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                                                                                                                                                                                                                                                                     WPI; 2005-769640/78.
                                                                          (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or treating cancer.
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                                                                                                                                                                            Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB99332;
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New antisense oligonucleotides targeted to nucleic acids encoding hematopoietic cell protein tyrosine kinase, useful for diagnosing treating cancer (e.g. leukemia), inflammation, diabetes or viral

infections

04-DEC-2001; 2001US-00007010. 04-DEC-2001; 2001US-00007010

03-JUL-2003

Borchers AH, Dobie KW; (ISIS-) ISIS PHARM INC.

2003-811000/76. N-PSDB; AAD62155

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New proteins which bind to human tyrosine kinase Hck for promotion of apoptosis and for the elucidation of the mechanism of Hck signal
                                    Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck; tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1; Hck signal transduction; human immunodeficiency virus; HIV infection;
                 Human tyrosine kinase Hck protein sequence SEQ ID NO:11.
                                                                                                                                                                                                                                                                                            Example 1; Page 33-35; 45pp; Japanese
                                                                                                                                                   26-OCT-2000; 2000WO-JP007500.
                                                                                                                                                                       99JP-00309957
 23-AUG-2001 (first entry)
                                                                                                                                                                                                             Taniyama T, Narita T;
                                                                                                                                                                                                                                 WPI; 2001-316440/33
                                                                                                                                                                                         (SSSE ) SSP CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 505 AA;
                                                                                                          WO200132869-A1.
                                                                                       Homo sapiens.
                                                                                                                                                                       29-OCT-1999;
                                                                                                                                                                                                                                                                        transduction
                                                                                                                               10-MAY-2001
                                                                     anticancer
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The present invention describes a protein, designated HSB-1, which binds to human tyrosine kinase Hck. Also described are: (1) nucleic acids encoding the protein and its derivatives; (2) recombinant vectors containing the nucleic acids; and (3) host cells transformed by the vectors and expressing the protein. HSB-1 has cytostatic activity, binds tyrosine kinase, enhances tumour necrosis factor alpha and promotes apoptosis. HSB-1 proteins are used for the elucidation of the mechanism of Hck signal transduction and of the role of Hck in human immunodeficiency virus (HIV) infection. They can be used for the transfunct of infections and other diseases with which Hck is associated. They promote the anticancer activity of tumour necrosis factor alpha. The present sequence represents the human tyrosine kinase Hck protein, which is used in an example from the present invention
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0; Indels Mismatches ö 9; Conservative σ Matches g

343 QIAEGMAFI 351

ABW01407 standard; protein; 505 AA (first entry) 15-JAN-2004 ABW01407; RESULT 30
ABW01407
ID ABW01
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AC ABW01
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DT 15-JA
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Human haematopoietic cell tyrosine kinase protein.

Haematopoietic cell; tyrosine kinase; hyperproliferative disorder; cancer; therapy; inflammation; diabetes; viral infection; inflammation; tumour; cytostatic; virucide; antisense therapy; human; enzyme.

Homo sapiens.

US2003125275-A1

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The invention relates to a compound targetted to a nucleic acid molecule encoding haematopoietic cell protein tyrosine kinase. The compound inhibits the expression of haematopoietic cell protein tyrosine kinase and it specifically hybridises with the nucleic acid molecule encoding the tyrosine kinase or with at least an 8-nucleobase portion of an active site on the nucleic acid molecule encoding the tyrosine kinase. The antisense compounds are useful for mcdulating the expression of haematopoietic cell protein tyrosine kinase and treating diseases or conditions associated with the expression of the tyrosine kinase, such as hyperproliferative disorders (e.g. cancer), inflammation, diabetes or a viral infection. The antisense compounds are also useful for diagnostics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapeutics, prophylaxis, e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The present sequence is human haematopoietic cell tyrosine
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                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 28-30; 59pp; English.
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Best Local Similarity
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Search completed: June 29, 2006, 09:13:00 Job time: 91.8313 secs

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ALIGNMENTS

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protein-tyrosine kinase (BC 2.7.1.112) tkl (similarity) - chicken
N;Alternate names: kinase-related transforming protein (tkl); T-cell surface antigen ass
C;Species: Gallus gallus (chicken)
C;Daces: Gallus gallus (chicken)
C;Accession: A42126; A3939
R;Chow, L.M.; Ratcliffe, M.J.; Veilletre, A.
Mol. Cell. Biol. 12, 1226-1233, 1992
A;Title: tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene.
A;Reference number: A42126; MUID:92186854; PMID:1545804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Experimental source: thymus, spleen
A, Experimental source: thymus, spleen
A, Note: sequence extracted from NGBI backbone (NCBIN:88831, NCBIP:88833)
B, Note: sequence extracted from NGBI backbone (NCBIN:88811, NCBIP:88833)
B, NCBI Acad. Sci. U.S.A. 84, 8778-8782, 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987
A, Title: Additional member of the protein-tyrosine kinase family: the src-and lck-relate
A, Reference number: A39939; MUID:88097370; PMID:3321053
A, Accession: A39939
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A;Residues: 52-507 <STR>
A;Residues: 52-507 <STR>
A;Cross-references: UNIPARC:UP100001713B3; GB:J03579; NID:g212712; PIDN:AAA49081.1; PID:
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Reywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;66-114/Domain: SH3 homology <SH3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;241-499/Domain: protein kinase homology <KIN>
F;249-257/Region: protein kinase ATP-binding morif
F;240-257/Region: protein kinase ATP-binding morif
F;22/Godified site: myristylated amino end (Gly) (in mature form) #status predicted
F;392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi
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A,Reference number: 148845; MUID:86146842; PMID:3081813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Stacus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-500 
A;Residues: 1-500 
A;Cross-references: UNIPROT:Q91X65; UNIPARC:UPI000000418D; EMBL:X03533; NID:g54813; PIDN
B;Marth, J.D.; Peet, R.; Krebs, E.G.; Perimutter, R.M.
Cell 43, 393-404, 1985
A;Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpress A;Reference number: A23639; MUID:86079521; PMID:2416464
A;Accession: A23639.
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A; Residues: 1-282, VP, 285-509 < MAR>
A; Residues: 1-282, VP, 285-509 < MAR>
A; Residues: 1-282, VP, 285-509 < MAR>
A; Cross-references: UNIPARC:UPIO000172586; GB:MI2056; NID:g198763
A; Note: the sequence is revised in GenBank entry MUSLCK, release 116.0, (PIDN:AAB59674.1)
R; Voronova, A.F.; Adler, H.T.; Sefton, B.M.
Mol. Cell. Biol. 7, 4407-4413, 1987
A; Title: Two lck transcripts containing different 5' untranslated regions are present in A; Reference number: 157629; MUID:88142832; PMID:3501824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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A,Molecule type: DNA
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A; Residues: 1-88 < CHO>
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                                                                                                                                                                                                                                                                                protein-tyrosine kinase (EC 2.7.1.112) hck - human C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Jan. Boc. 1989 # sequence_revision 10-Nov-1995 # text_change 05-Oct.2004
C; Accession: A27811; A27812; JC1149; C38268; S31103
R; Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J.M.; Pettenati, M.J.; Le Beau, M.M.; Dia Molin Cell. Biol. 7, 2267-2275, 1987
A; Title: Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and A; Title: Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and A; Title: Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and A; Maccession: A27811
A; Reference number: A27811
A; Residues: 1-505 < QUIP
A; Cross-references: UNIPROT: P08631; UNIPARC: UP1000015C528; GB: M16591
A; Note: the codon given for 3-Cys (TCG) is inconsistent with the authors' translation Mol. Cell. Biol. 7, 2276-2285, 1987,
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A;Gross-references: GDB:119303; OMIM:142370
A;Map position: 20q11-20q12
A;Introns: 20711, 258/1; 318/1; 343/3; 395/1; 439/1
C;Punction:
C;Function:
C;Superfamily: Tyrosine-protein kinase, prote-oncogene SRC type; protein kinase homology
C;Superfamily: Tyrosine-protein kinase, prote-oncogene SRC type; protein kinase homology
C;Reywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phc
F;2-505/Product: protein-tyrosine kinase hck #status predicted <MAT>
F;2-505/Promain: SH3 homology <SH3>
F;2-320/Domain: SH3 homology <SH2>
F;2-320/Domain: protein kinase homology <KIN>
F;23-497/Domain: protein kinase homology of SH3>
F;32-497/Domain: protein kinase ATP-binding motif
F;3/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: Lys #status predicted
F;309/Binding site: Lys #status predicted
F;309/Binding site: Lys #status predicted
F;300/Binding site: Dys #status predicted
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A; Residues: 1-505 <ZIES.
A; Cross-references: UNIPARC: UPI000015C528; GB:M16592; NID:g183913; PIDN:AAA52644.1; PID:
R; Hradetzky, D.; Strebhardt, K.; Ruebsamen-Waigmann, H.
Gene 113, 275-280, 1992
A; Title: The genomic locus of the human hemopoietic-specific cell protein tyrosine kinas
A; Reference number: JC1149; MUID:92241680; PMID:1572549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of A;Reference number: A27812; MUID:87257943; PMID:3453117
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A; Residues: 157-505
A; Residues: 157-505
A; Residues: 157-505
A; Residues: 157-505
A; Residues: 157-505
Broc. Natl. Acad. Sci. U.S.A. 87, 813-8917, 1990
A; Title: Putative tyrosine Kinases expressed in K-562 human leukemia cells.
A; Reference number: A38268; MUID:91062389; PMID:2247464
A; Reference number: A38268; MUID:91062389; PMID:2247464
A; Reference number: A38268; MUID:91062389; MID:9247464
A; Reference number: A38268; MID:9247464
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A; Reference number: A38268; MID:9247464
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A; Accession: JC1149

A;Accession: A27812

9; Conservative

Local Similarity

Query Match

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~ RESULT A39939 m

PID

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A;Molecule type: mRNA
A;Residues: 'A',316-509 <TRE>
A;Residues: 'A',316-509 <TRE>
A;Cross-references: UNIPARC:UPI000016AF39; EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PII
A;Cross-references: UNIPARC:UPI000016AF39; EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PII
B;Takadera, T.; Leung, S.; Gernone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.;
Mol. Cell. Biol. 9, 2173-2180, 1989
Mol. Cell. Biol. 9, 2173-2180, 1989
A;Title: Structure of the two promoters of the human lck gene: differential accumulatior A;Reference number: A32797; MUID:89313764; PMID:278774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UP100016ABFD; GB:M21510; NID:g187031; PIDN:AAA59501.1; PID: C;Comment: Protein tyrosine kinases play important roles in the control of cell growth a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP C; Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C; Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho F; C=099, Product: protein-tyrosine kinase lck #status predicted <MAT> F; C=09, Product: protein-tyrosine kinase lck #status predicted <MAT> F; C=0.15 / Domain: SH3 homology <SH3> F; C=0.15 / Domain: protein kinase homology <KIN> F; C=0.15 / Domain: protein kinase ATP-binding motif F; C=0.259 / Region: protein kinase ATP-binding motif F; C=0.05 / Region: protein kinase ATP-binding motif F; C=0.05 / Region: protein kinase ATP-binding motif F; C=0.05 / Region: protein kinase ATP-binding motif F; C=0.05 / Region: protein kinase ATP-binding motif F; C=0.05 / Region: protein kinase ATP-binding motif F; C=0.05 / Region: protein kinase ATP-binding motif F; C=0.05 / Region: protein kinase ATP-binding motif F; C=0.05 / Region: protein kinase ATP-binding motif F; C=0.05 / Region: protein kinase ATP-binding motif F; C=0.05 / Region: protein kinase ATP-binding motif F; C=0.05 / Region: protein kinase ATP-binding motif F; C=0.05 / Region: protein kinase ATP-binding motif F; C=0.05 / Region: protein kinase ATP-binding motif R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0.05 / R=0
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A;Residues: 1-50,'V',52-204,'R',206-305,'T',307-503 <REM>
A;Cross-references: UNIPARC:UPI0000170BD7; EMBL:X62345; NID:g57581; PIDN:CAA44218.1; PID
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A;Cross-references: UNIPROT:P50545; UNIPARC:UP1000012C350; GB:S74141; NID:g241436; PIDN.
A;Experimental source: megakaryocyte
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CiSpecies: Rattus norvegicus (Norway rat)
CiJate 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
CiJate 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
CiJate 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
CiJate 10131; S18974
RiOkano, Y.; Sugimoto, Y.; Fukuoka, M.; Matsui, A.; Nagata, K.; Nozawa, Y.
Biochen Biophys. Res. Commun. 181, 1137-1114, 1991
A;Title: Identification of rat cDNA encoding hck tyrosine kinase from megakaryocytes.
A;Reference number: JQ1321; MUID:92109719; PMID:1764064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-35 <TAK>
A; Residues: 1-35 <TAK>
A; Residues: 1-35 <TAK>
A; Cross-references: UNIPARC: UPI000016ABFF; GB: M26692; NID: 9341523; PIDN: AAA59503.1;
A; Cross-references: UNIPARC: UPI00016ABFF; GB: M2.0.7
Mol. Cell. Biol. 8, 3058-3064, 1988
A; Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma
A; Reference number: 157636; MUID: 89096891; PMID: 2850479
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A;Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
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submitted to the EMBL Data Library, December 1991
A;Reference number: $18974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GDB:119360; OMIM:153390
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A;Molecule type: DNA
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A; Molecule type: mRNA
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A/Cross-references: UNIPARC:UP1000016CE9D; GB:M18098; NID:g198766; PIDN:AAA39421.1; PID: R/Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A/Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cell A/Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cell A/Reference number: 157636; MUID:89096891; PMID:2850479
A/Reference number: 157636; MUID:89096891; PMID:2850479
A/Actatus: preliminary; translated from GB/EMBL/DDBJ
A/MOlecule type: DNA
A/Residues: 1-35, VRY *CGAR>
A/Gross-references: UNIPARC:UP100016CE9E; GB:M21511; NID:g198768; PIDN:AAA39422.1; PID: C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C;Reywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming prof F;68-116/Domain: SH2 homology *SH2>
F;241-259/Region: protein kinase APP-binding motif F;243-501/Domain: protein kinase homology <KIN>
F;243-501/Domain: protein kinase homology *KIN>
F;243-501/Domain: myristylated amino end (Gly) (in mature form) #status predicted F;273/Active site: Lys #status predicted
F;273/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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A; Residues: 1-86,'P',88-509 <PER>
A; Residues: 1-86,'P',88-509 <PER>
A; Residues: 1-86,'P', 88-509 <PER>
A; Cross-references: UNIPARC: UPID00163BD5; EMBL:X13529; NID:g34294; PIDN:CAA31884.1; PIL
B; K; Koga, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.
Eur. J. Immunol. 16, 1643-1646, 1986
A; Title: A human T cell-specific cDNA clone (YT16) encodes a protein with extensive home A; Reference number: S07200; MUID:87133831; PMID:3493153
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A;Molecule type: mRNA
A;Residues: 1-205,'ASAITPI',212-257,'RCGW',262,'TTT',266,'T',268-281,'AGRLP',287-503,'ST
A;Cross-references: UNIPARC:UPI000016B09E; EMBL:X05027; NID:g36807; PIDN:CAA28691.1; PID
R;Veillette, A.; Foss, F.M.; Sausville, E.A.; Bolen, J.B.; Rosen, N.
Oncogene Res. 1, 357-374, 1987
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A; Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56(LSTRA). A; Reference number: S07143; MUID:87000726; PMID:3489486
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C;Accession: JQ0152; S07822; S07200; S01879; S07143; A32797; I57636
R;Rouer, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R.
Gene 84, 105-113, 1989
A;Title: Structure of the human 1ck gene: differences in genomic organisation within A;Reference number: JQ0152; MUID:90108697; PMID:2558056
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R;Perlmutter, R.M.; Marth, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.
J. Cell. Biochem. 38, 117-126, 1998
A;Title: Structure and expression of 1ck transcripts in human lymphoid cells.
A;Reference number: S07822; MUID:89123626; PMID:3265417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 43; DB 1; 100.0%; Pred. No. 0.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 9, Conservative
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C;Date: 30-58p-1992 #sequence
C;Accession: JQ0152; S07822;
R;Rouer, E; Van Huynh, T.; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OIAEGMAFI 355
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A; Residues: 1-509 <ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA
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A;Map position: 8p23-8p22
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; tyro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Yi, T.; Bolen, J.B.; Ihle, J.N.
Mol. Cell. Biol. 11, 2391-2398, 1991
A;Title: Hematopoietic cells express two forms of lyn kinase differing by 21 amino acids A;Reference number: A39750; MUID:91203857; PMID:2017160
A;Accession: A39750
A;Accession: A39750
A;Accession: A39750; MUID:91203857; PMID:2017160
A;Accession: A39750
A;Accession: A39750
A;Cross-references: UNIPARC:UPI000016CEBF; GB:M57696; NID:9198940; PIDN:AAA39471.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Mesidues: 1.24,46-76,F',78-160,'I',162-278,'L',280-390,'I',392-424,'D',426-512 <YI2>
A; Kesidues: 1.24,46-76,'F',78-16000016CEC0; GB:MS7697; NID:g198942; PIDN:AAA39472.1; PID::
C; Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C; Keywords alternative splicinis, ARP; autophosphorylation; blocked amino end, lipoprote
F:1-21/Product: protein-tyrosine kinase lyn, long splice form #status predicted
F:1-24,46-512/Product: protein-tyrosine kinase lyn, short splice form #status predicted
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A;Residues: 1-512 <STA1>
A;Cross-references: UNIPROT:P25911; UNIPARC:UP1000016CEBE; GB:M64608; NID:g198938; PIDN:
A;Accession: B39719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein-tyrosine kinase (EC 2.7.1.112) lyn, long splice form - mouse
N.Contains: protein-tyrosine kinase lyn, short splice form
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Musculus (house mouse)
C.Species: Musculus 139719; May 139750; B39750
R.Species: Musculus 139719; Musculus 139919; Musculus II; Holtzman, D.A.; Lock, P.; Dunn, A.R.
Mol. Cell. Biol. 11, 3399-3406, 1991
A.Title: Alternatively spliced murine lyn mRNAs encode distinct proteins.
A.Reference number: A39719; MulD:91260683; PMID:1710766
                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: UNIPROT: P51451; UNIPARC: UP10000163B22; EMBL: Z33998; NID: 9601951;
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F;129-226/Domain: SH2 homology <8H2>
F;258-564/Domain: SH2 homology <8H2>
F;258-564/Pomain: protein kinase homology <KIN>
F;253-264/Region: protein kinase ATP-binding motif
F;27/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;65-113/Domain: SH3 homology <SH3>
F;124-220/Domain: SH2 homology <SH2>
F;124-220/Domain: Protein Kinase homology <KIN>
F;237-457/Domain: protein Kinase homology <KIN>
F;247-255/Region: protein Kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;269/Active site: Lys #status predicted
06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Oct-2004
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                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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Pred. No. 2.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:454114; OMIM:191305
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88.9%;
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A; Residues: 1-24,46-512 <STA2>
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Matches 8; Conserv
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                                   A;Gene: hck
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro
N;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro
N;Kinase
F;62-110/Domain: SH3 homology <8H3>
F;121-218/Domain: SH2 homology <8H2>
F;121-218/Domain: SH2 homology <8H3>
F;237-455/Domain: protein kinase homology <KIN>
F;245-253/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
                                                                                                                                                                                                                                                                                                                                                                           F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;267/Active site: Lys #status predicted
F;388/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology; Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phd;62-110/Domain: SH3 homology <SH3>
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A;Residues: 1-503 <HOL>
A;Cross-references: UNIPARC:UPI0000018DD; GB:J03023; NID:g192212; PIDN:AAA37305.1; PID:
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F;237-495/Domain: protein kinase homology <KIN>
F;237-495/Domain: protein kinase homology <KIN>
F;245-253/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;3/Active site: Lys #status predicted
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C;Dacte: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C;Dacte: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C;Accession: A.7282. A39973
R;Klemsz, M.J.; McKercher, S.R.; Maki, R.A.
Nucleici Cacida Res. 15, 9600, 1987
A;Title: Nucleotide sequence of the mouse hck gene.
A;Title: Nucleotide sequence of the mouse hck gene.
A;Reference number: A27282; MUID:88067781; PMID:3684607
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88.9%; Pred. No. 2.4;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 1; Length 503;
Pred. No. 2.4;
1; Mismatches 0; Indels
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Proc. Natl. Acad. Sci. U.S.A. 84, 8325-8329, 1987
A;Title: Isolation and sequence of a cDNA corresponding
A;Reference number: A39973; MUID:88068587; PMID:3317404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein-tyrosine kinase (EC 2.7.1.112) blk - human C;Species: Homo sapiens (man)
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Similarity 88.9%;
8; Conservative
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Conservative
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les 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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A;Molecule type: mRNA
A;Residues: 1-503 <KLE>
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A;Title: The yes-related cellular gene lyn encodes a possible tyrosine kinase similar to A;Reference number: A26719; MUID:87172710; PMID:3561390
A;Accession: A26719
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A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells. A;Reference number: A38268; MUID:91062389; PMID:2247464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RiBielke, W.; Ziemieki, A.; Kappos, L.; Miescher, G.C.
Blochem. Biophys. Res. Commun. 186, 1403-1409, 1992
A;Title: Expression of the B cell-associated tyrosine kinase gene lyn in primary neurobl
A;Reference number: PH0949; MUID:92378604; PMID:1510669
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A;Cross-references: UNIPARC:UPI000016AC37; GB:M79321; NID:g187270; PIDN:AAB50019.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP C; Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C; Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote yrosine-specific protein kinase kinase lyn, splice form A #status predicted <WATA> F; 2-24,46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <WATA> F; 2-24,46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <WATF: 2129-226/Domain: SH2 homology <SH3> F; 225-26/Domain: protein kinase homology <KIN> F; 245-504/Domain: protein kinase homology <KIN> F; 253-26/Region: protein kinase ATP-binding motif
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F;245-504/Domain: protein kinase homology <KIN>
F;245-501/Region: protein kinase ATP-binding motif
F;253-261/Region: protein kinase ATP-binding motif
F;2/Modified site: myristlylated amino end (Gly) (in mature form) #status predicted
F;3/Modified site: palmitate (Cys) (covalent) #status predicted
F;275/Active site: Lys #status predicted
F;275/Active site: Lys #status predicted
F;397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Experimental source: neuroblastoma SK-IN cell
R, Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.
Gane 138, 219-222, 1994
A, Title: The CDNAs encoding two forms of the LYN protein tyrosine kinase are expressed A, Reference number: I53715; MUID:94171041; PMID:8125304
A, Accession: I53715
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C;Species: Xiphophorus helleri
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 05-Oct-2004
C;Accession: IS1593
R;Hannig, G2, Ottilie, S2; Schartl, M.
Oncogene 6, 361-369, 1991
A;Title: Conservation of structure and expression of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of structure and expression of the c-yes and fyn genes in lower of structure and expression of the c-yes and fyn genes in lower of structure and expression of the c-yes and fyn genes in lower of structure and expression of the c-yes and fyn genes in lower of structure and expression of the c-yes and fyn genes in lower of structure and expression of the c-yes and fyn genes in lower of structure and expression of the c-yes and fyn genes in lower of structure and expression of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of the c-yes and fyn genes in lower of the c-yes and fyn genes of the c-yes and fyn genes in lower of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes of the c-yes and genes 
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Pred. No. 2.4;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GDB:120159; OMIM:165120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 369-424 <PAR>
A;Cross-references: UNIPARC:UP10000172583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 369-424 <BIE>
A;Cross-references: UNIPARC:UP10000172583
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              Cell. Biol. 7, 237-243, 1987
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C; Function:
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Best Local Similarity
                                                                                                                                                                                                      A; Molecule type: mRNA
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A,Title: Bacterially expressed rat p56lyn binds several proteins in rat basophilic leuke
A,Reference number: 156160
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A,Residues: 1-230,'L',232-307,'A',309-418,'Y',420-512 <RIDI>
A,Cross-references: UNIPARC:UPI0000170BE3; GB:L14782; NID:9294578; PIDN:AAA20944.1, PID:
A,Note: in Genbank entry RATLYNATYR, release 116.0, PIDN:AAA20944.1, the source is desig
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A;Cross-references: UNIPARC:UPI0000170BE2; GB:L14823; NID:g294580; PIDN:AAA20945.1; PID:A;Note: in Genbank entry RATIYNBTYR, release 116.0, PIDN:AAA20945.1, the source is desig C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C;Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote F;2-512/Product: protein-tyrosine kinase lyn, splice form A #status predicted <MATA>
F;2-24,46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <MATA>
                                                         (by autophosphorylation) #status pred
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N;Contains: protein-tyrosine kinase lyn, splice form B
C;Species: Homo sapiens (man)
C;Deters: Homo sapiens (man)
C;Actession: A26719; D38268; PH0949; IS3715
C;Accession: A26719; D38268; PH0949; IS3715
R;Yamanashi, Y.; Fukushige, S.I.; Semba, K.; Sukegawa, J.; Miyajima, N.; Matsubara, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q07014; UNIPARC:UP10000167AC2; GB:L14951; NID:g294582; PIDN:R;Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.
Gene 138, 219-222, 1994
A;Title: The CDNAs encoding two forms of the LYN protein tyrosine kinase are expressed in A;Reference number: I53715; MUID:94171041; PMID:8125304
A;Accession: I67811
A;Status: preliminary; translated from GB/EMBL/DDBJ
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;233-261/Region: protein kinase ATP-binding motif
;273-261/Region: protein kinase ATP-binding motif
;275/Active site: myristylated amino end (Gly) (in mature form) #status predicted
;275/Active site: Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - rat N;Contains: protein-tyrosine kinase lyn, splice form B C;Species: Rattus norvegicus (Norway rat C;Species: Rattus norvegicus (Norway rat C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004 C;Accession: 156160; 167811; 167812
5:Minnoguchi, K.; Nishikata, H.; Siraganian, R.P.
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                                                                                                                                                Length 512;
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                                                                                                                                                Score 40; DB 1;
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Pred. No. 2.4;
1; Mismatches
F;275/Active site: Lys #status predicted F;397,508/Binding site: phosphate (Tyr) (covalent)
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                                                                                                                                                                                            Pred. No. 2.4;
1; Mismatches
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88.9%;
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Best Local Similarity 85...
8; Conservative
                                                                                                                                            Query Match
Best Local Similarity 88.5
Matches 8; Conservative
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A; Residues: 1-512 <MIN>
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Length 528;

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C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; tran
F;88-137/Domain: SH3 homology <SH3>
                                                                                                                                                                                                                                                                                                                                            F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;265-523/Domain: protein kinase ATP-bincing motif
F;273-281/Region: protein kinase ATP-bincing motif
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Steele, R.E.; Irwin, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B. Oncogene Res. 1, 223-233, 1989
A;Title: The yes proto-oncogene is present in amphibians and contributes to the maternal A;Reference number: A45501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-250,'S',252-537 <ST2>
A;Cross-references: UNIPARC:UPI000013ACB9; EMBL:X14377; NID:g65272; PIDN:CAA32551.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: yes
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming prof
F;92-141/Domain: SH3 homology <SH3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;152-249/Domain: SH2 homology <SH2>
F;269-527/Domain: protein kinase homology <KIN>
F;277-285/Region: protein kinase ATP-binding motif
F;277-285/Region: protein kinase ATP-binding motif
F;277-285/Region: protein kinase ATP-binding motif
F;29/Acdified site: myristylated admino end (Gly) (in mature form) #status predicted
F;299/Active site: Lys #status predicted
F;420,531/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein-tyrosine kinase (EC 2.7.1.112) yes [similarity] - African clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.Alternate names: kinase-related transforming protein (yes)
C.Species: Xenopus laevis (African clawed frog)
C.Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C.Accession: A45501, S08517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P10936; UNIPARC:UP10000172588; GB:X14377 R;Steele, R.E.; Irwin, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B. submitted to the EMBL Data Library, February 1989
                                                                                                                                          C, Comment: This protein is synthesized as a gag-yes polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein-tyrosine kinase (EC 2.7.1.112) yes - chicken N;Alternate names: kinase-related transforming protein yes C;Species: Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.0%; Score 37; DB 1; 77.8%; Pred. No. 10; ative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.0%; Score 37; DB 1; 77.8%; Pred. No. 10;
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                                                                                                  A; Cross-references: UNIPARC: UPI000017258B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                    , Molecule type: genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 QIADGMAYI 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 QIADGMAYI 381
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Best Local Similarity
7, Conserve
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Best Local Similarity
7; Conserv?
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                                                                 A, Residues: 1-528 <KIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-537 <STE>
   A; Accession: A00633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S08517
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                                                                                           A;Nolecule type: mRNA
A;Residues: 1-544 <HAN>
A;Rolecule type: mRNA
A;Residues: 1-544 <HAN>
A;Ross-references: UNIPROT:P27447; UNIPARC:UPI000013ACBA; EMBL:X54970; NID:g64483; PIDN
C;Genetics:
A;Gene: Xyes
C;Genetics: Argentamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
C;Keywords: ATP; autophosphorylation; blocked amino end (ilpoprotein; myristylation; pho
F;99-148/Domain: SH2 homology <SH2>
F;79-148/Domain: BH2 homology <SH2>
F;76-534/Domain: protein kinase homology <KIN>
F;76-534/Domain: protein kinase homology <KIN>
F;76-534/Domain: protein kinase homology completed amino end (Gly) (in mature form) #status predicted
F;306/Accive site: Lys #status predicted
F;306/Accive site: Lys #status predicted
F;427,538/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein-tyrosine kinase (EC 2.7.1.112) yes - avian sarcoma virus Y73
C;Species: avian sarcoma virus Y73
A,Note: host Gallus (chicken)
A,Note: host Gallus (chicken)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 05-Oct-2004
C;Accession: A00633
R;Kitamura, N.; Kitamura, A.; Toyoshima, K.; Hirayama, Y.; Yoshida, M.
Nature 27, 205-208, 1982
A;Title: Avian sarcoma virus Y73 genome sequence and structural similarity of its transf A;Reference number: A00633; MUID:82195528; PMID:6281656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: MGI:88169
A,Map position: 14:28.0
S,Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C;Superfamily: Tyrosine-protein kinase homology C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho P;59-107/Domain: SH3 homology <SH3.>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: mRNA
A,Residues: 1-499 <DYM>
A,Cross-references: UNIPROT:P16277; UNIPARC:UPI0000151F18; GB:M30903; NID:g202076; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;233-491/Domain: protein kinase homology <KIN>
F;241-249/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;263/Active site: Lys #status predicted
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C;Species: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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R;Dymecki, S.M.; Niederhuber, J.E.; Desiderio, S.V.
Science 247, 332-336, 1990
A;Title: Specific expression of a tyrosine kinase gene,
A;Reference number: A40092; MUID:90117147; PMID:2404338
A;Accession: A40092
A; Reference number: I51592; MUID: 91187435; PMID: 1707152
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Pred. No. 3.8;
2; Mismatches (
                                                                     preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 2;
Pred. No. 2.6;
1; Mismatches
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88.9%;
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Best Local Similarity
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Best Local Similarity
Matches 7; Conserv
                                        A; Accession: I51593
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C,Genetics:
A,Gene: MGI:Blk
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Gaps

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Length 537; Indels

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F;303/Active site: Lys #status predicted
F;424,535/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status prec
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
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Fig. 543/Product: Drotein-tyrosine kinase yes-1 #status predicted <MAT>
Fig. 184-25/Domain: SH3 homology <SH3>
Fig. 184-25/Domain: SH3 homology <SH2>
Fig. 185-25/Domain: SH2 homology <KIN>
Fig. 185-25/Domain: protein kinase Annology <KIN>
Fig. 186-18/India site: myristylated amino end (Gly) (in mature form) #status predicted
Fig. 186-18/India site: palmitate (Cys) (covalent) #status predicted
Fig. 186-18/India site: Lys #status predicted
Fig. 186-18/India site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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C,Species: feline sarcoma virus
A,Note: host Felis sp. (cat)
C,Date: 27-Nov-1985 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004
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R;Hampe, A.; Gobet, M.; Sherr, C.J.; Galibert, F.
Proc. Natl. Acad. Sci. U.S.A. 81, 85-89, 1984
A;Title: Nucleotide sequence of the feline retroviral oncogene v-fms shows unexpected how
A;Reference number: A00654; MUID:84119469; PMID:6582485
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C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Oct-2004
C;Accession: A26714
R;Sukegawa, J.; Semba, K.; Yamanashi, Y.; Nishizawa, M.; Miyajima, N.; Yaman Mol. Cell. Biol. 7, 41-47, 1987
A;Title: Characterization of cDNA clones for the human c-yes gene.
A;Reference number: A26714; MUID:87172733; PMID:2436037
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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C;Comment: This protein is synthesized as a gag-fms polyprotein.
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                                                                                                                                                            Length
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                                                                                                                                                        5
                                                                                                                                              Score 37; DB 2
Pred. No. 10;
2; Mismatches
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A;Map position: 18p11.31-18p11.22
C;Function:
                                                                                                                                                        86.0%;
77.8%;
                                                                                                                                                   Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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Matches 7; Conservative
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377 QIADGMAYI 385
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QIADGMAYI 387
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N;Alternate names: gene c-yes protein
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 144318; S31645
R;Klages, S.; Adam, D.; Eiseman, E.; Fargnoli, J.; Dymecki, S.M.; Desiderio, S.V.; Bolen Oncogene 8, 713-719, 1993
A;Reference number: 148318
A;Reference number: 148318
A;Accession: 148318
A;Accession: 148318
A;Accession: 148318
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A;Ac
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A; Residues: 1-66, 'IHPLR', 72-81, 'Q', 83-541 < KAP>
A; Residues: 1-66, 'IHPLR', 72-81, 'Q', 83-541 < KAP>
A; Cross-references: UNIPARC: UPI0000171303; EMBL: X13207; NID: g63362; PIDN: CAA31595.1; PID
R; Sudol, M.; Kieswetter, C.; Zhao, Y.H.; Dorai, T.; Wang, L.H.; Hanafusa, H.
Nucleic Acids Res. 16, 9876, 1988
A; Title: Nucleotide sequence of a CDNA for the chick yes proto-oncogene: comparison with
A; Reference number: S01689; MUID: 89041591; PMID: 3054816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology; Reywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phd. 2-541/Product: protein-tyrosine kinase yes #status predicted <MAT>
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C,Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C,Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;96-145/Domain: SH3 homology <SH3>
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C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase home
C;Superfamily: Tyrosine-protein, blocked amino end; lipoprotein; myristylation
C;Seywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation
F;2-541/Product: protein-tyrosine kinase yes #status predicted <MAT>
F;96-145/Domain: SH3 homology <SH3>
F;26-145/Domain: SH2 homology <SH3>
F;213-531/Domain: protein kinase HPP-binding motif
F;213-531/Domain: protein kinase ATP-binding motif
F;21-045/Region: protein kinase ATP-binding motif
F;21-045/Region: protein kinase ATP-binding motif
F;21-05/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status
F;303/Active site: Lys #status predicted
F;303/Active site: Lys #status predicted
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F;156-253/Domain: SH2 homology <SH2>
F;273-531/Domain: protein kinase hology <KIN>
F;281-289/Region: protein kinase ATP-binding motif
F;281-289/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
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C;Date: 30-Jun-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004 C;Accession: S03134; S05283; S01689 R;Zheng, X.; Podell, S.; Sefton, B.M.; Kaplan, P.L. Oncogene 4, 99-104, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                    A;Title: The sequence of chicken c-yes and p61(c-yes). A;Reference number: S03324; MUID:89128204; PMID:2464785
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A;Residues: 1-237, S',239-541 <SUD>
A;Cross-references: UNIPARC:UP1000017258C; EMBL:X12461
C;Genetics:
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Pred. No. 10;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R, Kaplan, P.L.
submitted to the EMBL Data Library, October 1988
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A;Accession: S05283
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A; Residues: 1-541 <ZHE>
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Best Local Similarity
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R;Browning, P.J.; Bunn, H.F.; Cline, A.; Shuman, M.; Nienhuis, A.W.
Proc. Natl. Acad. Sci. U.S.A. 83, 7800-7804, 1986
A;Title: Replacement' of COOH-terminal truncation of v-fms with c-fms sequences markedly
A;Reference number: I59083; MUID:87017034; PMID:3532121
                                                                                                                                                                                                                                                           A;Status: translated from GB/EWBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Mossides: 874-972 cRES
A;Aresideuse: 874-972 cRES
A;Cross-references: UNIPARC: UPIO000000418; GB:M14193; NID:G182521; PIDN:AAA35834.1; PID::R;Nienhuis, A.W.; Bunn, H.F.; Turner, P.H.; Gopal, T.V.; Nash, W.G.; O'Brien, S.
Cell 142, 421-428, 1985
A;Title: Expression of the human c-fms proto-oncogene in hematopoietic cells and its delay.
A;Reference number: 152772; MUID:85282599; PMID:4028159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: GDB:CSF1R; FMS
A;Gene: GDB:CSF1R; FMS
A;Across-references: GDB:120600; OMIM:164770
A;Map position: 5q33.2-5q33.3
A;Introns: 17/1; 103/1; 198/1; 243/3; 297/1; 361/2; 400/1; 440/2; 504/1; 542/3; 585/1; 6
A;Introns: 17/1; 103/1; 198/1; 243/3; 297/1; 361/2; 400/1; 440/2; 504/1; 542/3; 585/1; 6
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Seywords: AfP: autophosphorylation; glycoprotein; kinase-related transforming protein; fic protein kinase
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;24-972/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT
;24-512/Domain: extracellular #status predicted <EXT>
;35-86/Domain: immunoglobulin homology <IMM1.
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Kfewwords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
fic protein kinase
F;1-19/Pomain: signal sequence #status predicted <SIG>
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A.Cross-references: UNIPARC:UPI000000000605; GB:M11067; NID:g182674; PIDN:AAA35848.1; PID:
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R;Rcthwell, V.M.; Rohrschneider, L.R.
R;Rcthwell, V.M.; Rohrschneider, L.R.
A;Orcogene Res. 1, 311-324, 1987
A;Title: Murine c-fms cDNA: cloning, sequence analysis and retroviral expression.
A;Reference number: S01880; MUID:88217329; PMID:2966922
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F;588-566/Region: protein kinase ATP-binding motifit
4,22-84,127-177,224-278,419-485/Disulfide bonds: #status predicted
F;45,73,153,240,275,302,335,353,412,428,480/Binding site: carbohydi
F;616,633,778/Active site: Ly8, Glu, Asp #status predicted
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A;Residues: 1-976 <ROT>
A;Cross-references: UNIPARC:UPI00001725B2; EMBL:X06369
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F;127-280/Domain: immunoglobulin homology <IMM3>
F;316-383/Domain: immunoglobulin homology <IMM4>
F;412-487/Domain: immunoglobulin homology <IMM5>
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A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Ratius: preliminary; translated from GB/EMBL/DDBJ
A/Ratius: preliminary; translated from GB/EMBL/DDBJ
A/Ratius: 1.16 *RRS
A/Cross-references: UNIPARC:UPI00000060C; GB:M14002; NID:g182676; PIDN:AAA35849.1; PID:
B/Cross-references: UNIPARC:UPI00000060C; GB:M14002; NID:g182676; PIDN:AAA35849.1; PID:
A/Cross-references: UNIPARC:UPI000000060C; GB:M14002; NID:g182676; PIDN:AAA35849.1; PID:
A/Accession: IS7648
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A/Acc
                C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
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                                                                                                                     :1-23/Domain: signal sequence #status predicted <SIG>
24-94-1/Product: protein-tyrosine kinase fms #status predicted
24-509/Domain: extracellular #status predicted <EXT>
35-86/Domain: immunoglobulin homology <IMMl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 1; Length 941;
Pred. No. 18;
3; Mismatches 0; Indels
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Query Match
Best Local Similarity 66.7
Matches 6; Conservative

QVAQGMAFL 767 QIAEGMAFI 9

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C; Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog C; Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein; fic protein kinase
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-380/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MATF;24-509/Domain: extracellular #status predicted <EXT>
F;28-509/Domain: immunoglobulin homology <IMMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                               macrophage colony-stimulating factor 1 receptor precursor - cat N; Contains: protein-tyrosine kinase (EC 2.7.1.112) csflr/fms C; Species: Felis silvestris catus (domestic cat) C; Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #cext_change 05-Oct-2004
                                                                                                                                                                                                                                                          A; Cross-references: UNIPROT: P13369; UNIPARC: UPI000012DDB9; EMBL: X03663
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Pred. No. 19;
                                                                                                     C; Accession: A31636
R; Woolford, J.; McAuliffe, A.; Rohrschneider, L.R.
Cell 55, 965-977, 1988
A; Title: Activation of the feline c-fms proto-oncogene: A; Reference number: A31636; MUID:89077553; PMID:2849512
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Pred. No. 12;
3; Mismatches
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759 QVAQGMAFL 767
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Best Local Similarity
6; Conserve
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A; Residues: 1-980 <WOO>
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Matches 6; Conser
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F;35-66/Domain: immunoglobulin homology <IMM1>
F;120-1795/Domain: immunoglobulin homology <IMM2>
F;120-1795/Domain: immunoglobulin homology <IMM2>
F;316-381/Domain: immunoglobulin homology <IMM3>
F;316-381/Domain: immunoglobulin homology <IMM4>
F;316-515/Domain: immunoglobulin homology <IMM5>
F;410-485/Domain: immunoglobulin homology <IMM5>
F;516-516-515/Domain: irransmembrane #status predicted <IMM5>
F;516-516-516/Domain: protein kinase ATP-binding motif F;58-514/Region: protein kinase ATP-binding motif F;58-54-278 417-483/Domain: protein kinase ATP-binding site: carbohydrate (Asn) (covalent) #status F;573-302,335,389,410,449,478,491/Binding site: carbohydrate (Asn) (covalent) #status F;614,631,776/Active site: Lys, Glu, Asp) #status predicted F;781,794/Binding site: magnesium (Asn, Asp) #status predicted
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Pred. No. 19;
3; Mismatches 0; Indels
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Best Local Similarity 60...
6; Conservative
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759 QVAQGMAFL 767
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protein-tyrosine kinase (EC 2.7.1.112) - feline sarcoma virus (fragment)
NyAlternate names: gag-onc fusion protein
CiSpecies: feline sarcoma virus
CiSpecies: feline sarcoma virus
CiSpecies: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
CiAccession: 804205
R;Kappes, B; Ziemiecki, A.; Mueller, R.G.; Theilen, G.H.; Bauer, H.; Barnekow, A.
Oncogene 4, 363-372, 1989
A;Title: The TP1 isolate of feline sarcoma virus encodes a fgr-related oncogene lacking
A;Reference number: 804205; MUID:89201884; PMID:2539576
A;Accession: S04205.
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A; Residues: 1-392 «KAP»
A; Residues: 1-392 «KAP»
A; Residues: 1-392 «KAP»
A; Cross-references: UNIPROT:Q28414; UNIPARC:UPI00001046DB; EMBL:X14842; NID:g1089; PIDN: C; Superfamily: feline sarcoma virus protein-tyrosine kinase fgr; protein kinase homology C; Keywords: ATP; autophosphorylation; myristylation; oncogene; phosphoprotein; phosphorr F; 7-104/Domain: SH2 homology «SH2»
F; 72-104/Domain: protein kinase homology «KIN»
F; 132-140/Region: protein kinase ATP-binding motif F; 134/Active site: Lys #status predicted
F; 154/Active site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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C; Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C; Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho: P; 72-121/Domain: SH3 homology <SH3.>
P; 132-229/Domain: SH3 homology <SH2.>
P; 249-507/Domain: SH2 homology <SH2.>
P; 249-507/Domain: protein kinase homology <KIN.>
P; 257-265/Region: protein kinase ATP-binding motif P; 277-265/Region: protein kinase ATP-binding motif P; 277-Additied site: myristylated amino end (Gly) (in mature form) #status predicted P; 279/Active site: Lys #status predicted P; 511/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence revision 30-Sep-1989 #text_change 05-Oct-2004
C;Date: 31-Dec-1988 #sequence revision 30-Sep-1989 #text_change 05-Oct-2004
C;Accession. A.27676; Rao, C.D.; Miki, T.; Cheah, M.S.C.; Tronick, S.R.; Robbins, Mol. Cell. Biol. 8, 259-266, 1988
A;Title: Primary structure of the human fgr proto-oncogene product p55(c-fgr).
A;Reference number: A27676; MUID:88094395; PMID:3275868
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R;Inoue, K.; Ikawa, S.; Semba, K.; Sukegawa, J.; Yamamoto, T.; Toyoshima, K.
cocgene I, 301-304, 1987
A;Title: Isolation and sequencing of cDNA clones homologous to the v-fgr oncogene from a A;Reference number: A28353; MUID:88262220; PMID:3330776
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A;Residues: 111-416 <REB>
A;Cross-references: UNIPARC:UPI000016A8FC; GB:M12724; NID:g182581; PIDN:AAA52762.1; PID:«
R)Erickell, P.M.; Patel, M.
Br. J. Cancer 58, 704-709, 1988
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R;Patel, M.; Leevers, S.J.; Brickell, P.M.
Orogene S, 201-206, 1990
A;Title: Structure of the complete human c-fgr proto-oncogene and identification of mult A;Reference number: S24306; MUID:90206622; PMID:1690869
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A;Cross.references: UNIPARC:UP1000017258D
R;Nishizawa, M.; Senba, K.; Yoshida, M.C.; Yamamoto, T.; Sasaki, M.; Toyoshima, K.
R;Nishizawa, M.; Senba, K.; 1986
MOI. Cell. Biol. 6, 511-517, 1986
A;Title: Structure, expression, and chromosomal location of the human c-fgr gene.
A;Reference number: A24842; MUID:87064334; PMID:3023853
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Pred. No. 16;
3; Mismatches
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66.7%;
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Best Local Similarity 66...
6; Conservative
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353 QVAEGMAYM 361
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A; Residues: 1-529 <REA>
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A; Molecule type: mRNA
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mIRNA
A; Molecule type: monocyte tumor cell line from strain Balb/c
R; Yi, T.L.; Willman, C.L.
Cncogene 4, 1081-1087, 1989
A; Title: Cloning of the murine c-fgr proto-oncogene cDNA and induction of c-fgr expressi
A; Accession: S10072
A; Reference number: S10072; MUID: 89385605; PMID: 2674883
A; Accession: S10072
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
C; Superferences: UNIPARC: UPID000028667; EMBL: X16440; NID: 950393; PIDN: CAA34463.1; PIC
C; Superfemily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C; Reywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
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F.249-507/Domain: SH2 homology cSH2>
F.249-507/Domain: protein kinase homology cKIXX>
F.257-265/Region: protein kinase ATP-binding motif
F.27/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F.279/Active site: Lys #status predicted
F.279/Active site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
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                                                                                                                                                                                                                                                                        N'Alternate names: kinase-related transforming protein (fgr)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-43n-1993 #sequence_revision 30-Jan-1993 #text_change 05-Oct-2004
C;Accession: A43807; S10072; A33127
R;King, F.J.; Cole, M.D.
Oncogens F, 337-344, 1990
A;Title: Molecular cloning and sequencing of the murine c-fgr gene.
A;Reference number: A43807; MUD:90191719; PMID:2179817
A;Molecular cloning and sequencing of the murine c-fgr gene.
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: S24547; PT0200
R;Yue, C.C.
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Score 36; DB 2; Pred. No. 16; 3; Mismatches

83.7%; 66.7%;

6; Conservative

Best Local Similarity Matches 6; Conserv

ે g C;Genetics: A;Gene: FGR

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6; Conservative
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627 QVAKGMAFL 635
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Matches 6; Conserv
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NiContains: amino end of core protein p30; core protein p12; core protein p15; protein-t
C,Species: feline sarcoma virus
A,Note: host Felis sp. (cat)
C,Dates: 04-Dec-1986 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C,Accession: A03936; A00655
R,Besmer, P.; Murphy, J.E.; George, P.C.; Qiu, F.; Bergold, P.J.; Lederman, L.; Snyder J
Nature 320, 415-421, 1986
A,Fitle: A new acute transforming feline retrovirus and relationship of its oncogene v-k
A,Reference number: A00655; MUID:86175044; PMID:3007997
Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology 
Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phd
                                                                                                                         F;84-133/Domain: SH3 homology <SH3>
F;144-241/Domain: SH2 homology <SH2>
F;144-241/Domain: SH2 homology <SH2>
F;269-277/Region: protein kinase homology <KIN>
F;269-277/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3,6/Binding site: palmitate (Cys) (covalent) #status predicted
F;291/Active site: Lys #status predicted
F;523/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein-tyrosine kinase (EC 2.7.1.112) fgr - feline sarcoma virus (strain Gardner-Rashee
C;Species: feline sarcoma virus
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A; Oroment: This protein is synthesized as a gag-fgr polyprotein.
C; Comment: This protein is synthesized as a gag-fgr polyprotein.
A; Gene: fgr
C; Superfamily: feline sarcoma virus protein-tyrosine kinase fgr; protein kinase homology
C; Superfamily: feline sarcoma virus protein-tyrosine kinase fgr; protein kinase homology
C; Superfamily: feline sarcoma virus protein-tyrosine kinase fgr; protein kinase homology
F; 1-118/Region: aga polyprotein similarity
F; 141-268/Region: actin similarity
F; 185-382/Domain: SH2 homology skin>
F; 140-418/Region: protein kinase homology skin>
F; 1410-418/Region: protein kinase homology ckin>
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C;Date: 27-Nov-1985 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: A00653; A03937
C;Accession: A00653; A03937
Science 223, 63-66, 1984
A;Title: Gene product of v-fgr onc: hybrid protein containing a portion of actin and a A;Reference number: A00653; MUID:84097512; PMID:6318314
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Pred. No. 21;
3; Mismatches 0; Indels
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Pred. No. 16;
3; Mismatches 0; Indels
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66.78;
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6; Conservative
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Best Local Similarity 60.,
6, Conservative
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| QVAEGMAYM 373
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Best Local Similarity
Matches 6; Conserv
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A;Residues: 1-790 <BES>
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    C;Superfamily:
C;Keywords: ATE
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A;Cross-references: UNIPROT:P04322; UNIPARC:UPI000017101D; GB:X03711; NID:g61535; PIDN:C
C;Genetics:
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N;Alternate names: mast/stem cell growth factor receptor; tyrosine kinase receptor c-kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 31-Mar-1991 #sequence revision 31-Mar-1991 #text change 05-0ct-2004
C; Accession: S01426; PC1015; A41815; B41815; 137948; 156954; 154336
C; Accession: S01426; PC1015; A41815; B41815; 137948; 156954; 154336
R; Yarden, Y; Kuang, W.J; Yang-Feng, T.; Coussens, L.; Munemitsu, S.; Dull, T.J.; Chen, EMBO J. 6, 3341-3351, 1987
A; Title: Human proto-oncogene c-kit: a new cell surface receptor tyrosine kinase for an A; Reference number: S01426; MUID:88111521; PMID:2448137
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A,Residues: 579-583,'L',585-589 <SPR>
A,Cross-references: UNIPARC:UF1000011F7BF; GB:S78819; NID:g244084; PIDN:AAB21234.1; PID:A,Note: sequence extracted from NCBI backbone (NCBIN:78839, NCBIP:78842)
A,Note: disease-related mutant from patient with piebaldism
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A;Cross-references: UNIPARC:UP1000011F7C0; GB:S78843; NID:g244086; PIDN:AAB21235.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:78843, NCBIP:78844)
A;Note: disease-related mutant from patient with piebaldism
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A)Cross-references: UNIPARC:UP1000011F7C1; GB:S78845; NID:9244088; PIDN:AAB21236.1; PID: A)Cross-references: UNIPARC:UP1000011F7C1; GB:S78845; NID:9244088; PIDN:AAB21236.1; PID: A)NOte: agguence extracted from NCBI backbone (NCBIN:78845, NCBIP:78846)
A)NOte: disease-related mutant from patient with piebaldism
R;Giebel, L.B.; Strunk, K.M.; Holmes, S.A.; Spritz, R.A.
A)Crocgene 7, 2207-2217, 1992
A)Title: Organization and nucleotide sequence of the human KIT (mast/stem cell growth fa A)Reference number: 137948; WUID:93064697; PMID:1279499
                                                                                A gene: gag-kit
C;Superfamily: feline sarcoma virus gag-kit polyprotein; protein kinase homology
C;Superfamily: feline sarcoma virus gag-kit polyprotein; protein; transforming j
C;Superfamily: feline sarcoma virus gag-kit polyprotein; transforming j
C;Reywords: ATP; core protein; miscatus predicted <LDP>
F;175-781/Product: gag-kit polyprotein #status predicted <MAT>
F;75-781/Product: core protein p12 #status predicted <C12>
F;72-7414/Product: core protein p12 #status predicted <C12>
F;272-414/Product: core protein p30 (fragment) #status predicted <P30>
F;439-783/Domain: protein kinase homology <KIN>
F;447-455/Region: protein kinase ATP-binding motif
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Chinese Biochem. J. 7, 618-629, 1991
A;Title: Nucleotide sequece of two neighbouring fragments of human c-kit proto-oncogene A;Reference number: PC1015
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A; Residues: 412-713 <-HUW>
A; Residues: 412-713 <-HUW>
A; Cross-references: UNIPARC: UPI00001725B3
A; Cross-references: Universe with English abstract
B; Spritz, R.A.; Glebel, L.B.; Holmes, S.A.
Am. J. Hum. Genet. 50, 261-269, 1992
A; Title: Dominant negative and loss of function mutations of the c-kit (mast/stem cell A; Reference number: A41815; MUID:92133600; PMID:1370874
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Pred. No. 24;
3; Mismatches
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776 QVAKGMAFL 784
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                                                                                                                                       A;Cross-references: UNIPARC:UPI000003F17D; EMBL:X69301; NID:934089; PIDN:CAA49159.1; PID A;Note: an alternative splice form omitting residues 510-513 is described R;Yamamoto, K.; Tojo, A.; Aoki, N.; Shibuya, M. Joncer Res. 84, 1136-1144, 1993
A;Title: Characterization of the promoter region of the human c-kit proto-oncogene. A;Reference number: 156954; MUID:94103107; PMID:7506248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-22 - KRE2,
A;Cross-references: UNIPARC:UPI00000737F3; GB:S67773; NID:g459358; PIDN:AAB29529.1; PID:
B;Spritz, R.A.; Holmes, S.A.; Berg, S.Z.; Nordlund, J.J.; Fukai, K.
A;Spritz, R.A.; Holmes, S.A.; Berg, S.Z.; Nordlund, J.J.; Fukai, K.
A;Title: A recurrent deletion in the KIT (mast/stem cell growth factor receptor) proto-c
A;Reference number: IS4336; MUID:94061059; PMID:7694728
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A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 242-250 <RE3>
A,Cross-references: UNIPARC:UPI0000072C21; GB:S67686; NID:g460545; PIDN:AAD13996.1; PID:
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A;Introns: 23/1; 113/1; 207/1; 252/3; 309/1; 372/2; 411/1; 449/2; 514/1; 549/3; 592/1;
A;Note: defects in this gene may result in piebaldism
C;Function:
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F;130,145,283,290,300,320,325,357,463,486/Binding site: carbohydrate (Asn) (covalent)
F;633,640,792/Active site: Lys, Glu, Asp #status predicted
F;797,810/Binding site: magnesium (Asn, Asp) #status predicted
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Pred. No. 30;
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Status: translated from GB/EMBL/DDBJ
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Best Local Similarity
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protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - aurochs C;Species: Bos primigenius (aurochs)
C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 05-Oct-2004
C;Accession: 145877
R;Kubota, T.; H;Kono, H.; Sasaki, E.; Sakurai, M.
Gene 141, 305-306, 1994
A;Title: Sequence of a bovine c-kit proto-oncogene cDNA.
A;Reference number: 145877; MUID:94215924; PMID:7512939

RESULT 30

brachydanio tetraodon n homo sapien mus musculu

mus musculu rattus norv mus musculu

tetraodon n m nod-deriv mus musculu xiphophorus

rattus

brachydanio tetraodon n tetraodon n

eptatretus rattus norv saimiri sci avian sarco xenopus lae xenopus tro xenopus lae xenopus lae

gallus gall mus musculu mus musculu

canis famil

041131 031623 031623 0406441 0407147 0407147 0407147 0407147 0407147 0407147 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040734 040733

pongo pygma mus musculu mus musculu equus cabal

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rattus norv homo sapien

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m nod-deriv mus musculu

mus musculu mus musculu rattus norv feline sarc felis silve mus musculu feline sarc xenopus lae xenopus tro

asterina mi mus musculu rattus norv m gardner-r

rattus norv m adult mal homo sapien feline sarc hahella che bos taurus mus musculu equus cabal sus scrofa equus cabal

Q5fw27 Q6rly5 P14234 Q63206 Q6gtf2 Q6p6u0 Q8bgm0 P09769 Q82m92

Q2s794 Q9myn0

Q3u1j6 Q5d4s1 097745 Q5fyr8

feline sarc

Q9eq22 P04048 Q28414 O93411

equus cabal rattus norv

P00545 P13369 O54967

Run

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LYN RAT
QARL31 TETNG
QARL31 TETNG
QATCS3_MOUSE
HCK MOUSE
YES_XIPHE
QEEWH1 BRARE
QARN20_TETNG
QANNY7 HIWAN
BLK_MOUSE
                                                                                                               037478 MOUSE
047897 RAT
087248 MOUSE
067P04 BRARE
04TEC2 TETNG
04TEC1 TETNG
0908V0 EPPBU
06AXQ3 RAT
LCK SAISC
                                                                                                                                                                                                                                                                                                             YES_CHICK
YES_CHICK
YES_MOUSE
QQC762_MOUSE
QQC9PB1 MOUSE
QQ99PW1 RAT
YES_HUMAN
QSREC4 PONPY
QJ144A HUMAN
GSREC4 PONPY
GSREC4 PONPY
GSTEC4 PONPY
GSTEC4 PONPY
GSTEC4 PONPY
GSTEC4 PONPY
GSTEC4 PONSE
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(66376 RAT
(66600 RAT
(886M0 MOUSE
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FGR FSVGR
(82M92 STRAW
(225794 9GAMM
(998700 BOUJN
(9911,46 MOUSE
(511,46 MOUSE
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                                                                                    ; Search time 105.831 Seconds (without alignments) 78.664 Million cell updates/sec
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Q95m32
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Q57yr0
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C5TYU7_EARRE
C513064_XENLA
Q306Q5_MOUSE
Q6CETO_MOUSE
Q6CETO_MOUSE
Q6CEMB9_CHICK
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Q3UD17_MOUSE
Q6JUD17_MOUSE
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Gapop 10.0 , Gapext 0.5
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uniprot_trembl:*
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Listing first 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 7.
Mammary gland RCB-0526 Jyg-MC(A) CDNA, RIKEN full-length enriched library, clone:6830026006 product:1ymphocyte protein tyrosine Kinase, full insert sequence. (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lamprey:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.; "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey isoform duplications around the divergence of cyclostomes and gnathostomes.";

J. Mol. Evol. 49:601-608(1999).

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                              01-MAY-2000, sequence version 1.
07-EBB-2006, entry version 28.
Src-like A (Fragment).
Sprc-like Durger: (Inshore hagfish).
Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes; Myxinidae; Eptatretinae; Eptatretus.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR00119; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002245; Tyr_pkinase.
InterPro; IPR003266; Tyr_pkinase_AS.
Pfam; PF07714; Pkinase_Tyr; 1.
PRINTS; PR00109; TYRKINASE.
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100.0%; Pred. No. 2.4;
                                                                                  249 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE, PSS0011; PROTEIN KINASE DOM; 1. PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
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SMART; SM00219; TyrKc; 1.
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Q3TLX4;
                                                                            Q9U8V6_EPTBU PRELIMINARY;
Q9U8V6;
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Best Local Similarity
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Q9U8V6; 1-249
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A Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., A Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Winning L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., A Yuan Z., Zavolan M., Zhu Y., Zamer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Arakawa A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Yasunishi A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Rahalysis of the mouse transcriptome based on functional annotation of 60,770 full-length, CDNAs.";
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Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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B., Washima-Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
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MEDIJIRE=20499374; Dubmed=11042159; DOI=10.1101/gr.145100;
MEDIJIRE=20499374; Dubmed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
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Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
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Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
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Muramatsu M., Hayashizaki Y.;

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MEDLINE-2188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.D., Collins F.S., Warone L.H., Derge J.G., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heigh F.,

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Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus nōrvēgicus (Rat).
Bukaryota; Metazoa; (Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                          EMBL; AK166263; BAE38668.1; -; mRNA.

MGI; MGI:96756; Lck.

GO:0004674; F:protein serine/threonine kinase activity; RCA.

InterPro; IPR00139; Prot kinase.

InterPro; IPR00139; Ser thr pkinase.

InterPro; IPR001845; Tyr pkinase.

InterPro; IPR001845; Tyr pkinase.

InterPro; IPR001846; Tyr pkinase.

Fram; PF001714; Pkinase AS.

Pfam; PF00171; SH2; 1.
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SMART; SM00219; TYrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS50011; PROTEIN KINASE TYR; 1.
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OF-FBB-2006, entry version 7.
LCk_mapped protein (Fragment).
Name=LCk_mapped;
                                                                                                                                                                                                                                                                                                                     PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00109; TYRKINASE.
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Les 9; Conservative
                                      tyrosine phosphate.
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                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schlein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
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26-SEP-2003, sequence version 2.
07-WAR-2006, entry version 39.
Tyrosine-protein kinase HCK (EC 2.7.1.112) (p56-HCK) (Hemopoietic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                     Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases. 
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Evarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                               SMR; Q4FZEG; 1-3-7

SMR; Q4FZEG; 1-3-7

R GO; GO:0000165; F: RATP binding; IEA.

GO; GO:0000165; F: RatP binding; IEA.

GO; GO:000013; F: Protein-tyrosine kinase activity; IEA.

GO; GO:000173; F: Protein-tyrosine kinase activity; IEA.

GO; GO:0001740; F: transferase activity; IEA.

GO; GO:00016740; F: transferase activity; IEA.

GO; GO:00016740; F: protein amino acid phosphorylation; IEA.

InterPro; IPR00220; Ser_thr_pkinase.

InterPro; IPR001290; Ser_thr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR00104; SH2; 1.

R PRINTS; PR00109; TYRKINASE.

R PRODOM; PD000001; Broc. kinase; 1.

R PRODOM; PD000001; SH2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 43; DB 2; Length 379; 100.0%; Pred. No. 3.6; 0; Indels cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 AA; 43336 MW; 7CDEB573BAFB53AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding; Kinase; Nucleotide-binding; Transferase;
                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00252; SH2; 1.
SMART; SM00219; TYrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                EMBL; BC099218; AAH99218.1; -; mRNA.
SMR; Q4FZR6; 2-379.
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                                                           sednences.";
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NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tyrosine-protein kinase.
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                                                                                                                                                                                                                             tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 ÇİAEĞMAFİ 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QIAEGMAFI 9
                                                                                                                         NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 9; Conserv
                                                                                                                                            TISSUE=Thymus;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCK MACFA
Q95M30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Picard C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=HCK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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Thesis (2001), University of Marseille, France.

-!- FUNCTION: May serve as part of a signaling pathway coupling the FC receptor to the activation of the respiratory burst. May also contribute to neutrophil and may regulate the degranulation process of neutrophils (By similarity).

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
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ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
Phosphotyrosine (by autocatalysis) (By
                                                                                                                                                                                                                                                                                        tyrosine phosphate.
-!- SUBCELLULALAR LOCATION: Membrane, peripheral membrane protein (By
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S-palmitoyl cysteine (By similarity)
B61F9322D2DE3436 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                    similarity).
-!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding, Kinase, Lipoprotein, Membrane, Myristate,
Nucleotide-binding, Palmitate, Phosyhorylation, SH2 domain,
SH3 domain, Transferase, Tyrosine-protein kinase.
INIT_MET 0 0 0 Tyrosine-protein kinase HCK.
CHAIN 1 503 Frid-PRO_000088103.
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SMART; SM00326; SH3; 1.
SMART; SM00319; TYPKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS500109; PROTEIN KINASE TY2; 1.
PROSITE; PS50010; SH3; 1.
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InterPro; IPR000108; Neu cyt_fact_2.
InterPro; IPR000108; Neu cyt_fact_2.
InterPro; IPR000109; Proc kinase.
InterPro; IPR001452; SH3.
InterPro; IPR001452; SH3.
InterPro; IPR001455; TYL_pkinase.
InterPro; IPR00145; TYL_pkinase_AS.
InterPro; IPR001245; TYL_pkinase_AS.
InterPro; IPR001245; TYL_pkinase_AS.
InterPro; IPR001245; TYL_pkinase_AS.
InterPro; IPR001245; TYL_pkinase_AS.
InterPro; IPR001245; TYL_pkinase_AS.
INTERPRO; IPR0013; SH3. 1; 1.
InterPro; IPR00101; SH2DOMAIN.
IPRINTS; PR00401; SH2DOMAIN.
IPRINTS; PR00109; TYRKINASE.
IPRODOM; PD0000001; IPRCLAMASE.
IPRODOM; PD0000001; IPRCLAMASE.
IPRODOM; PD0000001; INTERINASE.
IPRODOM; PD0000001; INTERINASE.
IPRODOM; PD0000001; INTERINASE.
IPRODOM; PD0000001; INTERINASE.
IPRODOM; PD0000001; INTERINASE.
IPRODOM; PD0000001; INTERINASE.
IPRODOM; PD0000001; INTERINASE.
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IPRODOM; PD0000001; INTERINASE.
IPRODOM; PD0000001; INTERINASE.
IPRODOM; PD0000001; INTERINASE.
IPRODOM; PD00000001;  INTERINASE.
IPRODOM; PD000000001; INTERINASE.
IPRODOM; PD0000000001; INTERINASE.
IPRODO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subfamily.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ320181; CAC44031.1; -; mRNA.
HSSP; P08631; 4HCK.
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Matches 9; Conservative
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88007370; PubMed=3321053; Strebbardt K., Mullins J.I., Bruck C., Ruebsamen-Waigmann H.; Strebbardt K., Mullins J.I., Bruck C., Ruebsamen-Waigmann H.; Strebbardt K., Mullins J.I., Bruck C., Ruebsamen-Waigmann H.; Strebbardt K., Mullins J.I., Bruck C., Ruebsamen-Waigmann H.; proc. Natl. Acad. Sci. U.S.A. 84:8778-8782(1987).

-!- FUNCTION: Tyrosine kinase that plays an essential role for the selection and maturation of developing T-cell in the thymus and in mature T-cell function. Is constitutively associated with the cytoplasmic portions of the CD4 and CD8 surface receptors and plays a key role in T-cell antigen receptor (TCR)-linked signal transduction pathways (B9 similarity).

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92186854; PubMed=1545804;
Chow L., Ratcliffe M., Veillette A.;
"tkl is the avian homolog of the mammalian lck tyrosine protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: Phosphorylated on Tyr-503. This phosphorylation downregulates catalytic activity. Phosphorylated on Tyr-392 either by itself or another kinase, leading to increased enzymatic activity. SIMILARITY: Belongs to the Tyr protein kinase family. SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tyrosine phosphate.
SUBUNIT: Binds to the cytoplasmic domain of cell surface receptors, such as CD4, CD8 (By similarity).
SUBCELLULAR LOCATION: Bound to the cytoplasmic domain of either
                                         942683; 053W88; 01-NOV-1995, integrated into UniProtKB/Swiss-Prot. 01-NOV-1995, sequence version 1. 07-MAR-2006, entry version 47. Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (Protein-tyrosine kinase C-TKL) (p56tkl).
                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Spleen;
Gaertner T., Khnel H., Strebhardt K., Ruebsamen-Waigmann H.;
Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X60380; CAA42930.1; -; mRNA.
EMBL; M8543; AAA49003.1; -; mRNA.
EMBL; M85639; AAA49003.1; -; mRNA.
HSSP; P06539; 1LCK.
SMR; P42683; 63-507.
INTERPO: IPR000719; Prot kinase.
INTERPO: IPR00019; Ser thr pkinase.
INTERPO: IPR001290; Ser thr pkinase.
INTERPO: IPR001452; SH3.
INTERPO: IPR001452; SH3.
INTERPO: IPR00145; Tyr pkinase.
INTERPO: IPR001455; Tyr pkinase.
Fam: PF07714; Pkinase Tyr; 1.
Pfam: PF00714; SH2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [MRNA] OF 1-88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Cell. Biol. 12:1226-1233(1992)
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                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE (MRNA).
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PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
                          STANDARD;
                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
LCK CHICK
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ALL DE LOCK CHICK
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Perez-Cuintero D.A., Vernot J.P.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.

1. PUNCTION: Tyrosine kinase that plays an essential role for the selection and maturation of developing T-cell in the thymus and in mature T-cell function. Is constitutively associated with the cytoplasmic portions of the CD4 and CD8 surface receptors and plays a key role in T-cell antigen receptor(TCR)-linked signal transduction pathways. Association of the TCR with a peptide antigen-bound WHC complex facilitates the interaction of CD4 and CD8 with MHC class II and class I molecules, respectively, and thereby recruits the associated LCK to the vicinity of the TCR/CD3 complex. LCK then phosphorylates tyrosines residues within the immunoreceptor tyrosines-based activation motifs (ITAMs) in the cytoplasmic tails of the TCRgamma chains and CD3 subunits,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphotyrosine (negative regulation) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aotus nancymaae (Ma's night monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Platyrrhini, Cebidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Proto-oncogene tyrosine-protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-NOV-2005, sequence version 3. 07-NAR-2006, entry version 13. Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK) (Lymphocyte cell-specific protein-tyrosine kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphotyrosine (by autocatalysis) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-myristoyl glycine (By similarity).
S-palmitoyl cyteine (By similarity)
S-palmitoyl cysteine (By similarity)
BC83C4FA891B6170 CRC64;
                                                                                                                                                                                                                                              PROSITE; PS50002; SH3; 1.
ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                domain; Transferase; Tyrosine-protein kinase. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proton acceptor (By similarity). ATP (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 43; DB 1; Length 507; 100.0%; Pred. No. 4.6; ive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                            LCK.
/FTId=PRO_000088128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein kinase.
ATP (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               508 AA
                                                                    SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 1.
SMART; SM00319; TYPKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
PD000001; Prot_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58009 MW;
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                          PD000093; SH2; 1.
PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243
249
362
271
                                                                                                                                                                                                                                                                                                                                SH2 domain; SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   503
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QSPXS1;
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BINDING
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ACT SITE
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initiating the TCR/CD3 signaling pathway. In addition, contributes to signaling by other receptor molecules. Associates directly with the cytoplasmic tail of CD2, and upon engagement of the CD2 molecule, LCK undergoes hyperphosphorylation and activation. Also plays a role in the IL2 receptor-linked signaling pathway that controls T-cell proliferative response. Binding of IL2 to its steeptor results in increased activity of LCK. Is expressed at all stages of thymocyte development and is required for the regulation of maturation events that are governed by both pre-TCR and mature alpha beta TCR (By similarity).

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                  tyrosine phosphate.

SUBUNIT: Binds to the cytoplasmic domain of cell surface subunits. Binds to the cytoplasmic domain of cell surface betoes, such as CD2, CD4, CD5, CD8, CD4, CD45, CD4, CD12. Also binds to effector molecules, such as PI4K, VAVI, RASAI, FYB and to other proteins kinases including CDC2, RAFI, ZAP70 and SYK. Binds to phosphatidylinositol 3 - kinase (PI3K) from T lymphocytes through its SH3 domain and to the tyrosine phosphorylated form of KHDRBSI(p70 through its SH2 domain. Interacts with SQSTMI. Interacts with CBLB (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proto-oncogene tyrosine-protein kinase
                                                                                                                                                                                                                                                                                                                                                                  similarity).
SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
Present in lipid rafts in an unactive form (By similarity).
DOMAIN: The SH2 domain mediates interaction with SQSTM1.
Interaction is regulated by Ser-58 phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
SH2 domain; 813 domain; Transferase; Tyrosine-protein kinase.
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (By similarity).
Interactions with CD4 and CD8 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
-!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTId=PRO_0000088123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00017; SH2; 1.
Pfam; PF00017; SH2; 1.
PRINTS; PR000401; SH3DOWAIN.
PRINTS; PR000401; SH3DOWAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD0000093; TYRKINASE.
ProDom; PD0000093; PH2; 1.
ProDom; PD000055; SH2; 1.
SWART; SM00252; SH2; 1.
SWART; SM00219; TYRK; 1.
PROSITE; PS00109; PROTEIN_KINASE ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subfamily.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001246; Tyr_pkinase.
Pfam; PP07714; Prinase_AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AY821852; AAV70114.2; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50001; SH2; 1
PROSITE; PS50002; SH3; 1
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497
258
71
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126
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NP BIND
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Proton acceptor (By similarity).

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ACT SITE

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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wright D.D., Sefton B.M., Kamps M.P.; "Oncogenic activation of the Lock protein accompanies translocation of the LCK gene in the human HSB2 T-cell leukemia."; Mol. Cell. Biol. 14:2429-2417(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure of the human lck gene: differences in genomic organisation within src-related genes affect only N-terminal exons."; Gene 84:105-113(1989).
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM SHORT), AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [MRNA].
MEDLINE-87133831; PubMed-3493153;
Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
Mak T.W.;
ATP (By similarity).
Phosphotyrosine (by autocatalysis) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=90108697; PubMed=2558056; DOI=10.1016/0378-1119(89)90144-3;
Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
Benarous R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Leukemic T-cell;
MEDLINE=96085119; PubMed=7495859; DOI=10.1016/0167-4781(95)00162-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Proto-oncogene tyrosine-protein kinase LCK (BC 2.7.1.112) (p56-LCK) (Lymphocyte cell-specific protein-tyrosine kinase) (LSK) (T cell-specific protein-tyrosine kinase).
                                                       Phosphotyrosine (negative regulation) similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mak T.W.;
"A human T cell-specific cDNA clone (YT16) encodes a protein with
"A human T cell-specific cDNA clone (YT16) encodes a protein with
sternsive homology to a family of protein-tyrosine kinases.";
Eur. J. Immunol. 16:1643-1646(1986).
                                                                                       N-myristoýl glycine (By similarity).
S-palmicoyl cysteine (By similarity)
S-palmicoyl cysteine (By similarity)
8B61951BC192A3A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                             LCK HUMAN STANDARD; PRT; 508 AA.
P06539; P07100; Q12850; Q13152; Q5TDH8; Q5TDH9; Q96DW4; Q9NVTB;
01-JM-1988, integrated into UniProcKB/Swiss-Prot.
01-FEB-1994, sequence version 5.
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Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure and expression of 1ck transcripts in human lymphoid
                                                                                                                                                                           100.0%; Score 43; DB 1; Length 508; 100.0%; Pred. No. 4.6;
                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vogel L.B., Arthur R., Fujita D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell. Biochem. 38:117-126(1988).
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                                                                                                                                         508 AA; 58041 MW;
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                                                                                                                                                         Query Match
Best Local Similarity luv...
9; Conservative
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393
                                                         504
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                                                         504
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                                                                                                                                         SEQUENCE
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MEDLINE=92347326; PubMed=1639064;

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Altschule R. D., Feingold E. A., Grouse L. H., Derged J. G. D., Altschule R. D., Colling F. S., Wagner L. H., Schemen C. M., Schuler G. D., Altschul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Bhat N. K., Hopkins R. F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A. A., Rubin G. M., Hong L., Stapleton M., Soares M. B., Bonaldo M. F., Casavant T. L., Scheetz T. E., Bronstein M. J., Usdin T. B., Toshiyuki S., Carninoi P., Prange C., Brah S., Loquellano N. A., Peters G. J., Abramson R. D., Mullahy S. J., Bosak S. A., McEwan P. J., McKernan K. J., Malek J. A., Gunaratne P. H., Richards S., Worley K. C., Hale S., Garcia A. M., Gay L. J., Hulyk S. W., Yillalon D. K., Muzny D. M., Sodergren E. J., Lu X., Gibbs R. A., Haley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A. Whiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G., Butterfield Y. S. N., Krzywinski M. I., Skalska U., Smailus D. E., Schnerch A., Schein J. B., Jones S. J. M., Marra M. A.; Generation and initial analysis of more than 15,000 full-length human Proc. Natl. Acad. Sci. U. S. A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Human T lymphocytes express a protein-tyrosine kinase homologous to p56LSTRA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Veillette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.; "Expression of the lck tyrosine kinase gene in human colon carcinoma and other non-lymphoid human tumor cell lines."; Oncogene Res. 1:357-374 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.

MEDLINE=89096891; PubMed=2850479;
Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;

Grittuture of the murine lck gene and its rearrangement in a murine lymphoma cell line.";

Mol. Cell. Biol. 8:3058-3064(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takadera T., Leung S., Gernone A., Koga Y., Takihara Y., Miyamoto N.G., Mak T.W.:
"Structure of the two promoters of the human lck gene: differential accumulation of two classes of lck transcripts in T cells.";
Mol. Cell. Biol. 9:2173-2180(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA] OF 374-508.
MEDLINE=87000726; PubMed=3489486; DOI=10.1016/0167-4889(86)90228-4;
Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Defective recruitment and activation of ZAP-70 in common variable immunodeficiency patients with T cell defects."; Eur. J. Immunol. 30:2632-2638(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=Peripheral blood lymphocyte;
MEDLINE=20462621; PubMed=11009097;
DOI=10.1002/1521-4141(200009)30:9<2632::AID-IMMU2632>3.0.CO;2-C;
Boncristiano M., Majolini M.B., D'Ellos M.M., Pacini S., Valensin Ulivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
                                                                                                                                                                              TISSUE=Lymph;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                          Human chromosome 1 international sequencing consortium;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3)
  aberrant lck mRNA in two human T-cell lines.";
                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
MEDLINE=89313764; PubMed=2787474;
                         lochim. Biophys. Acta 1264:168-172(1995)
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MEDLINE=88217332; PubMed=2835736;
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INTERACTION WITH KHDRBS1
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REATINGLY STORTHOWNS:

RA CATHING P. KRSURWA T. KRETAYMES S., GOUGH J., Frith M.C., Maeda N., RA CATHING P. KRSURWA T., KRETAYMES S., GOUGH J., Frith M.C., Maeda N., RA Gyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aldinis V., Allen J.E.,

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RA Tammoja K., Van Nimwegen B., Verardo R., Yagi K.,
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=86079521; PubMed=2416464; DOI=10.1016/0092-8674(85)90169-2; Marth 'D.D., Peet R. Krebs B.G., Perlanter R.M.; A. Iymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpressed in the murine T cell lymphoma LSTRA.";
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                                                                                                        100.0%; Score 43; DB 1; Length 508; 100.0%; Pred. No. 4.6; cive 0; Mismatches 0; Indels
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NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
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NUCLEOTIDE SEQUENCE [MRNA]
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Mus musculus (Mouse).
                                                                                                    Query Match
Best Local Similarity 100.
Matches 9; Conservative
[22] INTERACTION WITH LIME1.
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TRAINE-EVBONCE [LARGE SCALE MRNA].

STRAINE-PUB.

TISSUE-Salivary gland;

STRAINE-2788.7: TISSUE-Salivary gland;

RA MEDINE-238827; PubMed-12477932; DOI-10.1073/pnas.242603899;

STRAINE-278827; PubMed-12477932; DOI-10.1073/pnas.242603899;

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Schnerch A., Schein J
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MEDLINE=94019312; PubMed=8413237;
MEDLINE=94019312; PubMed=8413237;
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Biochem. J. 303:749-753(1994)
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Nature 365:156-160(1993).
                   MUTAGENESIS OF LYS-272
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Best Local Similarity 100.0%; Pred. No. 4.6 Matches 9; Conservative 0; Mismatches

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=22289034; PubMed=12401726;
Nervi S., Nicodeme S., Gartioux C., Atlan C., Lathrop M., Reviron D.
Naquet P., Matsuda F., Imbert J., Vialettes B.;
"No association between lck gene polymorphisms and protein level in type 1 diabetes.";
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1) Libbetes 51:3326-3330 (2002).

1- MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.
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15-DEC-2003, sequence version 1.
07-FEB-2006, entry version 13.
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Interpro; IPR002290; Ser thr_pkinase.
Interpro; IPR001452; SH3.
Interpro; IPR001452; SH3.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR008266; Tyr_pkinase_AS.
Pfam; PP07714; Pkinase_Tyr; 1.
Pfam; PP07017; SH2; 1.
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PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Proc kinase; 1.
ProDom; PD0000093; SH2; 1.
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QTRTZ3;
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SMART; SM00326; SH3; 1.
SMART; SM00219; Tyrkc; 1.
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1 QIAEGMAFI 9
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QC; GO:00045121; C:lipid raft; ISS.

QC; GO:0004522; C:pericentriolar material; ISS.

QC; GO:00004722; F:protein serine/threonine phosphatase activity; ISS.

QC; GO:0004713; F:protein-tyrosine kinase activity; ISS.

QC; GO:0004713; F:protein-tyrosine kinase activity; ISS.

R GC; GO:0006919; F:SHZ domain binding; ISS.

R GC; GO:0006917; P:nempoiesis; ISS.

R GC; GO:0006917; P:nempoiesis; ISS.

R GC; GO:0006917; P:nempoiesis; ISS.

R GC; GO:0006917; P:nempoiesis; ISS.

R GC; GO:0006917; P:nempoiesis; ISS.

R GC; GO:0006917; P:nempoiesis; ISS.

R GC; GO:000682; P:positive regulation of T cell activation; ISS.

R GC; GO:000074; P:regulation of Impropriention; ISS.

R GC; GO:0001249; P:regulation of Impropriention; ISS.

R GC; GO:0004249; P:regulation of Impropression through cell cycle; ISS.

R GC; GO:0004249; P:regulation of Impropression through cell cycle; ISS.

R GC; GO:0004249; P:regulation of Impropression through cell cycle; ISS.

R GC; GO:0004249; P:regulation of Impropression through cell cycle; ISS.

R GC; GO:0004249; P:rethiase.

R GC; GO:0004249; P:rethiase.

R GC; GO:0004249; R:Tyr_pkinase.

DR InterPro; IPR001245; Tyr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hylobates sp. (gibbon).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hylobatidae; Hylobates
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Thesis (2001), Department of Experimental Oncology laboratory, U.
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                                                                                                                                                                                 100.0%; Score 43; DB 2; Length 509; 100.0%; Pred. No. 4.6;
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                                                                                                                                         509 AA; 58001 MW; 44BFF0D43FFB420D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               509 AA
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS001019; PROTEIN KINASE TYR; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
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Q95M32;
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SMR; C
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EMBL; BC1002046; AA102047.1; ...

CG GO:0045121; C:lipid raft; ISS.

CG; GO:004722; F:protein serine/threonine phosphatase activity; ISS.

CG; GO:004722; F:protein-tyrosine kinase activity; ISS.

CG; GO:004716; F:protein-tyrosine kinase activity; ISS.

CG; GO:004716; F:protein-tyrosine kinase activity; ISS.

CG; GO:004716; F:protein-tyrosine kinase activity; ISS.

CG; GO:004716; F:protein-tyrosine kinase activity; ISS.

CG; GO:0006919; P:mamopolesis; ISS.

CG; GO:000741; P:induction of apoptosis; ISS.

CG; GO:007242; P:intracellular signaling cascade; ISS.

CG; GO:007242; P:intracellular signaling cascade; ISS.

CG; GO:0066468; P:protein amino acid phosphorytation; ISS.

CG; GO:0006468; P:protein amino acid phosphorytation; ISS.

CG; GO:0006468; P:protein amino acid phosphorytation; ISS.

CG; GO:000747; P:regulation of lymphocyte activation; ISS.

CG; GO:000074; P:regulation of progression through cell cycle; ISS.
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Distributed under the Creative Commons Attribution-NoDerivs License
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Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
Wagner L., Bala M., Barbauk S., Barber S., Babbkaiff R., Beland J.,
Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
Matsuo C., Mayo M., Santos R.X., Stort J., Tsai M., Wong D.,
Siddiqui A., Holt R., Jones S.J., Marra M.A.;
Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     509 AA; 57947 MW; FIBFR5C237C8DB7E CRC64;
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                                                               PEAM; PF00018; SH3_1; 1.

PRINTS; PR00401; SH3DOMAIN.

PRINTS; PR00452; SH3DOMAIN.

PRINTS; PR00109; TYRKINASE.

ProDom; PD0000093; SH2; 1.

ProDom; PD0000093; SH2; 1.

SMART; SM00252; SH2; 1.

SMART; SM00219; TYrKc; 1.

PROSITE; PS00109; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Q3ZCMO;
Pfam; PF07714; Pkinase Tyr; 1.
Pfam; PF00017; SH2; 1.
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Best Local Similarity luv...
Pest Some 9; Conservative
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PROSITE; PS50002; SH3; 1
SEQUENCE 509 AA, 5794
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InterPro; IPR000980; SH2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Naquet P. Imbert J.; A rate mann twelve specific protein tyrosine MA rate mRNA variant to the human lymphocyte-specific protein tyrosine kinaseLCK gene with intron B retention and exon 7 skipping encodes a putativeprotein with altered SH3-dependent molecular interactions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Nervi S., Guinamard R., Delaval B., Lecine P., Vialettes B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 43; DB 2; Length 509; 100.0%; Pred. No. 4.6;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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509 AA; 58116 MW; CE0E80DCD6D0F2F8 CRC64;
GO; GO:0042493; P:response to drug; ISS.
GO; GO:0030217; P:T cell differentiation; ISS.
GO; GO:0030217; P:T cell differentiation; ISS.
GO; GO:000682; P:zinc ion homeostasis; ISS.
InterPro; IPR002290; Ser_Thr_pkinase.
InterPro; IPR001452; SH3.
InterPro; IPR001452; SH3.
InterPro; IPR001455; TYr_pkinase.
InterPro; IPR001455; TYr_pkinase.
InterPro; IPR001455; TYr_pkinase.
Pfam; PP00017; SH2; I.
Pfam; PP00017; SH3; I.
PRINTS; PR00401; SH3; I.
PRINTS; PR00401; SH3; I.
PRINTS; PR00401; SH3; I.
PRODOM; PD000009; TYRKINASE.
ProDom; PD000009; Prot kinase; I.
ProDom; PD0000019; Prot kinase; I.
ProDom; PD0000019; Prot kinase; I.
ProDom; PD0000019; Prot kinase; I.
PROSITE; PS00107; PROTEIN KINASE ATP; I.
PROSITE; PS00107; PROTEIN KINASE DOM; I.
PROSITE; PS00107; PROTEIN KINASE TYR; I.
PROSITE; PS00107; PROTEIN KINASE TYR; I.
PROSITE; PS00107; PROTEIN KINASE TYR; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q573B4_HUMAN PRELIMINARY; PRT;
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1es 9; Conservative
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                 SO DE RESERVA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE
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RA OLD T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., RA Sekihe M., Obayashi K., Sato H., Nagai K., Kimura K., Makita H., Satoli M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J., Salto K., Kawai Y., Ishono Y., Nakamura Y., Nagahari K., Ramamoto J., Salto K., Kawai Y., Ishono Y., Nakamura Y., Nagahari K., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Sado H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Rahabashi M., Kanda K., Yokoi T., Fukwa E., Chimara M., Ranabashi T., Yamashita H., Murakawa K., Fujimori K., Anaita M., Matanabe M., Hiraoka S., Chiba Y., Ishida S., Ranehori K., Takahashi T., Yamashita H., Murakawa K., Fujimori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y., Ranehori K., Yuuki H., Oshima A., Sasaki N., Antta M., Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Antta M., Imose N., Momyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Ry Yamazaki M., Watanabe K., Kunagai A., Itakura S., Fukuzumi Y., Rahasaki H., Watanabe K., Kunagai A., Itakura S., Fukuzumi Y., Ryamada K., Fujimori Y., Yamada M., Tashiro M., Ohmori Y., Antta M., Watanabe M., Tashiro M., Ohmori Y., Antta M., Haili Y., Ozaaki K., Hirao M., Ohmori Y., Antta M., Haili Y., Ozaaki K., Hirao M., Chanoto S., Anttami R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Anttami R., Rawakami T., Noguchi S., Itoh T., Shigeta K., Samari R., Matumura K., Nagase T., Momura M., Kikuchi H., Masuho Y., Yamadita R., Matumura K., Nagase T., Nomura M., Kikuchi H., Masuho Y., Yamadita R., Nagase T., Nomura N., Kikuchi H., Masuho Y., Sugano S., R., Chuna M., Watanara Y., Ohama M., Kikuchi H., Masuho Y., Isagano S., Itoh R., Yada T., Nagase T., Nomura N., Kikuchi H., Masuho Y., Sagani R., Nakai K., Yada T., Nakamura Y., Ohama M., Kikuchi H., Masuho Y., Sagani R., Nakai K., Yada T., Nakamura Y., Ohama M., Kikuchi H., Masuho Y., Sagani MUCLECTIDE SEQUENCE LLAKGE SCALE GENOMIC DUAL).

MUCLECTIDE SEQUENCE LLAKGE SCALE GENOMIC DUAL).

MUCLINE SEQUENCE LLAKGE SCALE GENOMIC DUAL).

MICHAGE M., SELVENCE G., Almeida J.P., Babbage A.K., Bagguley C.L.,

Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

A Jones M., Stavrides G., Almeida J.P., Barbage A.K., Bagguley C.L.,

Bailey J., Barlow K.F., Bates K.N., Barden B.M., Brown A.J.,

Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

A Collappan J.C., Clamp M., Clark G.N., Clark S.Y., Clee C.M.,

Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

A crafham D.V., Griffiths G.J., Heath P.D., Ho S., Holden J.L., Howden P.J.,

Huckle E., Hunt A.R., Hunt S.E., Moscon M.D., Gwilliam R., Hall R.E.,

Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson D.,

KAY M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

Maine S.L., Martin S.L., Mocre M.J.E., Mullikin J.C., Nickerson T.,

A Milne S.A., Mistry D., Moore M.J.E., Mullikin J.C., Nickerson T.,

A Whine S.M., Sycamore M.J. F.N., Panes B. W., Thorpe A.,

Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,

Swann R.M., Sycamore M., Taylor R., Tee L., Thomas D.W., Thorpe A.,

Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Milliey D.L., Williams L., Williams S.A.,

Mitchead S.L., Whitteker P., Willey D.L., Williams L., Williams L.,

M. Proper G.L., Specker J., Durbin R.M., Bentley D.R., Beck S.,

Brown R.M., Beck S.,

M. Proper B. Willing L., Durbin R.M., Bentley D.R., Beck S.,

Brown R.M., Belling L., Willing L., William B. M., Bentley D.R., Beck S., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marza M.A.;
"Generation and initial analysis of more than 15,000 full-length human Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [4] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 21-525. [5]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] TISSUE=Ileal mucosa; PubMed=14702039; DOI=10.1038/ng1285; mouse cDNA sequences."; Genet. 36:40-45(2004). and

Rogers J.;

MEDLINE=9763487; PubMed=9109402; DOI=10.1016/S0014-5793(97)00255-X; Zhang W., Smithgall T.E., Gmeiner W.H.; Zhang W., Smithgall T.E., Gmeiner W.H.; Sequential assignment and secondary structure determination for the "Sequential assignment and secondary structure determination for the "Sequential assignment and secondary structure determination for the Src homology 2 domain of hematopoietic cellular kinase."; FBBS Lett. 406:131-135(1997).

-!- FUNCTION: May serve as part of a signaling pathway coupling the FC receptor to the activation of the respiratory burst. May also contribute to neutrophil migration and may regulate the degranulation process of neutrophils.

-!- CATALIVITY: ATP + a protein tyrosine = ADP + a protein MEDILINE=98239731; PubMed=9571048; DOI=10.1006/jmbi.1998.1690; Horita D.A., Baldisseri D.M., Zhang W., Altieri A.S., Smithgall T.E., Gmeiner W.H., Byrd R.A., Salution structure of the human Hck SH3 domain and identification of its ligand binding site."; Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Dunn A.R.; "Two isoforms of murine hck, generated by utilization of alternative translational initiation codons, exhibit different patterns of "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001). TISSUE-Spleen; MEDLINE-92241680; PubMed=1572549; DOI=10.1016/0378-1119(92)90407-G; tyrosine phosphate. -!- SUBUNIT: May bind to HIV-1 Nef and VIF through its SH3 domain. This interaction would stimulates its tyrosine-kinase activity. Hradetzky D., Strebhardt K., Ruesamen-Waigmann H.;
The genomic locus of the human hempoietic-specific cell protein
tyrosine kinaee (PTK) -encoding gene (HCK) confirms conservation of
exon-intron structure among human PTKs of the src family."; INTERACTION WITH HIV-1 NEF.

MEDLINE=97364702; PubMed=9218412; DOI=10.1074/jbc.272.29.17899;
Briggs S.D., Sharkey M., Stevenson M., Smithgall T.E.;
Briggs S.D., Sharkey M., Stevenson M., Smithgall T.E.;
"SH3-mediated Hck tyrosine kinase activation and fibroblast transformation by the Nef protein of HIV-1."; X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 80-136.
MEDLINE=98453315; PubMed=9778343; DOI=10.1021/bi9809899;
Arold S., O'Brien R., Franken P., Strub M.P., Hoh F., Dumas C.,
Ladburty J.E.; Pranken P., Strub M.P., Hoh F., Dumas C.,
"RT loop flexibility enhances the specificity of Src family SH3
domains for HIV-1 Nef."; PubMed=11278465; DOI=10.1074/jbc.M009076200; Hassaine G., Courcoul M., Bessou G., Barthalay Y., Picard C., Olive D., Collette Y., Vigne R., Decroly B.; "The tyrosine kinase Hck is an inhibitor of HIV-1 replication counteracted by the viral vif protein."; -:- INTERACTION: 092969:- (xeno); NDExp=2; IntAct=EBI-346340, EBI-710506; X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-525.
MEDLINE=97177106; PubMed=9024658; DOI=10.1038/385602a0;
Sicheri F., Moarefi I., Kuriyan J.;
"Crystal structure of the Src family tyrosine kinase Hck.";
Nature 385:602-609(1997). NUCLEOTIDE SEQUENCE OF 1-21, AND ALTERNATIVE INITIATION. Mol. Cell. Biol. 11:4363-4370(1991). Siochemistry 37:14683-14691(1998). WEDLINE=91342636; PubMed=1875927; Mol. Biol. 278:253-265(1998). NUCLEOTIDE SEQUENCE OF 178-525. STRUCTURE BY NMR OF 138-244. INTERACTION WITH HIV-1 VIF. subcellular localization." STRUCTURE BY NMR OF 77-137. Gene 113:275-280(1992).

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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Staplecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
P26660:- (xeno); NDExp=1; IntAct=EB1-346340, EB1-706322; P27958:- (xeno); NDExp=5; IntAct=EB1-34640, EB1-706378; Q13545:-; NDExp=1; IntAct=EB1-346340, EB1-346574; Q9UOG1:-; NDExp=1; IntAct=EB1-346340, EB1-346577; Q9WMX2:- (xeno); NDExp=1; IntAct=EB1-346340, EB1-34697; Q9VMX2:- (xeno); NDExp=1; IntAct=EB1-346340, EB1-24697; Q9ULH1:DDER1; NDExp=1; IntAct=EB1-346340, EB1-34652; P50570:DNM2; NDExp=1; IntAct=EB1-346340, EB1-34652; Q9US55:ELMO1; NDExp=1; IntAct=EB1-346340, EB1-346547; Q9US55:ELMO1; NDExp=1; IntAct=EB1-346340, EB1-34653; Q9US8; VLJ; NDExp=1; IntAct=EB1-346340, EB1-34653; Q9US8; REAUS; NDExp=1; IntAct=EB1-346340, EB1-34653; Q9USS; REAUS; NDExp=1; IntAct=EB1-346340, EB1-34653; Q9USS; REAUS; NDExp=1; IntAct=EB1-346340, EB1-34653; Q9USS; REAUS; NDExp=1; IntAct=EB1-346340, EB1-34639, EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1-34630; EB1
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                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 43; DB 1; Length 525; 100.0%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                               P61978:HNRPK; NbExp=1; IntAct=EBI-346340, EBI-304185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-2005, integrated into UniProtKB/TrEMBL.
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-!- SIMILARITY: Contains 1 SH3 domain.
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Q504RS_HUMAN PRELIMINARY; PRT;
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Hypothetical protein (Fragment).
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Matches 9; Conservative
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NIH MGC Project;
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MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
A Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Butcow K.H., Scheafer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenok L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquallano N.A., Peters G.J., Abramon R.D., Mullahy S.J.,
Bosak S.A., McDwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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               GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006468; P:protein anino acid phosphorylation; IEA.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR002290; Ser thr pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SH3 domain; Transferase; Tyrosine-protein Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JAN-2006, integrated into UniProtKB/TrEMBL. 10-JAN-2006, sequence version 1. 07-MAR-2006, entry version 4. Hypothetical protein (Fragment). Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           580 AA.
ENSG0000101336; Homo sapiens.
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TISSUE=PCR rescued clones;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408 QIAEGMAFI 416
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Best Local Similarity
Matches 9; Conserv
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ProDom; PD000001; Prot_kinase; 1.
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Q4RR72 TETNG
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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Oones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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MEDLINE=200330; PubMed=10552041;
Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
"Protein tyrosine kinase cDMAs from amphioxus, hagfish, and lamprey isoform duplications around the divergence of cyclostomes and
                                                                                                                                                                                                NISSUB-PCR rescued clones;
NIH MGC Project;
Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gnathostomes.";
J. Mol. Evol. 49:601-608(1999).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Hyperoartia,
Petromyzontiformes, Petromyzontidae, Lethenteron.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC108931; AA108932.1; -; mRNA.
EMBL; BC108930; AA108931.1; -; mRNA.
ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
SH3 domain; Transferase; Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 43; DB 2; Length 580; 100.0%; Pred. No. 5.2;
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SMR; O9PVVO; 1.246.
SO, GO:0005524, F-ATE binding; IEA.
GO; GO:0004713; F-protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    580 AA; 65343 MW; A9D2E429B128891A CRC64;
                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR008265; Tyr_pkinase.
Pfam; PF07714; Pkinase Tyr; 1.
PRINTS; PR00109; TYRINASE.
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HSSP; P08631; 1AD5.
SMR; Q9PVV0; 1-246.
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                                                                                                                and mouse cDNA sequences."
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The meanly vertebrate proto-karyotype.";
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary data. We will be control of the eukaryotic cell subcritor. Plays a key role in the control of the eukaryotic cell cycle. It is required in higher cells for entry into S-phase and mitosis. Component of the kinase complex that phosphorylates the
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19-JUL-2005, sequence version 1.
07-FBE-2006, entry version 6.
Chromosome 14 SCAF15003, whole genome shotgun sequence. (Fragment).
ORFNAmes=GSTENG00030294001;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
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Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                           Length 249;
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SEQUENCE 249 AA; 28627 MW; DAC9DBA041F3D941 CRC64;
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                                                                                                                                                                                                                                                              97.7%; Score 42; DB 2;
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1; Mismatches
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SMART; SM00219; TYRKC; 1.
PROSITE; PS50011; PROTEIN KINASE DOM;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
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Matches 8; Conservative
                                                                                                            Tyrosine-protein kinase.
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ProDom; PD000066; SH3; 1.
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NUCLEOTIDE SEQUENCE.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

Cyprinidae; Danio.

NCBI_TaxID=7955;
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GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:001646; F:protein-tyrosine kinase activity; IEA.
GO; GO:001646; P:protein amino acid phosphorylation; IEA.
InterPro; IPR00229; Fort kinase.
InterPro; IPR001245; Tyr_bkinase.
InterPro; IPR001245; Tyr_bkinase.
InterPro; IPR001245; Tyr_bkinase.
InterPro; IPR00129; Tyr_kinase.
InterPro; IPR00129; Tyr_kinase.
INTERPRO; IPRO0109; FORTEIN KINASE AFP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ATP-binding; Kinase, Nucleotide-binding; Transferase;
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R Ensembl; BX842684; CAH69080.1; -; Genomic_DNA.

SMR; Q5TVU7; 42-485.

R Ensembl; BX842680000007783; Danio rerio.

R ZFIN; ZDB-GENE-040724-106; Si:dkey-33i22.2.

GO; GO:0004713; F:ATP binding; IEA.

GO; GO:0004713; F:Drotein-tyrosine kinase activity; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

R InterPro; IPR00019; Prot kinase.

R InterPro; IPR0019; SH2.

R InterPro; IPR001452; SH3.

R InterPro; IPR001452; SH3.

R InterPro; IPR001452; TYr_Dkinase.

R InterPro; IPR001452; TYr_Dkinase.

R InterPro; IPR001452; TYr_Dkinase.

R PF00714; Pkinase_TYr; 1.

R Pfm; PF00017; SH2; 1.

R PRINTS; PR00401; SH2DOMAIN.

R PRINTS; PR00401; SH2DOMAIN.

R PRINTS; PR00109; TYRKINASE.

R PRODOM: DD00001; Prot kinase; 1.
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88.9%; Pred. No. 13;
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OSTYUT;
07-DEC-2004, integrated into UniProtKB/TrEMBL.
07-DEC-2004, sequence version 1.
07-EEB-2006, entry version 8.
Novel protein tyrosine 8.
Novel protein tyrosine 8.
Name-si cikey-33i22.2; Synonyms=OTTDARP00000004623;
ORFNames=DKEY-33i22.2-001;
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Distributed under the Creative Commons Attribution-NoDerivs License
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Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Xenopus.
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RSPP; P08631; 1AD5.

ROWG O03064; 43.488.

GO; GO:00004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0007422; F:protein-tyrosine kinase activity; IEA.

GO; GO:00004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:00004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:00004713; F:protein-tyrosine kinase.

R GO; GO:00004713; F:protein-tyrosine kinase.

R GO; GO:0006468; P:protein-amino acid phosphorylation; IEA.

R InterPro; IPR00290; Ser_thr_pkinase.

R InterPro; IPR00145; Fyr_pkinase.

R InterPro; IPR00145; Tyr_pkinase.

R InterPro; IPR00145; Tyr_pkinase.

R Pfam; PF0011; SH2; 1.

R PRINTS; PR00104; SH3; 1.

R PRINTS; PR00105; TYRKINASE.

R PRODOM; PD000004; SH3; 1.

R PRODOM; PD000066; SH3; 1.

R SMART; SM00125; SH3; 1.

R SMART; SM00125; SH3; 1.

R RSMART; SM00109; TYRKINASE ATP; 1.

R PROSITE; PS0011; PROTEIN KINASE ATP; 1.

R PROSITE; PS0011; PROTEIN KINASE ATP; 1.

R PROSITE; PS50011; PROTEIN KINASE TYR; 1.

R PROSITE; PS50011; PROTEIN KINASE TYR; 1.

R PROSITE; PS50011; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                  Score 40; DB 2; Length 485;
Pred. No. 19;
1; Mismatches 0; Indels
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Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                          485 AA; 55644 MW; 3ED1878453666747 CRC64;
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SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 1.
SMART; SM00219; TYPKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS500109; PROTEIN KINASE_TYR; 1.
PROSITE; PS50001; SH2; 1.
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88.9%;
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nes 8, Conservative
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RC STRAINS-CS-PBL/66; TISSUB-BONE marrow;

RAY NUCLECUTION S. SUCIENCE.

RAY MARCASTBL/66; TISSUB-BONE marrow;

RAY OYAMA R., RASUKAWA T., KATAYAMA S., GOUGH J., Frith M.C., Maeda N., OYAMA R., RAYAMA T., Lenhard B., Wells C., KOdzius R., Shimokawa K., RA Bajic V. B., Brenner S. B., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Ajdinis V., Allen J.E., Bono H., Chalk A.M., RA Ambesi-Impiombato A., Apwailer R., Aturaliya R.N., Balley T.L., Randsil M., Barter L., Dalla E., Wellson T., Clutterbuck D.R., Choudhary V., Christoffels A., Clutterbuck D.R., Choudhary V., Christoffels A., Clutterbuck D.R., Chall R.M., R. Bresano T., Bono H., Chalk A.M., RA Crow M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Gingeras T.R., Golopori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., RA Georgil-Hemming P., Gingeras T.R., Golopori T., Green R.E., Gustincich S., Harbers M., Katoh M., Kanapin A., Katoh M., Kanapin A., Katoh M., Kanabu S.P., Kruger A., Kummerfeld S.K., Ktano H., Kolliam G., Kitoh M., Madera M., Machiliam S., McMilliam S., McMilliam S., McMaln Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Migmone F. Miyake S., Morris R. Mottada H., Matsuzawa S., Miki H., Migmone F. Miyake S., Ringwald M., Reptrovsky N., Piazza S., Rika J., Sandelin A., Schneider C., Sekiguchi S., Reded J., Reid J.F., Ring B.Z., Ringwald M., Shibata Y., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H., Shimada H.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6J; TISSUB-Bone marrow; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninol P., Hayashizaki Y.; Hayashizaki Y.; Hayahizaki Y.; High-efficiency Full-length CDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                                           Gaps
                                                                                                                                                                                                                                                 11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 5.
Bone marrow macrophage cDNA, RIKEN full-length enriched library,
clone:1830119M13 product:Yamaguchi sarcoma viral (v-yes-1) oncogene
                                                                           .;
0
                                            2; Length 488;
                                                                          0; Indels
                488 AA; 55795 MW; B7E70668B6EA92B2 CRC64;
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Pred. No. 19;
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88.9%;
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Best Local Similarity 88.۶
دم 8، Conservative
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Kinase.
SEQUENCE
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RC MEDLINE-2235468; PubMed=12466851; DOI=10.1038/nature01266; RX MUGLEACTINE SEQUENCE.

RX OKAZAKI Y., FURLUNO M., KASUKAWA T., Adachi J., BOND H., KONDOS., RA OKAZAKI Y., FURLUNO M., KASUKAWA T., Adachi J., BOND H., KONDOS T., RIYOSAWA H., YAMMARKA I., ADACHI J., BOND H., KONDOS T., RA YAGI K., TOMATU Y., Hasegawa Y., NOGAMI A., SCHONDACH C., GOJODOTI T., RA BAIGATELLI K., HILL D.P., BULL C., HUME D.A., QUACKENBUS M. J., CALTINI L.M., KARADIN A., MATSUGA H., BARAGION S., Beisel K. W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Balake J.A., Bradt D., HITOKAWA N., Jackson I.J., Jarvis E.D., RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., RAMAJI H., KAWABAMA Y., KAUGELETSKI R.M., KING B.L., KORAGAYA A., KURCOKKIN I.V., Lee Y., Lenhard B., Lyons P.A., KAWAJI H., NAMATHA W., PRAN W., Perten G., Perton G., Ramachandran S., KORAGARIMA T., Ramachandran S., Ragashima T., Numata K., Okido T., Pavan W.J., Ramachandran S., Petrovsky N., Pillai R., Pontius J.U., Oli D., Ramachandran S., Petrovsky N., Schheider K., Jengle C.A., Secoul M., Shimade K., Asul L., Wanlbark-Boris A., Yamagiswa M., Yang I., Yang L., Yang L., Yang L., Wanghaw-Boris A., Yangiswa T., Ramachandran S., Vanna Z., Zavolan M., Zhu Y., Zimmer A., Harbizume W., Imotani K., Ishinagawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishinagawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishinagawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishinagawa T., Fukuda S., Birney E., Hayashizaki Y., Sasaki D., Shibade K., Shinagawa T., Rusakaki A., Sakai K., Sasaki D., Shibade K., Shinagawa T., Rusakaki A., Sakai K., Sasaki D., Shibade K., Shinagawa T., Rusakaki A., Shinalaki Y., Shinagawa T., Rusakaki A., Shinalaki Y., Shinadaki A., Sasaki D., Shibade K., Shinagawa T., Rusakaki A., Shina B., Hayashizaki Y., Sasaki D., Shibade K., Shinagawa T., Birney E., Hayashizaki Y., Sasaki D., Shibade K., Shinagawa T., Rusaka D., Shila M., STRAIN-C57BL/65; TISSUE-Bone marrow;

KRAIN-C57BL/65; TISSUE-Bone marrow;

KRAIN-C57BL/65; TISSUE-Bone marrow;

KRAIN-C57BL/65; PubMed=11217851; DOI=10.1038/3505500;

KRAIN-C57BL/66; PubMed=11217851; DOI=10.1038/3505500;

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Whymshaw-Bootis A., Yoshida K., Hasegewa Y., Kawaji H., Kohteuki S.,

Narachiati. Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., STRAIN=C57BL/6J; TISSUE=Bone marrow; PubMed=16141073; DOI=10.1126/science.1112009; PubMed=16141073; DOI=10.1126/science.1112009; RIKING Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antiseense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566 (2005). "Functional annotation of a full-length mouse cDNA collection."; "The transcriptional landscape of the mammalian genome."; STRAIN=C57BL/6J; TISSUE=Bone marrow; Science 309:1559-1563(2005). Nature 409:685-690(2001). Nature 420:563-573 (2002). NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE dayashizaki Y.; Hayashizaki Y.; ragami M.

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                                                                                                                                                                                                                             Namu-Zius (Mouse).
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/61; TISSUE=Pancreas; MBDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; High-efficiency full-length cDNA cloning."; MH40h-efficiency 1011-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suzuki S.,
H., Kawai J.,
                                                                                                                                                                     (v-yes-1) oncogene
                                                                                          01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 21.
10 day old male pancreas cDNA, RIKEN full-length enriched library,
clone:1810073A02 product:Yamaguchi sarcoma viral (v-yes-1) oncogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nishio T., Okada M., Plessy C., Shibata K., Shiraki T.,
Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki
Hayashizaki Y.,
                                                                      01-MAR-2003, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Pancreas;
PubMed=16141072; DOI=10.1126/science.1112014;
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PubMed=16141073; DOI=10.1126/science.1112009;
                          491 AA.
                          PRT;
                                                                                                                                                                                      homolog, full insert sequence
                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 309:1559-1563(2005).
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QBCEIO;
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Gaps

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Indels

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1; Mismatches

Local Similarity 88.

Best Loca Matches

Query Match

93.0%; Score 40; DB 2; Length 491; 88.9%; Pred. No. 19;

AEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

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A Nazaki Y., Furno M., Kasukawa T., Adachi J., Bono H., Kondo S., R. Arginko S., Collano M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Adachi J., Bono H., Koyosawa H., Ragi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Baldarelli R., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S., Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S., R. Adasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., R.A Kanaji H., Kawasia Y., Kedzierski R.M., King B.L., Kawaji H., Kawasia Y., Kedzierski R.M., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., R., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Ravasi T., Numata K., Okido T., Pavan W.J., Peraca G., Peesle G., Petrovsky N., Pillai R., Pontius J.U., Oi D., Ramachandran S., Schneider C., Semple C.A., Setou M., Shimada K., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Mulming L.G., Wynshaw-Boris A., Yanagisawa T., Radama R., Hakanizume W., Imnoranici P., Hayashisau N., RA Hara A., Hashizume W., Imnorani A., Takawa T., Ronno H., Nakamura M., Sakazume N., Sakai K., Sasaki D., Shibata K., Shinagawa A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Ranalysis of the mouse transcriptome based on functional annotation of G., 770 full-length cDNAs., PN N.
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STRAING-CSTBL/60: TISSUE-pancreas;

MEDLINE=21085660; PubMed=11217851; DOI=10.1038/3505500;

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Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sakai H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Whymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Whymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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  and Genome Science Group
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                                                                                                                                                  STRAIN=CS7BL/GJ; TISSUE=Pancreas;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
                  (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566 (2005).
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STRAIN=C57BL/6J; TISSUE=Pancreas;
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Distributed under the Creative Commons Attribution-NoDerivs License
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           Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., sequencing pipeline with 384 multicapillary sequencer.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0004713; F:procein-tyrosine kinase activity; IDA.
GO; GO:0007242; P:intracellular signaling cascade; IDA.
GO; GO:0007242; P:intracellular signaling cascade; IDA.
GO; GO:001808; P:peptidyl-tyrosine phosphorylation; IDA.
GO; GO:0046777; P:procein amino acid autophosphorylation; IDA.
GO; GO:0046777; P:protein amino acid autophosphorylation; IDA.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR00990; SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 491;
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SMR; Q8CEI0; 46-491.
Ensembl; ENSMG50000042228; Mus musculus.
MGI; MGI:96892; Lyn.
GO; GO:0005515; F:protein binding; IPI.
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Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AK028112; BAC25753.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pkinase_AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3 1; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR008264; Tyr_pkinase_
Pfam; PF07714; Pkinase_Tyr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.0%;
88.9%;
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SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 1.
SMART; SM00219; TyrKc; 1.
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nes 8; Conserv
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QSZMB9 CHI
ID QSZMB
AC QSZMB
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NCBI_TaxID=10116;
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01-0CT-1996, integrated into UniProtKB/Swiss-Prot.
26-SEP-2003, sequence version 2.
07-WAR-2006, entry version 54.
Tyrosine-protein kinase HCK (EC 2.7.1.112) (p56-HCK) (Hemopoietic cell kinase).
23-NOV-2004, integrated into UniProtkB/TrEMBL.
23-NOV-2004, sequence version 1.
970-FEB-2006, entry version 8.
Hypothetical protein.
ORFNames=RCJMB04 218.
Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                        STRAIN=CB; TISSUE=Bursa; Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J., Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M., Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.; "Full-length cDNAs from chicken bursal lymphocytes to facilitate genefunction analysis."; Genome Biol. 6:R6-R6(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                    SMK; O2XMB9; 46-492.

BMG; GO: 0004713; F:ATP binding; IEA.

GO; GO: 0004713; F:Protein-tyrosine kinase activity; IEA.

GO; GO: 0007242; F:ATP binding; IEA.

GO; GO: 0007413; F:Protein-tyrosine kinase activity; IEA.

GO; GO: 000748; P:Protein-tyrosine kinase activity; IEA.

GO; GO: 000648; P:Protein-amino acid phosphorylation; IEA.

InterPro; IRR00199; Prot kinase.

RIGERPO; IRR00199; Ser Thr pkinase.

RIGERPO; IRR001990; Ser Thr pkinase.

RIGERPO; IRR001245; Tyr pkinase.

RIGERPO; IRR001245; Tyr pkinase.

RIGERPO; IRR001245; Tyr pkinase.

RIGERPO; IRR001245; Tyr pkinase.

RIGERPO; IRR001245; Tyr pkinase.

RIGERPO; IRR001245; Tyr pkinase.

RIGERPO; IRR001245; Tyr pkinase.

RIGERPO; IRR00125; SH3; 1.

RIGERPO; RR00109; TYRINASE.

RR PRODON; PROUDO; RH2DOMAIN.

RR PRODON; PROUDO; SH3; 1.

RR SMART; SM00212; SH3; 1.

RR SMART; SM00219; TYRK; 1.

RR SMART; SM00219; TYRK; 1.

RR PROSITE; PSG0010; PROTEIN KINASE ATP; 1.

RR PROSITE; PSG0019; PROTEIN KINASE TYR; 1.

RR PROSITE; PSG0019; PROTEIN KINASE TYR; 1.

RR PROSITE; PSG0019; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.0%; Score 40; DB 2; Length 492; 88.9%; Pred. No. 19;
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492 AA; 56202 MW; 69D2F0534E33CC1E CRC64;
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                                                                                                                                                                                                                                                                   EMBL; AJ719465; CAG31124.1; -; mRNA.
SMR; Q5ZMB9; 46-492.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
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                                                                                                                             NUCLEOTIDE SEQUENCE.
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                                                                                            Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
SEQUENCE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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HCK_RAT
ID HCK_R
AC PSOS
DT 01-OC
DT 26-SE
DT 07-MA
DE TYPOS
DE Kinas
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OR Battus novegicus (REAL)

OR BARATUS ACRIGATES, Detailates, Vertebrates, Buteleostomi; OR BARATUS ACRIGATION (ACRIGATES)

OR BARATUS ACRIGATION (ACRIGATES)

OR BARATUS ACRIGATION (ACRIGATES)

MINITARY SEQUENCE (MENA);

REDINGS-20191719; PubMedal1660421

MINITARY OCCUPATION (ACRIGATES)

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PS00109; PROTEIN KINASE TYR; 1.
          PS50001; SH2; 1.
PS50002; SH3; 1.
                                                                                                                     340 OIAEGMAYI 348
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                                                                                                  1 OIAEGMAFI
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
          PROSITE;
PROSITE;
 PROSITE;
                                       SEQUENCE
                                                                                                                                                  RESULT 25
Q3UD17 MOUSE
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                              Kinase
  % % R B B B
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                                                                                                                                                                                Gaps
                          Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
Phosphotyrosine (by autocatalysis) (By
                                                                                similarity).
N-myristoyl glycine (By similarity).
S-palmitoyl cysteine (By similarity).
F > W (in Ref. 2).
K -> R (in Ref. 2).
I -> T (in Ref. 2).
                                                                                                                                                                                                                                                                                                 01-MAR-2001, sequence version 1.

07-FSB-2006, entry version 20.

Src-family tyrosine kinase SCK.

Salmo salar (Atlantic salmon).

Bararyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei;

Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMR; Q9DKG; 54-502.

GO; GO:0004713; F:ATP binding; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR00179; Prot kinase.

InterPro; IPR001990; SHZ.

InterPro; IPR001452; SH3.

InterPro; IPR001452; SH3.

InterPro; IPR001452; Tyr_pkinase.

InterPro; IPR001452; Tyr_pkinase.

InterPro; IPR008266; Tyr_pkinase_AS.

Pfam; PF07714; Pkinase_Tyr; 1.
                                                                                                                                                              93.0%; Score 40; DB 1; Length 502;
                                                                                                                                                                                0; Indels
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                    4CFC1F3F0E82EADF CRC64;
  'FTId=PRO_0000088104
                                                                                                                                                                                                                                                                                          01-MAR-2001, integrated into UniProtKB/TrEMBI
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                                                                                                                                                                      Pred. No. 19;
1; Mismatches
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SMART; SM00252; SH3; 1.
SMART; SM00219; TYRC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                              similarity)
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QĐDDK6;
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ProDom; PD000093; SH2; 1.
ProDom; PD000066; SH3; 1.
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2
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305
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56885 MW;
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PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
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            1114
2117
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252
357
366
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204
305
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502 AA;
                                                                                                                                                                     Local Similarity
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ACT_SITE
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MOD_RES
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          DOMAIN
DOMAIN
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SMR; Q
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Mus.
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STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
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STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
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                                                                        Length 502;
                                                                                                                                                        0; Indels
502 AA; 56600 MW; 82DF0D677AA99980 CRC64;
                                                                        Score 40; DB 2;
Pred. No. 19;
1; Mismatches
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"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
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                                                                            93.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q3UD17_MOUSE PRELIMINARY;
Q3UD17;
                                Query Match
Best Local Similarity 88.5%,
Shes 8; Conservative
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RA MEDILINE-1223-8683; PUDNGGGGL346-851; DOI=10.1038/naure012266;
RA MEDILINE-1223-8683; PUDNGGGGL346-851; DOI=10.1038/naure012.666;
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Ra Baldarelli R., Hill D.P., Bult C., Hundle C., Gojobori T., Ra Baldarelli R., Hill D.P., Bult C., Hundle C., Gojobori T., Ra Baldarelli R., Ranapin A., Matsuda H., Batalov S., Beisel K.W., Rabadin T., Gariboldi M., Gissi C., Corbani L.E., Cousins S., Ra Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Balda J., Kawaji H., Kawasawa Y., Kadzierski R., Gough J., Ranai A., Kawaji H., Kawasawa Y., Kadzierski R., Yong B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons B.A., Madlais L., Marchionni L., McKenzie L., Miki H., Rayashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Oli D., Ramachandran S., Schneider C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Seton M., Shimada K., Autana R., Takenaka Y., Yonno H., Yanagisawa M., Yang I., Yang L., Wanshaw-Boris A., Yanagisawa M., Yang I., Yang L., Wanshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yang L., Yana Z., Zavolan M., Zhu Y., Xang H., Nakamura M., Yang I., Yang L., Yang L., Yana Z., Zavolan M., Zhu Y., Zimmer A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I., Rhazaki A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I., Rharisti T., Waki K., Kawai Y., Kahii Y., Ishinagawa A., Waninishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., Ranachillan R., Ishiata R., Sakai K., Sasaki D., Shibata R., Shinagawa A., Birney E., Hayashizaki Y., Ranachillan R., Ishiatume W., Ishibata R., Ishiatume W., Ishibata R., Shinagawa A., Birney E., Hayashizaki Y., Ranachillan R., Ishiatume W., Ishibata R., Shinagawa A., Birney E., Hayashizaki Y., Ranachillan R., Ishiatume W., Ishibata R., Shinagawa A., Birney E., Hayashizaki Y., Ranachillan R., Ranachillan R., Ranachillan R., Ranachillan R., Ranachillan R., R
Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schoubach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shihada H., Silvab D., Sinclair B., Shenga H., Shihada R., Silvab D., Sinclair B., Takenka Y., Takenka B., Sugiura K., Sultana R., Takenka Y., Taki K., A Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Vamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., A Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., A Rulda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakwa T., A Lida J., Imamura K., Itch M., Kato T., Kawaji H., Kawagashira N., A Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., A Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The transcriptional landscape of the mammalian genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 309:1559-1563(2005).
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Distributed under the Creative Commons Attribution-NoDerivs License
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Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6J, and NOD; TISSUE-Activated spleen, Bone marrow, and
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Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Immura K., Inotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.,
                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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EMBL; AK149736; BAE29054.1; -; mRNA.
GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
INTERPRO; IPRO00108; Neu cyt fact 2.
INTERPRO; IPR000109; Prof_kinase.
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
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EMBL; AK150709; BAE29787.1; -; mRNA.
EMBL; AK155975; BAE33532.1; -; mRNA.
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Length 503;

DB 2;

Score 40;

93.0%;

Query Match

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Name=BLK;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Aspleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Monse Chan and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchoncoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
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Director MGC Project;
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                              1; Mismatches
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PRINTS; PR00401; SH2DOMAIN.
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                          QGAYV7 RAT
QGAYV7;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hck protein
                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning and chromosomal iocalization of the human homologue of a B-lymphocyte specific protein tyrosine kinase (blk)."; Oncogene 10:477-486(1995).
-!- FUNCTION: May function in a signal transduction pathway that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLK_HUMAN STANDARD; PRT; 504 AA.
P51451; Q16291;
01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
01-OCT-1996, sequence version 1.
07-MAR-2006, entry version 48.
Tyrosine-protein kinase BLK (EC 2.7.1.112) (B lymphocyte kinase) (p55-
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLBOTIDE SEQUENCE [MRNA].
MEDLINE=95123078; PubMed=7822795;
Islam K.B., Rabbani H., Larsson C., Sanders R., Smith C.I.;
"Molecular cloning, characterization, and chromosomal localization of a human lymphoid tyrosine Kinase related to murine Blk.";
J. Immunol. 154:1265-1272(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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-!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.0%; Score 40; DB 2; Length 503; 88.9%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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MEDLINE=91148218; PubMed=7845672;
Drebin J.A., Hartzell S.W., Griffin C., Campbell M.J.,
Niederhuber J.B.;
                                                                                                                                                                                                                                                                                                                                                                                                     56968 MW; 4D4D0777FF3AAC99 CRC64;
                                                                                                                                              SMART; SM00322; SH3; 1.
SMART; SM00326; SH3; 1.
SWART; SM00319; TYKK; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DCM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
SEQUENCE 503 AA; 56968 MW; 4D4D0777FF3P
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H-InvDB; HIX0007315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subfamily.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
PR00452; SH3DOMAIN.
PR00109; TYRKINASE.
PD000001; Prot_kinase; 1.
PD000003; SH2; 1.
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BMBL; S76617, ABA33265.1; -; mRNA.
PNR; 137206; 137206.
HSSP; P16277; 1BLK.
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nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 QISEGMAFI 349
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Feingold E.A., Grouse L.H., Derge J.G.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-myristovl glycine (By similarity).
M -> V (in Ref. 2).
I -> Y (in Ref. 2).
BDBIDF50EC7370C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding; Phosphorylation; SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase. By similarity.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SH2.
Protein kinase.
Proton acceptor (By similarity).
ATP (By similarity).
                MIN, 191305, gard.

RIM, 191305, gard.

RO; GO:0004713; F:protein-tyrosine kinase activity; TAS.

RO; GO:0004713; F:protein kinase cascade; TAS.

RO; GO:0007243; P:protein kinase.

RIMERPRO; IPR002290; Ser_thr_pkinase.

RIMERPRO; IPR001290; SH2.

RIMERPRO; IPR001245; SH3.

RIMERPRO; IPR001245; TYr_pkinase.

RIMERPRO; IPR001245; TYr_pkinase.

RIMERPRO; IPR001245; TYr_pkinase.

REATH PF00114; PR13.

REATH PF00115; SH3.

REATH PF00109; SH3.

REATH PF00000019; SH3.

REATH PF00000019; SH3.

REATH PF00000019; SH3.

REATH PF00000019; SH3.

REATH PF00000019; SH3.

REATH PF00000019; SH3.

REATH PF000000019; SH3.

REATH PF000000019; SH3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00252; SH2; 1.
SMART; SM00252; SH3; 1.
SMART; SM00219; TYPKC; 1.
PROSITE; PS001107; PROTEIN KINASE ATP; 1.
PROSITE; PS00110; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE TYR; FALSE NEG.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DBC-2001, integrated into UniProtKB/TrEMBL 01-DBC-2001, sequence version 1. 07-FBB-2006, entry version 24. B lymphoid tyrosine kinase.
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Q96INI;
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HGNC; HGNC:1057; BLK.
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Kausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Hotschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haiber F., Diatchenko L., Marusina R., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina R., Farmer A.A., Rubin G.M., Hong L., Scheetz T.B., Repleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raplacton M., Loquellano N.B., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Pheton B.J., Lu X., Glibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., And monse CDNA seminan and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human
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R Ensembl; ENSG000013673; Homo sapiens.

R GO; GO:0004713; F:ATP binding; IEA.

GO; GO:0004713; F:ATP binding; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR001459; Ser_thr_pkinase.

R InterPro; IPR001452; SH3.

R InterPro; IPR001452; SH3.

R Pfam; PF00017; SH2; 1.

R Pfam; PF00017; SH2; 1.

R Pfam; PF00017; SH2; 1.

R R PRINTS; PR00401; SH3DOMAIN.

R RRINTS; PR00401; SH3DOMAIN.

R RRINTS; PR000109; TYRKINASE.

R ProDom; PD0000015; SH2; 1.

R PRODOM; PD000066; SH3; 1.

R PRODOM; PR000066; SH3; 1.

R PRODOM; PR0017; PROTEIN KINASE ATP; 1.

R PROSITE; PS0011; PROTEIN KINASE ATP; 1.

R PROSITE; PS0011; PROTEIN KINASE DOM; 1.
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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EMBL; BCO24713; AAH22413.1; -; mRNA.
HSEP; P16277; 1BLK.
SMR; Q961N1; 63-505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences."
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                     11-077-2004, integrated into UniFrotKB/TrEMBL.
11-0CT-2004, sequence version 1.
07-FEB-2006, entry version 11.
                            510 AA.
                           PRELIMINARY; PRT;
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PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKIRASE.
PRODOM; PD000001; Prot_kinase; 1.
ProDom; PD000003; SH2; 1.
ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                       and mouse cDNA sequences.
343 QIAEGMAYI 351
                                                                                                   NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00017;
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                           Q66104_BRARE
Q66104;
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NUCLEOTIDE SEQUENCE [MRNA] OF 368-423
Query Match
Best Local Similarity 88.>
8, Conservative
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P07948;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusha K., Farmer A.A., Rubin G.W., Hong L.,
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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Richards J., Helton E., Kettemen M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
R. Generation and initial analysis of more than 15,000 full-length human
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                                                                  OSCRNAMOS = 29C:92124;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Meopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae; Danio.
NCBI_TaxID=7955;
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SMR; Q66104; 65-510.

E Bresembl; ENSDARG0000031715; Danio rerio.

ZFLN; ZDB-GENE-040912-7; ZGG:92124.

GO; GO:00004713; F:ATP binding; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0006468; P:protein-tyrosine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR00079; Prot kinase.

InterPro; IPR00079; Ser Thr_pkinase.

InterPro; IPR00145; SH3.

InterPro; IPR00145; SH3.

InterPro; IPR00145; Tyr_pkinase.

InterPro; IPR00145; Tyr_pkinase.

InterPro; IPR00145; Tyr_pkinase.

InterPro; IPR00149; Tyr_pkinase.

InterPro; IPR00149; Tyr_pkinase.

InterPro; IPR00149; Tyr_pkinase.
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Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
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WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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X Alusner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

Altscheko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Porner A.A., Rubin G.M., Hong L.,

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Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

X Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Cheneration and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDILMES 8712710; PubMed=3561390;
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Yamanashi Y., Fukushige S., Semba K., Sukegawa J., Miyajima N.,
Matsubara K., Yamamoto T., Toyoshima K.;
Matsubara K., Yamamoto T., Toyoshima K.;
"The yes-related cellular gene lyn encodes a possible tyrosine kinase similar to p561ck.";
MOTO PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONENT PERMONEN
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MEDLINE=94171041; PubMed=8125304; DOI=10.1016/0378-1119(94)90811-7;
Rider L.G., Raben N., Miller L., Jelsema C.;
"The cDMAs encoding two forms of the LNN protein tyrosine kinase are expressed in rat mast cells and human myeloid cells.";
Gene 138:219-222(1994).
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Pred. No. 20;
1; Mismatches
SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 1.
PMO81T; SM00219; TYPKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS0001; SH2; 1.
PROSITE; PS50002; SH3; 1.
SEQUENCE 510 AA; 58258 MW; 5EE8F6822656
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Fyrosine-protein kinase Lyn (EC 2.7.1.112)
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88.9%;
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Search completed: June 29, 2006, 09:29:23
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REMEL; M79321; AAB5019.1; -; mRNA.
REMEL; M79321; AAB50019.1; -; mRNA.
REMEL; RC075001; AAH75001.1; -; mRNA.
REMEL; RC075002; AAH75002.1; -; mRNA.
REMEL; RC075002; AAH75002.1; -; mRNA.
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                                            Partanen J., Maekelae T.P., Alitalo R., Lehvaeslaiho H., Alitalo K.; "Putative tyrosine kinases expressed in K-562 human leukemia cells."; Proc. Natl. Acad. Sci. U.S.A. 87:8913-8917(1990).
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PubMed=1552245; DOI=10.1038/nbt1046;
Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
Zha X.-M., Polakiewicz R.D., Comb M.J.;
"Immunoaffinity profiling of tyrosine phosphorylation in cancer
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-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.

-tyrosine phosphate.

-!- SUBUNIT: Interacts with phosphorylated LIME1 upon BCR activation. Interacts with Epstein-Barr virus LMP2A.

-!- INTERACTION:
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                                                                                                                                                                                                        MUCLEOTIDE SEQUENCE [MRNA] OF 368-423.

MEDLINE=92378604; PubMed=1510669;
Bielke W., Ziemieki A., Kappos L., Miescher G.C.;
Expression of the B cell-associated tyrosine kinase gene Lyn in primary neuroblastoma tumours and its modulation during the differentiation of neuroblastoma cell lines.";
Biochem. Biophys. Res. Commun. 186:1403-1409(1992).
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Event_Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miller C.L., Burkhardt A.L., Lee J.H., Stealey B., Longnecker R.
Bolen J.B., Kieff E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Integral membrane protein 2 of Epstein-Barr virus regulates reactivation from latency through dominant negative effects oprotein-tyrosine kinases.";
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-!- SIMILARITY: Contains 1 SH3 domain.
MEDLINE=91062389; PubMed=2247464;
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3D-structure, Alternative splicing, ATP-binding, Kinase, Lipoprotein, Myristate, Nucleotide-binding, Palmitate, Phosphorylation, Prote-oncogene, SH2 domain, SH3 domain, Transferase, Tyrosine-protein kinase.

By similarity.

CHAIN

1 511 Tyrosine-protein kinase Lyn.
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ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
Phosphotyrosine (by autocatalysis) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphotyrosine.
N-myristoyl glycine (By similarity).
S-palmitoyl cysteine (By similarity).
Missing (in isoform LYN B).
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Pred. No. 20;
1; Mismatches 0; Indels
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Tyrosine-protein kinase Lyn./FTId=PRO_0000088129.
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PRINTS; PR0018; SH3 1; 1.

PRINTS; PR00162; SH3 DOMAIN.

PRINTS; PR00109; TYRKINASE.

ProDom; PD0000093; SH2; 1.

ProDom; PD0000093; SH2; 1.

SMART; SM00252; SH2; 1.

SMART; SM00219; TYRK; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 1.

PROSITE; PS00101; SH3; 1.

PROSITE; PS00101; SH3; 1.
GO:0007165; P:signal transduction; TAS.
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          InterPro; IPR00219; Prot kinase.
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InterPro; IPR001452; SH3.
InterPro; IPR001452; SH3.
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Pfam; PP00714; Pkinase_Tyr; 1.
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	OM protein - protein search, using		Title: US-10-062-257A-16 Perfect score: 49 Sequence: 1 DVWSFGILL 9	Scoring table: BLOSUM62 Gapop 10.0 , Gapext	Searched: 2589679 segs, 4572	Total number of hits satisfying ch	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 100% Maximum Match 100% Listing first 100 s	Database : A Geneseq 8:*	4 0 c			0	No.	score greater than or equal and is derived by analysis o	d	Query	score macon bengul bb	49 100.0 9 4 49 100.0 9 6	49 100.0 9 8	49 100.0 12 2	49 100.0 15 3	49 100.0 30 1	49 100.0 30 2 49 100.0 30 3	1 49 100.0 43 4	2 49 100.0 43 4 3 49 100.0 43 4	4 49 100.0 43 4 5 49 100.0 43 4	9 100.0 43 4	4 49 100.00 43 4	49 100.0 43 5	1 49 100.0 49 5

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The invention relates to a method for the detection of antigen specific recells in a blood sample involving the use of a plurality of antigenic peptides. The method comprises sampling of peripheral blood monocytes; stimulation of the collected peripheral blood monocytes with antigens without direct use of antigen presenting cells; and detection of T-cells specific to the antigen in the stimulated monocytes. The method is particularly used for the detection of cancer as it can be used in semi-apparticularly used for the detection of cancer specific T-cells. It can also be used for cancer vaccine therapy for patients with cervical or prostate cancer. The method can additionally be used to monitor of callular immunity and cancer immune therapy by detection of specific T-cell frequencies. Sequences ABR84165 represent HLA-A2 (human leukocyte antigen) peptides of human origin used in an example from the
                                                                                                                                                                                                 A detection method of antigen specific T-cells, comprises the use of plural antigenic peptides, useful in semi-quantitative determination of cancer specific T-cell frequencies and for monitoring cellular immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; ubiquitin; Ub; T-cell target; melanoma; sarcoma; Hodgkins; Imphoma; non-Hodgkins; leukaemia; neuroblaastoma; myeloma; lung cancer; stomach; skin; thyroid; ovary; prostate; womb; pancreas; colon; bladder; breast; oseophagus; kidney; brain; human; epitope; Lck.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genetic vaccine/ubiquitin (Ub)/Lck-related epitope peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 49; DB 6; Length 9; 100.0%; Pred. No. 2.1e+06;
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                                                                                                                                                                                                                                                          Example 7; Page 8; 18pp; Japanese
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                                                                                  18-SEP-2001; 2001JP-00283413
                                                                                                              13-NOV-2000; 2000JP-00345094
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Best Local Similarity
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                             JP2002365286-A.
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  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and polynucleotides encoding them for treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen specific T-cell; detection; diagnosis; cancer specific T-cell; cancer; tumour; cervical cancer; prostate cancer; cellular immunity; immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
                                                                                                                                                                                                                                                                       Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
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Ady52635 F
Ady52634 F
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                                                                                    ALIGNMENTS
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ADY52642
ADY52636
ADY52635
ADY52634
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                                                                                                                                                         AAB73132 standard; peptide; 9 AA
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nes 9; Conservative
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The invention relates to a novel genetic vaccine containing the ubiquitin gene together with a gene encoding an antigenic protein containing a T-cell target sequence. The vaccine of the invention may be useful for prevention and treatment of cancers including melanoma, sarcoma, lymphoma (Hodgkins or non-Hodgkins), leukaemia, neuroblastoma, myeloma and cancer of the lung, stomach, skin, thyroid, ovary, prostate, womb, pancreas, colon, bladder, breast, oceophagus, kidney or brain. The current sequence is that of a human genetic vaccine/ubiquitin (Ub)-related epitope peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                src-family tyrosine kinase; serine phosphorylation-mediated degradation;
mutation; T cell activation; immune response; screening; cancerous cell;
therapy; immunity; allogenic transplant; xenogeneic organ transplant.
                                                      Gene vaccine containing cancer antigen genes ligated to ubiquitin genes or cytokine genes for prevention and treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide fragment from kinase domain of src-family tyrosine kinases.
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                                                                                               Disclosure; SEQ ID NO 143; 266pp; Japanese
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 Maehara Y;
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Matches 9; Conservative C
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Furue M,
                         WPI; 2004-357144/33
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                                                                                                                                                                                                                                                                                                                                                                    1 DVWSFGILL
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Misc-difference
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Himeno K,
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                                                                                                                                                                                                                                                                                               Query Match
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Claim 21, 23; Page 23; 48pp; English.

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immune response. They can also be used for screening candidate the repense. They can also be used for screening candidate stimulating or blocking the antigen-specific immune response. Identification and development of such compounds and protocols is useful for enhancing, decreasing or preventing antigen-specific immune responses. Therapies which enhance the immune response aid in the development of immunity to antigens derived from pathogens and cancerous cells. Therapies which prevent or decrease the development of an antigenspecific immune response are useful in preventing an immune response to
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                         This represents a peptide fragment from the kinase domain of src-family tyrosine kinase polypeptide. The invention provides src-family tyrosine kinase peptide fragments (AAM80586 to AAM80591), which on mutation reduces the serine phosphorylation-mediated degradation of the polypeptide. The mutation could be a mutation of the serine residue incoated at the amino terminus to alamine and/or could be a mutation that results in a leucine leucine to alamine-alamine change in the polypeptide. The invention also provides methods for detecting the level of T cell activation; for detecting a compound that modulates T cell in the contraction of the mutation is the serine compound that modulates the serine cannot be serine that modulates the serine cannot be serine the serine cannot be serine that modulates the serine cannot be serine that modulates the serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine that modulates the serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine cannot be serine can
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                                                                                                                                                                                                                                                                                                         activation, and for generating a src-family tyrosine kinase polypeptide that has a reduced level of serine phosphorylation-mediated degradation. The methods can be used for the rapid detection of an antigen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigens derived from e.g. allogenic or xenogeneic organ transplants
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84US-00001304.
87US-00039534.
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16-APR-1987;
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Mismatches 0; Indels
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of a portion of the protein, the receptor molecule having been raised to an immunogen containing the polypeptide. High yields of monoclonal receptors can be obtained which bind to or immunoreact with known predetermined epitopes of protein molecules such as oncoproteins. The receptors can be used for e.g. detection of oncoprotein ligands or in affinity sorbants for binding and purifying oncoprotein ligands. (Updated on 27-MUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncoprotein, epitope, oncogene, retroviral; infection, cellular; monoclonal; antibody; MAb; purification, cancer; tumour; growth factor; mitogenic; expression; detection; diagnosis; prognosis; immunoassay; growth; development; neoplasia; foetus; non-invasive, oncoprotein.
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                                                                                                                                                                                   Query Match 100.0%; Score 49; DB 2; Length 15; Best Local Similarity 100.0%; Pred. No. 0.069; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             v-fes encoded oncoprotein epitope #4
                                                                                                                                                                                                                                                                                                                                                                                              AAY52604 standard; peptide; 15 AA
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85US-00736545.
91US-00772702.
94US-00300068.
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21-MAY-1985;
07-OCT-1991;
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28-FEB-2000
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caused by retroviruses. It may also be used for the prognostication of foetal development (and other growth states including neoplasia) using either urine or other body fluid obtained by non invasive methods, the antibodies being used to assay for oncoprotein. As the antibodies bind epitopes of known amino acid sequence, the type of oncoprotein being expressed in the patient may be determined. (Updated on 06-AUG-2003 to correct OS field.)
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85US-00702954.
85US-00736545.
91US-00772702.
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(first entry)
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Best Local Similarity
9; Conserv?
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21-MAY-1985;
07-OCT-1991;
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antibody; immunoglobulin; ligand;

(revised)
(first entry)

85US-00701954

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immunogen; epitope; oncoprotein; detection.
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                            AAW14803 standard; peptide; 30 AA.
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17-AUG-1984;
16-APR-1987;
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23-MAY-1997
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    AAW14803
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caused by retroviruses. It may also be used for the prognostication of foctal development (and other growth states including neoplasia) using either urine or other body fluid obtained by non invasive methods, the antibodies being used to assay for oncoprotein. As the antibodies bind expitopes of known amino acid sequence, the type of oncoprotein being expressed in the patient may be determined. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic polypeptide(s) - useful for immunisation against neoplastic growth and in detection of neoplastic disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP40384 standard; peptide; 30 AA.
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nes 9; Conservative
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09-JAN-1992
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                                                                                                                                                       Monoclonal receptors to protein, esp. onco-protein ligands - prepd. using a polypeptide corresp. to a portion of the protein aminoacid sequence.
                                                                                                                                                                                                                                                                        The sequences given in AAW14803-32 represent peptides derived from oncogenes which are bound by the monoclonal receptors of the invention. The monoclonal receptor molecules are immunoglobulins which bind to both (a) a protein ligand and (b) a polypeptide having an amino acid residue sequence containing 7-40 amino acid residues corresponding to a sequence of a portion of the protein, the receptor molecule having been raised to an immunogen containing the polypeptide. High yields of monoclonal receptors can be obtained which bind to or immunoreact with known predetermined epitopes of protein molecules such as oncoproteins. The receptors can be used for e.g. detection of oncoprotein ligands or in affinity sorbants for binding and purifying oncoprotein ligands. (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncoprotein; epitope; oncogene; retroviral; infection; cellular; amonoclonal; antibody; Mab; purification; cancer; tumour; growth factor; mitogenic; expression; detection; diagnosis; prognosis; immunoassay; growth; development; néoplasia; foetus; non-invasive. oncoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY52601 standard; peptide; 30 AA.
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                                                                                                                                                                                                                                 Disclosure; Page; 41pp; English.
83US-00524084.
84US-00001304.
87US-00039534.
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(first entry)
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Best Local Similarity 100...
9, Conservative
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Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                          gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 22441; 487pp; English
                                                                                                                                                                                                                                                                                               Chen W, Rank DR
                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                          03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                          30-JAN-2001; 2001WO-US000670.
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                                                                                                                          30-JUN-2000;
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                                                                                  04-FEB-2000;
                                                                                                        26-MAY-2000;
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09-AUG-2001
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ABB36636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences AAY52601-Y52675 represent oncoprotein epitopes used to raise monoclonal antibodies which bind to both the epitopes and the proteins chat comprise them. Certain retroviruses are able to cause the formation of solid tumours within a short period of time after infection of the host. Oncogenes, and the oncoproteins they encode, are responsible for the tumorigenic potential of these retroviruses. Retroviral oncogenes are closely related to and are derived from cellular oncogenes, which encode proteins with mitogenic activity such as growth factors. The invention closely relates to monoclonal anti-oncoprotein antibodies, and the method used to purify them. The method of the invention may be used for obtaining purified oncoprotein ligands from aqueous solutions. It may be used in this way to detect proteins produced in tumour cells to diagnose cancers caused by retroviruses. It may also be used for the prognostication of cented development (and other growth states including neoplasia) using either urine or other body fluid obtained by non invasive methods, the antibodies being used to assay for oncoprotein. As the antibodies bind to epitopes of known amino acid sequence, the type of oncoprotein being expressed in the patient may be determined. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                Purifying oncoprotein ligands using monoclonal antibodies, useful for diagnosing cancers caused by retroviruses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; human; microarray; gene expression; cervical epithelial cell;
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Feline sarcoma virus; strain Snyder-Theilen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Col 23-24; 52pp; English.
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                                                                                                                                                           84WO-US001304.
85US-00702954.
85US-00736545.
91US-00772702.
94US-00300068.
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                                                                                                                                                                                    15-FEB-1985;
21-MAY-1985;
07-OCT-1991;
                                                                                                                          02-JUN-1995;
                                                                                                                                                                                                                                                     02-SEP-1994;
                                                                                                                                                                  17-AUG-1984;
                                        US5985587-A
                                                                                  16-NOV-1999
                                                                                                                                                                                                                                                                                                                                            Lerner RA,
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(SENP: see A110068-A120859). The present sequence is a peptide proceed by one such probe. The SENPs are derived from human HeLa cells. The SENPs are because the sea be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; foetal liver; gene expression; single exon nucleic acid probe
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                                                                                                                                                                                                                               100.0%; Score 49; DB 4; Length 43; 100.0%; Pred. No. 0.2;
                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB36636 standard; peptide; 43 AA
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2000US-00608408.
2000US-00632366.
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2000US-0236359P.
2000GB-00024263.
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27-SEP-2000;
04-OCT-2000;
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WO200157278-A2

Homo sapiens

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ID AAM17
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XX
AC AAM17
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DT 12-0'
XX
DE PEPT
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KW Prob
KW CETV
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 44 cells. The method involves contacting the probes with a collection of detectably labelled mucleic acids derived from mRNA of human breast, and then measuring the label bound to each probes of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional conformation from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed
such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide #4074 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New spatially-addressable set of single exon nucleic acid probes, for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID NO 14391; 327pp + Sequence Listing; English.
                                                                                                                                           100.0%; Score 49; DB 4; Length 43; 100.0%; Pred. No. 0.2; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                       ABB31423 standard; peptide; 43 AA.
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; 2000US-0234687P.
; 2000US-0236359P.
; 2000GB-00024263.
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2000US-00608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2002 (first entry)
                                                                                                                                                                                        9; Conservative
                                                             human genetic disorders
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                                                                                                                                                                  Local Similarity
                                                                                                       Sequence 43 AA;
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30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
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                                                                                                                                               Query Match
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                                                                                                                                                                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences
                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
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                                                                                                                                                                                      Claim 27; SEQ ID NO 29271; 639pp + Sequence Listing; English.
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                                          Rank DR
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  (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-2000; 2000US-0207456P.
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21-SEP-2000; 2000US-0234687P
27-SEP-2000; 2000US-0236359P
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                                        Chen
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                                          Hanzel DK,
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                                                                                WPI; 2001-483447/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM30133;
                                        Penn SG,
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Matches

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The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one

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AAM69792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  measuring human gene expression in a sample derived from human heart (see ABA21555-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, monitoring and proponsing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                  expression.
specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single exon nucleic acid probes for analyzing gene expression in human hearts.
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes for
                                                                              ö
                                                                                                                                                                                                                                                  Protein #3969 encoded by probe for measuring heart cell gene
                                                                                                                                                                                                                                                                       Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 49; DB 4; Length 43; 100.0%; Pred. No. 0.2; ive 0; Mismatches 0; Indels
                                                        DB 4; Length 43;
                                                                              0; Indels
                                                                  0.2;
                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15; SEQ ID NO 23740; 530pp; English
                                                      100.0%; Score 49; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank
                                                                                                                                                                               ABB21970 standard; protein; 43 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023458PP.
27-SEP-2000; 2000US-0234559P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US000666
                                                                                                                                                                                                                           (first entry)
                                                                             9; Conservative
                                                                                                                                                                                                                                                                                             congenital heart disease
                                                                                                                      DVWSFGILL 31
                                                                                                  1 DVWSFGILL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488899/53
                                                        Query Match
Best Local Similarity
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                                   Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                         WO200157274-A2
                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                           23-JAN-2002
                                                                                                                                                                                                     ABB21970;
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                                                                                                                                                      RESULT 15
ABB21970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human brain expressed single exon probe encoded protein SEQ ID NO: 29504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                            Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                       Human bone marrow expressed probe encoded protein SEQ ID NO: 30098.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 49; DB 4; Length 43; 100.0%; Pred. No. 0.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qene expression in human bone marrow.
                                                                                                                                    AAM69792 standard; protein; 43 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM57399 standard; protein; 43 AA
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2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
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2000US-00608408.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488900/53.
DVWSFGILL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                               WO200157276-A2.
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                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000;
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Gaps

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Best Local Similarity 100. Matches 9; Conservative

Query Match

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(MOLE-) MOLECULAR DYNAMICS INC
 30-JUN-2000; 2000US-00608408
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Matches 9: Conserm
                                                                                                                                                                                                                                                                                                                                                                              23 DVWSFGILL
                                                                                                                                                                                                                                                                                                      Sequence 43 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM05274;
                                                                         Penn SG,
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 19
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                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
          Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
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                                                                                                                                                                                                                                                                         Example 4; SEQ ID NO 29504; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 49; DB 4; Length 43; 100.0%; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                           Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human liver peptide, SEQ ID No 30135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG51487 standard; peptide; 43 AA.
                                                                                                            04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0224687P.
27-SEP-2000; 2000US-0234637P.
                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                          Chen W,
                                                                                            30-JAN-2001; 2001WO-US000667
                                                                                                                                                                     2000GB-00024263
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26-MAY-2000; 2000US-0207456P
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Best Local Similarity 100.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                          Penn SG, Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 43 AA;
                                                       WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157273-A2
         brain
                                     Homo sapiens
                                                                                                                                                                     04-OCT-2000;
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                                                                         09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG51487;
                                                                                                                                                                                                                                                        brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 18
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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #3956 encoded by probe for measuring breast gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 49; DB 4; Length 43; 100.0%; Pred. No. 0.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID NO 30135; 658pp; English.
                                                                                                                                                                                                                                             Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM05274 standard; protein; 43 AA.
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                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
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200005-00633366
200005-0234687P.
200005-0236359P.
2000GB-00024263.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                                                                                    04-OCT-2000; 2000GB-00024263
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2000US-0207456P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31
                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DVWSFGILL 9
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The present invention relates to novel single exon nucleic acid probes use AA100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory disease of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                  Novel single exon nucleic acid probe used to measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human peptide encoded by genome-derived single exon probe SEQ ID 29086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; single exon probe; asthma; lung cancer; COPD; ILD; bronic Obstructive pulmonary disease; interstital lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Plok disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 49; DB 4; Length 43; 100.0%; Pred. No. 0.2;
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                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 14014; 322pp; English.
                               Rank DR;
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                                   Chen W,
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03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
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                                   Hanzel DK,
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                                                                                                                                                                                                         human breast
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                                   Penn SG,
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes of the human lung, comprising the novel set of probes of the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, in the above mentioned microarray; assigning exons to a single gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The the above mainting exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or call types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or call types indicates that expression of the exons in the tissues and/or call types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORP). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung cancer, chronic obstructive pulmonary disease such as asthma. Jung cancer, chronic obstructive pulmonary diseases (ODP), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, cuberous sclerosis, quanter a disease, Niemann-Pick disease, Hermansky-budlak syndrome, sarcoidosis, pulmonary hamenosiderosis, primary chistiocytosis, lymphangioleiomyomicosis, pulmonary alveolar proteinosis, dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, JAK, protein kinase signalling; protein tyrosine kinase; enzyme; kinase like domain; pseudo-substrate loop; anti-asthmatic; anti-allergic; dermatological; anti-inflammatory; anti-tumour; cytostatic; immunostimulant; JAK inhibitor; JAK modulator; asthma; eczema;
                                                                                                         Spatially-addressable set of single exon nucleic acid probes, used to
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                                                                                                                                      measure gene expression in human lung samples.
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                                                                                                                                                                                         Claim 27; SEQ ID NO 29086; 634pp; English
Chen W, Rank DR
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Matches 9; Conservative
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Hanzel DK,
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WO2004082458-A2

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The present invention describes a method (M1) of selecting or designing a compound for the regulation of JAK activity involving assessing the ability of the compound to modulate the interaction of the pseudocation of the pseudocation of the pseudocation of the pseudocation of the pseudocation of the pseudocation of the pseudocation interactes with the kinade of the compound (C1) which reduces the KLD (interacts with the binding of the PSL with the KLD), which reduces the activity of the JAK compared to that of the JAK in the absence of the compound. JAK has anti-asthmatic, anti-callergic, dermatological, anti-inflammatory, immunostimulant, anti-tumour and cytostatic. The method can be used for designing or selecting a compound with the ability to regulate JAK activity; for the treatment of a subject suffering from a JAK-associated disease state such as asthma, cezema, food allergy, inflammatory bowel disease, Crohn's disease, Crohn's disease, Lumour and prostate cancer. The method provides a number of target points at which a chemical entity regulates JAK activity. The present sequence represents a JAK family related amino acid sequence, which is given in
                                                                                                                                                                                                                                                                                                                                                                                                                            Method of selecting or designing a compound useful in the treatment of e.g. asthma by assessing the ability of the compound to modulate the interaction of the pseudo-substrate loop with the kinase like domain.
food allergy; inflammatory bowel disease; Crohn's disease; leukaemia; lymphoma; cutaneous inflammation; immune suppression; solid tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 23; 82pp; English.
                                                                                                                                                                                                                 30-JAN-2002; 2002WO-AU000088
                                                                                                                                                                                                                                                           30-JAN-2001; 2001AU-00002791
                                                                                                                                                                                                                                                                                                   (CYTO-) CYTOPIA PTY LTD.
                                                                                                                                                                                                                                                                                                                                            Atkin J,
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-608498/65
                                            prostate cancer.
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                                                                                                                             WO200260927-A1
                                                                                        Homo sapiens
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                                             100.0%; Score 49; DB 5; Length 49; 100.0%; Pred. No. 0.23;
                                                             0; Indels
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                                                                                                                                                                                 Rat FES partial protein sequence SeqID9.
                                                                                                                                 ADT00021 standard; protein; 65 AA.
                                                                                                                                                                16-DEC-2004 (first entry)
                                                             9; Conservative
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tyrosine kinase; cancer; anti-cancer agent; signalling molecule; tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FES; GUCY2F; MCCK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor;

guanylate cyclase stimulator; rat

Rattus norvegicus.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel activated mutant protein tyrosine kinases and associated methods for diagnosing cancer and screening for anti-cancer agents. Protein kinases are signalling molecules involved in tumourigenesis. Mutational analysis of the human tyrosine kinase gene family identified somatic alteration sin 1 in 5 colorectal cancers, with the majority of mutations occurring in the NTRK3, FES, GUCY2F and MCCK/MLK4 genes. Most were identified in the kinase domain. The invention may be useful for the production of compounds with a cytostatic activity acting as protein tyrosine kinase inhibitors or guanylate cyclase stimulators. The invention may be useful for developing methods for detecting mutations involved in cancer or screening for anti-cancer agents. The present sequence is that of a partial protein which was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tyrosine kinase; cancer; anti-cancer agent; signalling molecule; tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FBS; GUCY2F; MCCK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor; guanylate cyclase stimulator; chicken.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and MCCK) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCCK) ar
associated methods for diagnosing cancer and screening for anti-cancer
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                                                                                                                                     18-FEB-2004; 2004WO-US004452
                                                                                                                                                                                                    21-FEB-2003; 2003US-0448537P.
29-MAY-2003; 2003US-0473895P.
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29-MAY-2003; 2003US-0473895P.
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Vogelstein

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This invention relates to a novel activated mutant protein tyrosine kinases and associated methods for diagnosing cancer and screening for anti-cancer agents. Protein kinases are signalling molecules involved in tumourigenesis. Mutational analysis of the human tyrosine kinase gene family identified somatic alteration sin 1 in 5 colorectal cancers, with the majority of mutations occurring in the NTRK3, FES, GUCY2F and MCCK/MLK4 genes. Most were identified in the kinase domain. The invention may be useful for the production of compounds with a cytostatic activity acting as protein tyrosine kinase inhibitors or guanylate cyclase stimulators. The invention may be useful for developing methods for detecting mutations involved in cancer or screening for anti-cancer agents. The present sequence is that of a partial protein which was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine kinase; cancer; anti-cancer agent; signalling molecule;
tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FES;
GUCY2F; MCCK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor;
                                                                            Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCCK) and associated methods for diagnosing cancer and screening for anti-cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 49; DB 8; Length 66; 100.0%; Pred. No. 0.32; cive 0; Mismatches 0; Indels
             Kinzler KW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human FES partial protein sequence SeqID6
                                                                                                                                            Example 4; SEQ ID NO 10; 363pp; English.
             Velculescu V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         guanylate cyclase stimulator; human
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29-MAY-2003; 2003US-0473895P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 100
Matches 9; Conservative
               Parsons W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DVWSFGILL 9
                                             WPI; 2004-718702/70
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 66 AA;
             Bardelli A,
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Gaps

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This invention relates to a novel activated mutant protein tyrosine kinases and associated methods for diagnosing cancer and screening for anti-cancer agents. Protein kinases are signalling molecules involved in tumourigenesis. Mutational analysis of the human tyrosine kinase gene family identified somatic alteration sin 1 in 5 colorectal cancers, with the majority of mutations occurring in the NTRK3, FSE, gUCY2F and MCCK/MLK4 genes. Most were identified in the kinase domain. The invention may be useful for the production of compounds with a cytostatic activity acting as protein tyrosine kinase inhibitors or guanylate cyclase
Vogelstein B;
                                                                                                                                                                                 Activated mutant protein tyrosine kinases (e.g. NTRK3, associated methods for diagnosing cancer and screening
    Kinzler KW,
                                                                                                                                                                                                                                                                                                                                                                  Example 4; SEQ ID NO 7; 363pp; English.
    Velculescu V,
    Parsons W,
                                                                                        WPI; 2004-718702/70.
    Bardelli A,
                                                                                                                                                                                                                                                                                  agents.
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and MCCK) and anti-cancer

Activated mutant protein tyrosine kinases (e.g. NTRK3, FES associated methods for diagnosing cancer and screening for

Example 4; SEQ ID NO 6; 363pp; English.

Vogelstein

Velculescu V, Kinzler KW,

(UYJO) UNIV JOHNS HOPKINS.

Bardelli A, Parsons W,

WPI; 2004-718702/70

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     This invention relates to a novel activated mutant protein tyrosine kinases and associated methods for diagnosing cancer and screening for anti-cancer agents. Protein kinases are signalling molecules involved in tumourigenesis. Mutational analysis of the human tyrosine kinase gene family identified somatic alteration sin i in 5 colorectal cancers, with the majority of mutations occurring in the NTRK3. FES, GUCY2F and MCCK/MLK4 genes. Most were identified in the kinase domain. The invention may be useful for the production of compounds with a cytostatic activity acting as protein tyrosine kinase inhibitors or guanylate cyclase stimulacors. The invention may be useful for developing methods for detecting mutations involved in cancer or screening for anti-cancer in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine kinase; cancer; anti-cancer agent; signalling molecule; tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FES; GUCY2F; MCCK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor; guanylate cyclase stimulator; cat; feline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FES and MCCK) and for anti-cancer
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                                                                                                                                                                                                                                    100.0%; Score 49; DB 8; Length 66; 100.0%; Pred. No. 0.32;
                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                Mismatches
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29-MAY-2003; 2003US-0473895P.
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                                                                                                                                                                                                                                                Local Similarity 100.
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                                                                                                                                                                                                           Sequence 66 AA;
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Matches
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This invention relates to a novel activated mutant protein tyrosine kinases and associated methods for diagnosing cancer and screening for anti-cancer agents. Protein kinases are signalling molecules involved in tumourigenesis. Mutational analysis of the human tyrosine kinase gene family identified somatic alteration sin 1 in 5 colorectal cancers, with the majority of mutations occurring in the NTRK3 FES, GUCYSP and MCCK/MLK4 genes. Most were identified in the kinase domain. The invention may be useful for the production of compounds with a cytostatic activity acting as protein tyrosine kinase inhibitors or guanylate cyclase stimularors. The invention may be useful for developing methods for activity mutations involved in cancer or screening for anti-cancer agents. The present sequence is that of a partial protein which was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    tyrosine kinase; cancer; anti-cancer agent; signalling molecule; tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FES; GUCY2F; MCCK; MLK4; Kinase domain; cytostatic; tyrosine kinase inhibitor; guanylate cyclase stimulator; mouse; murine.
stimulators. The invention may be useful for developing methods for detecting mutations involved in cancer or screening for anti-cancer agents. The present sequence is that of a partial protein which was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCCK) and associated methods for diagnosing cancer and screening for anti-cancer
                                                                                                                                                          Gaps
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                                                                                                                         DB 8; Length 66;
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                                                                                                                     100.0%; Score 49; DB 8; 100.0%; Pred. No. 0.32;
                                                                                                                                                         Mismatches
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29-MAY-2003; 2003US-0473895P.
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                                                                                                                                                       Conservative
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Best Local Similarity
...... 9; Conserv?
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                                                                                     Sequence 66 AA;
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The invention relates to a crystal (I) of human janus kinase 3 (JAK3)

domain, domain comprising JAK3 domain, a computer (composition comprising a machine-
readable data storage medium, working memory, CPU and output hardware),

using a computer for selecting an orientation of a chemical entity that
interacts favorably with a binding pocket/domain, using a computer for
selecting an orientation of a chemical entity with a favorable shape

complementarity in a binding pocket of JAK3, identifying a candidate
inhibitor of a molecule/molecular complex comprising a binding pocket of domain, designing a compound/complex that interacts with a binding

pocket/domain, utilizing molecular replacement to obtain structural
information of a molecule/a molecular complex of unknown structura (
information of a molecule/a molecular complex of unknown structural
information of a molecule/a molecular complex of unknown structural
information of a candidate inhibitor that interacts with a binding site of information and a chemical entity chosen from adenosine, ATP, ATP

che molecule is sufficiently homologous to human JAK3 domain); and
identifying a candidate inhibitor that interacts with a binding site of a
chuman JAK3 domain and a chemical entity chosen from adenosine, ATP, ATP

chosphate and active site inhibitor (preferably AMP-PNP). The JAK3 domain
is chosen from amino acid residues 810-1100, 810-1104, 810-1115, 810-1124

for screening kinase inhibitor useful as drugs for treating severe
combined immunodeficiency (SCID). The present sequence is the alpha-FG

region from another tyrosine kinase used as comparator for the alpha-FG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of human janus kinase 3 domain, domain complex or its homolog,
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                                                                                                                                                                                                                                                                                             c-Src; tyrosine kinase; protein structure; crystallography; protein co-ordinate data; drug discovery; severe combined immunodeficiency; immunostimulant.
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                                                                                                                                                                                                                                                        Tyrosine kinase alpha-FG region from c-Src.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for screening kinase inhibitor.
                                                                                                                                     AED85831 standard; protein; 70 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-2005; 2005WO-US014216.
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08-APR-2005; 2005US-0669771P.
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Matches 9; Conservative
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                    DVWSFGILL
DVWSFGILL
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                                                                                                                                                                                                                                                                                                                                                                               Unidentified
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Query Match
100.0%; Score 49; DB 8; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels

55 DVWSFGILL 63

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed construction of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed activity of (II) or to treat disease states involving (II). (II) is cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cusful for generating antibodies against it, detecting or quantitating a supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capacities, forensics, genemapphig, identification of mutations of diagnostics, forensics, genemapphig, identification of mutations and to produce other types of date and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from WHD at celectronic format directly from WHD at celectronic format directly from WHD at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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Local Similarity 100.0%; Pred. No. 0.41;
les 9; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                Novel human diagnostic protein #22253.
                                                                                                                                    ABG22262 standard; protein; 85 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT;
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                       18-FEB-2002
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Polymucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polymucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; and antagonists may have neuroprotective; cytostatic; cardioactive; and communicative mascular active general; vulnerary; gastrointestinal communication also includes antibodies specific for the protein or polymucleotide sequences. The lung cancer associated polymucleotide sequences may be used for detection of lung cancer, chromosome cor research purposes. The proteins may be used to treat disorders such as contract, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases.

Colymucleotide sequences AAF18425 - AAF18433 and peptide AAB5849 are used in the course of the invention for the identification and characterisation of the polymucleotide and protein sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                              Human, lung cancer associated protein, neuroprotective, cytostatic, cardioactive; immunomodulatory; muscular active; vulnerary; cardioactive; immunomodulatory; muscular active; synecological; astrointestinal; nephrotropic; antiinfective; synecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer.
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                                                                                                                           cancer associated polypeptide sequence SEQ ID 526.
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               AAB58188 standard; protein; 90 AA.
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(ROSE/) ROSEN C A.
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Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease; Human protein encoded by clone HLUNG20011260. ADB64505 standard; protein; 114 AA (HELI-) HELIX RES INST. (REAS-) RES ASSOC BIOTECHNOLOGY. 05-NOV-2001; 2001JP-00379298. 25-JAN-2002; 2002US-00350978. 28-MAR-2002; 2002EP-00007401. 04-DEC-2003 (first entry) cancer; tumour. Homo sapiens. EP1308459-A2 07-MAY-2003. ADB64505; ADB64505

Otsuki T, Wakamatsu A, Sato H, Ishii S; Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I; Otsuka M, Nagahari K, Masuho Y;

Isogai T, Sugiyama T, Yamamoto J, Isono Y, Seki N, Yoshikawa T, WPI; 2003-450961/43.

N-PSDB; ADB62535

New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.

Claim 1; Page; 222pp; English.

The invention discloses a polymucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel colling defined nucleotide sequences which encode novel to polymeptides. Also claimed is a polymeptide encoded by the polymucleotide or peptide or paptide or peptide, an antibody binding to the polymeptide or peptide or peptide of the polymucleotide, immunologically assaying the polymeptide or peptide or peptide of the polymucleotide by contacting the polymucleotide or peptide or peptide of the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polymucleotide in an expressible manner and an antisense polymucleotide. The oligonucleotide or as a probe for detecting the polymucleotide. The polymucleotide and encoded proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and adiagnostic marker or medicines for regulation of their expression and activity, or as targets of genes many be included in them, for developing a diagnostic marker or configuration. Membrane proteins, signal transduction-related proteins, tisease-related proteins, transcription-related proteins, disease-related proteins, creamedicion membrane proteins, disease-related proteins are conding them can be used as indicactors for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence data for this patent is not represented in the printed proverse parton, but is based on sequence information supplied by the European Patent Office.

Sequence 114 AA;

ö Gaps ; 0 / Match 100.0%; Score 49; DB 7; Length 114; Local Similarity 100.0%; Pred. No. 0.55; nes 9; Conservative 0; Mismatches 0; Indels Query Match Matches

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ALIGNMENTS

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NyAlternate names: protein-tyrosine kinase cyl; protein-tyrosine kinase T2 (Species: Homo sapiens (man) (C.Species: Homo sapiens (man) (C.Species: Homo sapiens (man) (C.Species: Jo-Uun-1992 #sequence revision 20-Aug-1994 #text_change 05-Oct-2004 (C.Speciesion: JH0559; 838818; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 819024; 8
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A;Residues: 1-450 <BRA>
A;Cross-references: UNIPROT:P41240; UNIPARC:UPI0000128541; EMBL:X59932; NID:g30255; PIDN
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A;Title: Characterization of the human CSK locus.
A;Reference number: S38818; MUID:93241739; PMID:7683131
A;Accession: S38818
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Best Local Similarity 1000.
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A;Molecule type: DNA
A;Residues: 1-450 <BR2>
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A;Molecule type: mRNA
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Cispecies: dallus gallus (chicken)
Cispecies: dallus gallus (chicken)
Cispecies: 13-59-1996 #sequence_revision 13-5ep-1996 #text_change 09-Jul-2004
Cibacesion: 13-60406
Ripfaff, S.L.; Zhou, R.
Ripfaff, S.L.; Zhou, R.
Aittle: Defining the borders of the chicken proto-fps gene, a precursor of Fujinami sar Aittle: Defining the borders of the Chicken proto-fps gene, a precursor of Fujinami sar Aittle: Defining the borders of the Chicken proto-fps gene, a precursor of Fujinami sar Aittle: Defining the borders of the Chicken GB/EMBL/DDBJ
Aittle: Dreliminary; translated from GB/EMBL/DDBJ
Aistle: Dreliminary; translated from GB/EMBL/DDBJ
Aistle: Dreliminary; translated from GB/EMBL/DDBJ
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C;Species: Rattus norregicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: S04328
R;Letwin, K.; Vee, S.P.; Pawson, T.
Oncogene 3, 621-627, 1988
A;Title: Novel protein-tyrosine kinase cDNAs related to fps/fes and eph cloned using ant A;Reference number: S04327; MUID:94167102; PMID:2485255
A;Accession: S04328
A;Molecule type: mRNA
A;Residues: 1-323 <-LET>
A;Cross-references: UNIPROT:P09760; UNIPARC:UPI000012AA08; EMBL:X13412; NID:g56169; PIDN C;Genetics:
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C; Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
C; Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; tyrosine-speci
F; 62-322/Domain: protein kinase homology <KIN>
F; 70-78/Region: protein kinase ATP-binding motif
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protein-tyrosine kinase (EC 2.7.1.112) - feline sarcoma virus (fragment)

Nathernate names: gag-onc fusion protein

C; Species: feline sarcoma virus

C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C; Accession: S04205

R; Kappes, B; Ziemiecki, A.; Mueller, R.G.; Theilen, G.H.; Bauer, H.; Barnekow, A.

Oncogene 4, 363-372, 1989

A; Title: The TP1 isolate of feline sarcoma virus encodes a fgr-related oncogene lacking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Introns: 41/2; 94/1; 135/1
C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
C;Reywords: ATP
F;1-180/Domain: protein kinase homology (fragment) <KIN>
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Matches 9; Conservative 0; Mismatches
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Best Local Similarity 100.
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A; Molecule type: DNA
A; Residues: 1-392 «KAP»
A; Cross-references: UNIPROT:Q28414; UNIPARC:UPI00001046DB; EMBL:X14842; NID:g1089; PIDN:G
C; Superfamily: feline sarcoma virus protein-tyrosine kinase fgr; protein kinase homology,
C; Keywords: ATP; autophosphorylation; myristylation; oncogene; phosphoprotein; phosphotr:
F;7-104/Domain: SH2 homology «SH2»
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
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A,Experimental source: adult amygdala; clone DKFZp761P1010
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                                                                                                                                                                                                                                                                                                                               F;154/Active site: Lys #status predicted
F;275,386/Binding site: phosphate (Tyr) (covalent)
                                                                                                                                                                                                                                                       F;124-382/Domain: protein kinase homology «KIN»
F;132-140/Region: protein kinase ATP-binding motif
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A; Experimental source: sciatic nerve C; Genetics: S, A; Experimental source: sciatic nerve C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; G
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R;Klages, S.; Adam, D.; Class, K.; Fargnoli, J.; Bolen, J.B.; Penhallow, R.C.
Proc. Natl. Acad. Sci. U.S.A. 91, 2597-2601, 1994
A;Title: Ctk: a protein-tyrosine kinase related to Csk that defines an enzyme family. A;Reference number: A53469; MUID:94195789; PMID:7511815
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Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
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C;Species: Gallus gallus (chicken)
C;Date: 31-nen-1000 H-1
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F;201-209/Region: protein kinase ATP-binding motif
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A,Molecule type: DNA
A,Residues: 1-450 <SAB>
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A;Residues: 1-450 <RES>
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A, Molecule type: mRNA
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A;Cross-references: UNIPARC:UPI0000128541; EMBL:X60114; NID:930314; PIDN:CAA42713.1; PID
R;Holtrich, U.; Braeuninger, A.; Strebhardt, K.; Ruebsamen-Waigmann, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 10411-10415, 1991
A;Title: Two additional protein-tyrosine kinases expressed in human lung: fourth member
A;Reference number: S19025; MUID:92073297; PMID:1720539
A;Cross-references: UNIPARC:UPI0000128541; EMBL:X74765; NID:g402582; PIDN:CAB58562.1; PIR:Partanen, J.; Armstrong, E.; Bergman, M.; Maekelae, T.P.; Hirvonen, H.; Huebner, K.; A Oncogene 6, 2013-2018, 1991
A;Title: cyl encodes a putative cytoplasmic tyrosine kinase lacking the conserved tyrosine A;Reference number: S19024; MUID:92050797; PMID:1945408
A;Accession: S19024
A;Status: preliminary
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A; Map position: 15q23-15q25
A; Map position: 15q23-15q25
A; Introin: 5/3; 43/3; 81/2; 154/3; 186/1; 208/1; 241/2; 271/3; 296/2; 361/3; 390/3
C; Function:
A; Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C; Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C; Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F; 16-65/Domain: SH3 homology <SH3>
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A; Cross-references: UNIPARC: UPI0000128541; EMBL: X59932; NID: 930255; PIDN: CAA42556.1; PID A; Note: this sequence was submitted to the EMBL Data Library, June 1991
C; Comment: This protein lacks the N-myristylation and autophosphorylation sites present
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A;Accession: PT0195
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 05-Oct-2004
C;Accession: 815094; S18500; PT0195
R;Nada, S.; Okada, M.; MacAuley, A.; Cooper, J.A.; Nakagawa, H.
Asture 315, 69-72, 1991
A;Title: Cloning of a complementary DNA for a protein-tyrosine kinase that specifically A;Reference number: 815094; MUID:91226538; PMID:1709258
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Modecule type: mRNA
A,Residues: 1-450 <MND1>
A,Cross-references: UNIPROT:P32577; UNIPARC:UP100001132C9; EMBL:X58631; NID:957507; PIDN
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A;Residues: 44-49;54-67;77-86;126-137;330-337;352-360;367-376;394-401 <NAD>
A;Cross-references: UNIPARC:UPI000017258F; UNIPARC:UPI0000172590; UNIPARC:UPI0000172591
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F;193-447/Domain: protein kinase homology <KIN>
F;201-209/Region: protein kinase ATP-binding motif
F;222/Active site: Lys #status predicted
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A;Residues: 319-367 <LAI>
A;Cross-references: UNIPARC:UP10000149DAC
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R;Lai, C.; Lemke, G.
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protein-tyrosine kinase (EC 2.7.1.112)
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Conservative 0
  100.08;
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Best Local Similarity 100.vv
Pest 100 9; Conservative
                                                                                                                                                                                                                                                         C; Species: feline sarcoma virus
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
9; Conserve
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                                                                      1 DVWSFGILL
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A;Residues: 1-477 <HAM>
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         C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C;Keywords: APP; phosphotransferase; tyrosine-specific protein kinase
E;16-68/Domain: SH3 homology SH3>
E;82-171/Domain: SH2 homology SH2>
F;82-171/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Howo sapiens (man)
C;Species: Howo sapiens (man)
C;Accession: 549016
R;Mitchell, P.J.; Barker, K.T.; Martindale, J.E.; Kamalati, T.; Lowe, P.N.; Page, M.J.;
R;Mitchell, P.J.; Barker, K.T.; Martindale, J.E.; Kamalati, T.; Lowe, P.N.; Page, M.J.;
A;Title: Cloning and characterisation of CDNAs encoding a novel non-receptor tyrosine ki
A;Reference number: S49016; MUID:94309916; PMID:8036022
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A;Residues: 1-453 <RES>
A;Cross-references: UNIPROT:Q61561; UNIPARC:UPI0000289C9; GB:M32054; NID:g193276; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q13882; UNIPARC:UPI000004F1D9; EMBL:X78549; NID:g515025; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Dec-2004
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Dec-2004
C;Accession: 149663
Mol. Cell. Biol. 10, 146-153, 1990
A;Fitle: A murine fer testis-specific transcript (ferT) encodes a truncated fer prot A;Reference number: 149663; MUID:90097822; PMID:2294399
A;Accession: 149663
A;Status: preliminary; translated from GB/EMBL/DDBJ
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F/78-170/Domain: SH2 homology <SH2>
F/78-170/Domain: protein kinase homology <KIN>
F/197-205/Region: protein kinase ATP-binding motif
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F;91-177/Domain: SH2 homology <SH2>
F;91-1732-457/Domain: protein kinase homology <KIN>
F;200-208/Region: protein kinase ATP-binding motif
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                               368 DVWSFGILL 376
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A; Status: preliminary
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- feline sarcoma virus (strain Snyder-Theilen)
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C,Date: 2.7Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C,Accession: A00652
R;Hampe, A.; Laprevotte, I.; Galibert, F.; Fedele, L.A.; Sherr, C.J.
75-785, 1982
A;Title: Nucleotide sequences of feline retroviral oncogenes (v-fes) provide evidence for A;Reference number: A00651; WUID:83050963; PMID:6183005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology C;Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; transfe,115-200/Domain: SH2 homology <SH2> F;115-200/Domain: BH2 homology <KIN> F;212-230/Region: protein kinase ATP-binding motif F;222-230/Region: protein kinase ATP-binding motif F;245/Active site: Lys #status predicted
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A;Cross-references: UNIPROT:045539; UNIPARC:UPI00001755F8; EMBL:281543; PIDN:CAB04427.1;
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A,Introns: 82/3, 123/2, 153/1; 219/1; 242/3; 330/3; 427/1
C,Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology,
C,Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; thiol
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;4/Binding site: palmitate (Cys) (covalent) #status predicted
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Species: Caenorhabditis elegans
Spate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004
       Gaps
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C;Comment: This protein is synthesized as a gag-fes polyprotein.
   Indels
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submitted to the EMBL Data Library, November 1996
A;Reference number: 219561
A;Acession: T22405
Mismatches
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F;237-495/Domain: protein kinase homology «KIN»
F;245-253/Region: protein kinase ATP-binding motif
F;245-253/Region: protein kinase ATP-binding motif
F;246-253/Region: protein kinase ATP-binding motif
F;246-253/Region: protein kinase ATP-binding motif
F;34/Rodified site: myrathate (Cys) (covalent) #status predicted
F;267/Active site: Lys #status predicted
F;388/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
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F;62-110/Domain: BH3 homology <SH3>
F;237-495/Domain: protein kinase homology <KIN>
F;237-495/Domain: protein kinase ATP-binding motif
F;245-253/Region: protein kinase ATP-binding motif
F;245-253/Region: protein kinase ATP-binding motif
F;246-74ctive site: myristylated amino end (Gly) (in mature form) #status predicted
F;348,499/Rinding site: palmitate (Cys) (covalent) #status predicted
F;367/Active site: Lys #status predicted
F;388,499/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Holtzman, D.A.; Cook, W.D.; Dunn, A.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 8325-8329, 1987
A;Title: Isolation and sequence of a cDNA corresponding to a src-related gene expressed
A;Reference number: A39973; MUID:88068587; PMID:3317404
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NyAlternate names: kinase-related transforming protein (bmk)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C;Accession: A27282; A39973
R;Klemsz, M.J; McKercher, S.R.; Maki, R.A.
Nucleic Acids Res. 15, 9600, 1987
A;Title: Nucleotide sequence of the mouse hck gene.
A;Reference number: A27282; MUID:88067781; PMID:3684607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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F;121-218/Domain: SH2 homology <SH2>
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A;Residues: 1-50,'V',52-204,'R',206-305,'T',307-503 <REM>
A;Cross-references: UNIPARC:UPI0000170BD7; EMBL:X62345; NID:g57581; PIDN:CAA44218.1; PID
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C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro
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A;Residues: 1-503 <OKA>
A;Cross-references: UNIPROT:P50545; UNIPARC:UPI000012C350; GB:S74141; NID:g241436; PIDN:
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R; Okano, Y.; Sugimoto, Y.; Fukuoka, M.; Matsui, A.; Nagata, K.; Nozawa, Y.
Biochem. Biophys. Res. Commun. 181, 1137-1144, 1991
A; Title: Identification of rat cDNA encoding hck tyrosine kinase from megakaryocytes. A; Reference number: JQ1321; MUID:92109719; PMID:1764064
                                                                                                                                                                                                                                                                                                                                                                             R.; Takeda, N.; Chiba,
                                                                                                                                                                                                                                                                                                              C;Accession: A56040; I56322
R;Kohmura, N.; Yagi, T.; Tomcoka, Y.; Oyanagi, M.; Kominami, R.; Takeda, N.; Chiba, Mol. Cell. Biol. 14, 6915-6925, 1994
A;Title: A novel nonreceptor tyrosine kinase, Srm: cloning and targeted disruption. A;Reference number: A56040; MUID:95021220; PMID:7935409
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                                                                                                                                                                                 protein-tyrosine kinase (BC 2.7.1.112) Srm, nonreceptor type - mouse C;Species: Mus musculus (house mouse)
C;Date: 01-Dec:1995 #sequence_revision 01-Dec-1995 #text_change 31-Dec-2004
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: JQ1321; S18974
R;Okano, Y.; Sugimoto, Y.; Fukuoka, M.; Matsui, A.; Nagata, K.; Nozawa, Y.
Biochem. Biophys. Res. Commun. 181, 1137-1144, 1991
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F;232-491/Domain: protein kinase homology <KIN>
F;240-248/Region: protein kinase ATP-binding motif
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submitted to the EMBL Data Library, December 1991
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C,Superfamily: SH2 homology; SH3 homology
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A;Accession: S18974
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A; Residues: 1-496 <KOH>
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A, Status: preliminary
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A;Cross-references: UNIPROT:P42685; UNIPARC:UP1000012AC35; EMBL:U00803; NID:g392887; PID
                                                                                                                                                                      C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase F;49-105/Domain: SH3 homology <SH3>
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C;Species: Gallus Glicken)
C;Species: Gallus Glicken)
C;Date: 16-Jun-2000 #sequence-revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: A47126; A39939
R;Chow, L.M.; Ratcliffe, M.J.; Veillette, A.
A)Ol. Cell. Biol. 12, 1226-1233, 1992
A;Title: tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene.
A;Reference number: A42126; MUID:92186854; PMID:1545804
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A;Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBIP:88833)
A;Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBIP:88833)
B;Strebhardt, K., Mullins, J.I., Bruck, C.; Ruebsamen-Waigmann, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987
A;Title: Additional member of the protein-tyrosine kinase family: the src-and lck-related A;Reference number: A39939; MUID:88097370; PMID:3321053
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A;Residues: 52-507 <STR>
A;Cross-references: UNIPARC:UP100001713B3; GB:J03579; NID:g212712; PIDN:AAA490B1.1; PID:
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F; 125-22/Domain: SH3 homology <SH3>
F; 241-499/Domain: Brotein kinase homology <KIN>
F; 241-499/Domain: protein kinase homology <KIN>
F; 249-257/Region: protein kinase ATP-binding motify (in mature form) #status predicted F; 392,503/Binding site: myristylated amino end (GJy) (in mature form) #status predicted F; 392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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F;232-494/Domain: protein kinase homology <KIN>
F;240-248/Region: protein kinase ATP-binding motif
F;262/Active site: Lys #status predicted
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                                                                                                A;Cross-references: GDB:355675
A;Map position: 4q35-4q35
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Best Local Similarity 100.
Matches 9; Conservative
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A; Residues: 1-88 < CHO>
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                                                                      A; Gene: GDB: FRK
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A; Map position: 20q1-20q12
A; Map position: 20q1-20q12
A; Map position: 20q1-20q12
A; Map position: 20q1-20q12
A; Map position: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C; Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C; Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
C; Superfamily: Tyrosine kinase hok #status predicted <MAT>
F; A: 2005/Product: protein-tyrosine kinase hok #status predicted <MAT>
F; A: 112/Domain: SH3 homology <SH2>
F; A: 2005/Domain: protein kinase homology <KIN>
F; A: 2005/Region: protein kinase homology <KIN>
F; A: 2005/Region: protein kinase ATP-binding motif
F; A: 2006/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F; 3/Binding site: palmitate (Cys) (covalent) #status predicted
F; 300/Binding site: Lys #status predicted
F; 300/Binding site: Dys #status predicted
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A;Cross-references: UNIPARC:UPI000015C528; GB:M16592; NID:g183913; PIDN:AAA52644.1; PID:
R;Hradetzky, D.; Strebhardt, K.; Ruebsamen-Waigmann, H.
Gene 113, 275-280, 1992
A;Title: The genomic locus of the human hemopoietic-specific cell protein tyrosine kinas
A;Reference number: JC1149; MUID:92241680; PMID:1572549
                                                                                                                                                    A; Note: the codon given for 3-Cys (TCG) is inconsistent with the authors' translation R; Ziegler, S.F.; Marth, J.D.; Lewis, D.B.; Perlmutter, R.M. Mol. Cell. Biol. 7, 2276-2285, 1987
A; Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of A; Reference number: A27812; MUID:87257943; PMID:3453117
A; Accession: A27812
A; Molecule type: mRNA
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A;Reference number: 138396; MUID:94171047; PMID:7510261
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A; Residues: 157-505 < HRA>
A; Residues: 157-505 < HRA>
A; Cross references: UNIPARC:UP10000172589; EMBL:X59741
B; Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lebraeslaiho, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A; Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A; Reference number: A38268; MUID:91062389; PMID:2247464
A; Accession: C38268
A; Status: nucleic acid sequence not shown; not compared with conceptual translation
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A,Accession: A27811
A,Molccule type: mcs Cont.
A,Residues: 1-505 cOUL>
A,Ccoss-references: UNIPROT:P08631; UNIPARC:UPI000015C528; GB:M16591
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A; Residues: 362-417 < PAR>
A; Cross-references: UNIPARC:UPI000017258A
C; Genetics:
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DVWSFGILL 426
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-505 <RES>
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A; Residues: 1-205, 'ASAITPI', 212-257,'RCGW', 262,'TTT', 266,'T', 268-281,'AGRLP', 287-503,'STA; Cross-references: UNIPARC: UP1000016809E; EMBL: X05027; NID: 936807; PIDN: CAA28691.1; PID R; Valilette, A.; Foss, F.M.; Sausville, E.A.; Bolen, J.B.; Rosen, N. Oncogene Res. 1, 357-374, 1987
A; Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in human colon carcinoma and other not a state of the lock tyrosine kinase gene in the lock tyrosine kinase gene in the lock tyrosine kinase gene in the lock tyrosine kinase gene in t
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A; Residues: 368-471, H', 473-509 < VEI>
A; Cresidues: 368-471, H', 473-509 < VEI>
A; Cresidues: 368-471, H', 473-509 < VEI>
B; Crevillyan, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Linna, T.J.
Biochim. Biophys. Acta 888, 286-295, 1986
A; Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56 (LSTRA).
A; Reference number: S07143; MUID:87000726; PMID:3489486
A; Accession: S07143
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A;Title: Structure of the two promoters of the human lck gene: differential accumulation A;Reference number: A32797; MUID:89313764; PMID:2787474
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KGazvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cell
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A;Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
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251-259/Region: protein kinase ATP-binding motif
251-259/Region: protein kinase ATP-binding motif
251-259/Region: myristylated amino end (Gly) (in mature form) #status predicted
3,5/Binding site: palmitate (Cyg) (covalent) #status predicted
273/Active site: Lys #status predicted
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Pred. No. 3;
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A;Residues: 'A',376-509 <TRE>
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A;Residues: 1-35,'VR' <RES>
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A; Molecule types: mRNA
A; Residues: 1-282, 'VP', 285-509 <MAR>
A; Residues: 1-282, 'VP', 285-509 <MAR>
A; Residues: 10-282, 'VP', 285-509 <MAR>
A; Note: the sequence is revised in GenBank entry MUSLCK, release 116.0, (PIDN:AABS9674.1
R; Voronova, A.F.; Adler, H.T.; Sefton, B.M.
Mol. Cell. Biol. 7, 4407-4413, 1987
A; Title: Two lck transcripts containing different 5' untranslated regions are present in A; Reference number: 157629; MUID:88142832; PMID:3501824
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-11 <VOR>
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Mol. Cell. Biol. 8, 3058-3064, 1988
AjTitle: Structure of the murine lck gene and its rearrangement in a murine lymphoma cell A; Reference number: 157636; MUID:89096891; PMID:2850479
A,Accession: 177452
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A,Accession: 177452
A,Accession: 1774
                                             A;Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promote
A;Reference number: 148845; MUID:86146842; PMID:3081813
A;Accession: 148845
                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:091X65; UNIPARC:UPI00000018D; EMBL:X03533; NID:g54813; PIDN R;Marth, J.D.; Peet, R.; Krebs, B.G.; Perimutter, R.M. 393-404, 1985
A;Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpres A;Reference number: A23639; MUID:86079521; PMID:2416464
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F;243-501/Domain: protein kinase homology <KIN>
F;243-501/Domain: protein kinase homology <KIN>
F;251-29/Region: protein kinase ATP-binding motif
F;21/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;273/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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A;Reference number: JQ0152; MUID:90108697; PMID:2558056
A;Accession: JQ0152
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A; Residues: 1-509 <ROU>
A; Cross-references: UNIPROT: P06239; UNIPARC: UPI0000151F17; EMBL: X14053
A; Cross-references: UNIPART: D.B.; Peet, R.; Ziegler, S.F.; Wilson, J. Cell. Biochem. 38, 117-126, 1988
A; Title: Structure and expression of lck transcripts in human lymphoid cells.
A; Reference number: S07822; MUID: 89123626; PMID: 3265417
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C;Date: 30-Sep-1992 #text change 05-Oct-2004
C;Accession: JQ0152; S07822; $07200; S01879; S07143; A32797; I57636
R;Rouer, B.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, Gene 84, 105-113, 1989
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N.Alternate names: kinase-related transforming protein (lck)
                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-509 <VOR1>
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100.0%; Pred. No. 3;
:ive 0; Mismatches
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RjBielke, W.; Ziemieki, A.; Kappos, L.; Miescher, G.C.
Biochem. Blophys. Res. Commun. 186, 1403-1409, 1992
A;Title: Expression of the B cell-associated tyrosine kinase gene lyn in primary neurobla
A;Reference number: PH0949; MUID:92378604; PMID:1510669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Experimental source: neuroblastoma SK-IN cell R; Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C. Gene 138, 219-222, 1994 A; Title: The CDNAs encoding two forms of the LYN protein tyrosine kinase are expressed in A; Reference number: IS3715; MUID:94171041; PMID:8125304 A; Accession: IS3715
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A;Cross-references: UNIPROT:Q61364; UNIPARC:UPI00000E734B; GB:L36132; NID:g556287; PIDN:;A;Cross-references: UNIPROT:Q61364; UNIPARC:UPI0000E734B; GB:L36132; NID:g556287; PIDN:;A;Thuveson, M.; Albrecht, D.; Zurcher, G.; Andres, A.C.; Ziemiecki, A. Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. Psop. 582-539; 1995
A;Title: iyk, a novel intracellular protein tyrosine kinase differentially expressed in this A;Reference number: 148608; MUID:95251656; PMID:7733928
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F;253-26J/Region: protein kinase ATP-binding motif
F;2Nodified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;275/Active site: bys #status predicted
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
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Status: not compared with conceptual translation
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                                                                                          A, Residues: 369-424 < PAR>
A, Cross-references: UNIPARC:UP10000172583
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 369-424 <BIE>
A;Cross-references: UNIPARC:UP10000172583
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A; Residues: 1-24,46-512 <RID>
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les 9; Conserv
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                                                       Molecule type: mRNA
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A; Residues: 1-24,46-230, L',232-307, 'A',309-418, 'Y',420-512 <RID2>

A; Cross-references: UNIPARC:UPI0000170BE2; GB:L1482; NID:2994580; PIDN:AAA20945.1; PID:

A; Cross-references: UNIPARC:UPI0000170BE2; GB:L1482; NID:3294580; L, the source is designed by the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
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R.7Accession: A.6719; D38268; PH0949; I53715

R.7Yamanashi, Y.; Prukushige, S.I.; Semba, K.; Sukegawa, J.; Miyajima, N.; Matsubara, K.; Mol. Cell. Biol. 7, 237-243, 1987

A.Title: The yes-related cellular gene lyn encodes a possible tyrosine kinase similar to A; Reference number: A.6719; MUID:87172710; PMID:3561390

A.Accession: A.6719

A.Molecule type: mRNA

A; Residues: I-512 - YAMA

A; Mackelae: C. YAMA

A; Mackelae: U.S. A; Ralfalo, R.; Lehvaeslaiho, H.; Alitalo, K.

Proc. Natl. Acad. Sci. U.S. A. 87, 8913-8917, 1990

A; Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.

A; Reference number: A38268; MUID:91062389; PMID:2247464
                                                                                                                                                                                                                  C)Date: 18-Feb-2000 #sequence revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: I56160; I67811; I67812
R;Minoguchi, K.; Nishikata, H.; Siraganian, R.P.
J: Immunol. 150, 222, 1993
A;Title: Bacterially expressed rat p561yn binds several proteins in rat basophilic leuke
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Ksesidues: 1-230,'L',322-307,'A',309-418,'Y',420-512 <RID1>
A;Cross-references: UNIPARC:UP10000170BE3; GB:L14782; NID:g294578; PIDN:AAA20944.1; PID:
A;Note: in Genbank entry RATLYNATYR, release 116.0, PIDN:AAA20944.1, the source is desig
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-512 <MIN>
A;Cross-references: UNIPROT:Q07014; UNIPARC:UP10000167AC2; GB:L14951; NID:g294582; PIDN:
R;Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.
Gene 138, 219-222, 1994
A;Title: The cDNAs encoding two forms of the LYN protein tyrosine kinase are expressed in A;Reference number: I53715; MUID:94171041; PMID:8125304
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                                                                                          protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - rat
N;Contains: protein-tyrosine kinase lyn, splice form B
C;Species: Rattus norvegicus (Norway rat)
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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100.0%; Pred. No. 3;
iive 0; Mismatches
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A;Cross-references: UNIPROT:Q63206; UNIPARC:UP100000E7676; EMBL:X57018; NID:956145; PIDN
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A;Title: Novel putative protein kinase clones from a rat large granular lymphocyte tumox A;Reference number: PT0196; MUID:91287726; PMID:2062320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;72-121/Domain: SH3 homology <SH3>
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F;249-507/Domain: protein kinase homology <KIN>
F;257-265/Region: protein kinase ATP-binding motif
F;277-265/Region: protein kinase ATP-binding motif
F;27/Wodified site: myristylated amino end (Gly) (in mature form) #status predicted
F;279/Active site: Lys #status predicted
F;279/Active site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
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Vicology 189, 556-567, 1992
A;Title: Small deletion in v-src SH3 domain of a transformation defective mutant of Rous
A;Reference number: A42994; MUID:92351554; PMID:1322589
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F;207-279/Region: protein kinase ATP-binding motif
F;270-279/Region: protein kinase ATP-binding motif
F;22/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;29/Active site: Lys #status predicted
F;413/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experime
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: S24547; PT0200
R;Yue, C.C.
submitted to the EMBL Data Library, December 1990
A;Reference number: S24547
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A;Residues: 1-523 <DEZ>
A;Cross-references: UNIPROT:P31693; UNIPARC:UPI0000135F2B; GB:M84475
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A;Residues: 371-427 <YU2>
A;Cross-references: UNIPARC:UP100001755F4
A;Experimental source: lymphocyte cell line
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-517 <YUE>
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Matches 9; Conserv
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                                                    A; Molecule type: mRNA
A; Residues: 1-153, Tr., 155-236, Hr., 238-512 < RE2>
A; Residues: 1-153, Tr., 155-236, Hr., 238-512 < RE2>
A; Cross-references: UNIPARC:UP100000E8172; EMBL: 248757; NID: 9736263; PIDN: CAA88658.1; PI C; Genetics:
A; Gene: BSK
C; Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C; Reywords: ATP: blocked amino end; intestine; lipoprotein; myristylation; phosphotransf F; 56-112/Domain: SH3 homology < SH3>
F; 123-15/Domain: protein kinase homology < KIN>
F; 239-501/Domain: protein kinase ATP-binding motif F; A77-255/Region: protein kinase ATP-binding motif F; Amdified site: myristylated amino end (Gly) (in mature form) #status predicted
F; SH30-504/Active site: Dalmitate (Cys) (covalent) #status predicted
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A,Status: preliminary
A,Molecule type: mRNA
A,Robicsule type: mRNA
A,Robicsule type: mRNA
A,Residues: 1-40, NN. 42-211, 'Q', 213-517 < YIA>
A,Residues: 1-40, NN. 42-211, 'Q', 213-517 < YIA>
A,Cross-references: UNIPARC:UP1000028C67; EMBL:X16440; NID:950393; PIDN:CAA34463.1; PIC
C,Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C,Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
E,72-121/Domain: SH3 homology < SH2>
F,72-121/Domain: SH2 homology < SH2>
F,249-507/Domain: protein kinase homology < KIXX>
F,249-507/Domain: protein kinase ATP-binding motif
F,257-265/Region: protein kinase ATP-binding motif
F,257-265/Region: myristylated amino end (Gly) (in mature form) #status predicted
F,279/Active site: Lys #status predicted
F,511/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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A; Residues: 1-517 < KIN>
A; Cross-references: UNIPROT:P14234; UNIPARC:UPI0000041D4; GB:X52191; NID:g50395; PIDN:C
A; Experimental source: monocyte tumor cell line from strain Balb/c
R; Yi, T.L.; Willman, C.L.
Oncogene 4, 1081-1187, 1989
A; Title: Cloning of the murine c-fgr proto-oncogene cDNA and induction of c-fgr expressi
A; Reference number: S10072; WUID:89385605; PMID:2674853
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N'Alternate names: kinase-related transforming protein (fgr)
C;Species: Mus musculus (house mouse)
C;Date: 30-3na-1993 #sequence_revision 30-Jan-1993 #text_change 05-Oct-2004
C;Accession: A43807; S10072; Ā33127
R;King, F.J.; Cole, M.D.
Oncogene 5, 337-344, 1990
A;Title: Molecular cloning and sequencing of the murine c-fgr gene.
A;Reference number: A43807; MUD:90191719; PMID:2179817
A;Molecular A43807.
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100.0%; Pred. No. 3;
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protein-tyrosine kinase (BC 2.7.1.112) fgr
                        A;Status: translated from GB/EMBL/DDBJ
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A)Reference number: A38018; MUID:83059858; PMID:6292477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onco F;88-137/Domain: SH3 homology <SH3>
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F;265-523/Domain: protein kinase homology <KIN>
F;253-281/Region: protein kinase ATP-binding motif
F;273-281/Region: protein kinase ATP-binding motif
F;21%-oditied site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experimen
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F;88-137/Domain: SH3 homology <SH3>
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F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;273-281/Region: protein kinase ATP-binding motif
F;273-281/Region: protein kinase ATP-binding motif
F;295/Active site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experimen
                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-15,'C',17-94,'RT',97-116,'D',118-337,'T',339-526 <TA2>
A;Cross-references: UNIPARC:UP10000135F24; GB:K00928; NID:g210187; PIDN:AAA42565.1;
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C;Date: 01-Sep-1981 #sequence_revision 17-Dec-1982 #text_change 05-Oct-2004
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R;Schwartz, D.; Tizard, R.; Gilbert, W.
submitted to the Nucleic Acid Sequence Database, September 1982
A;Reference number: A00632
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R;Neil, J.C.; Ghysdael, J.; Vogt, P.K.; Smart, J.E.
Nature 291, 675-677, 1981
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C.Species: Rous sarcoma virus
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R.Czerniofsky, A.P.; Levinson, A.D.; Varmus, H.B.; Bishop, J.M.; Tischer, E.; Goodman, Nature 301, 736-738, 1983
A.Title: Corrections to the mucleotide sequence of the src gene of Rous sarcoma virus.
A.Rocession: A38017
A.Rocession: A38017
A.Rocession: A38017
A.Rocession: A38017
A.Rocession: A38017
A.Rocession: A38017
A.Rocession: A38017
A.Rocession: A38017
A.Rocession: Rounder: Schaidt-Ruppin
R.Takeya, T.; Handrus, H.
Cell 32, 881-990, 1983
A.Title: Structure and sequence of the cellular gene homologous to the RSV sec gene and A.Rocession: A00631
A.Rocession: A00631
A.Rocession: A00631
A.Rocession: Rounder: A00630; MUD: 8315564; PMID: 6299580
A.Rocession: A00631
A.Rocession: A00631
A.Rocession: A00631
A.Rocession: A00631
A.Rocession: Rounder: Strain Schmidt-Ruppin strain of Rous Sarcom A.Rocession: Solids Res. 17, 1252, 1989
A.Title: Nucleotide sequence of the src gene of the Schmidt-Ruppin strain of Rous A.Rocession: S02756
A.Rocession: S02766
A.Rocession: S02786
A.Rocession: S02786
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A.Rocession: S02786
A.Rocession: Rounder: Waller A.R.; Hanafusa, H.
B.Rocession: Rouse-references UNIPARC:UPI0000135F2C; EMBL:X13745; NID:g61908; PIDN:CASA32012.1; PILR
B.R.Takeya, T.; Peldman, R.A.; Hanafusa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: translation not shown
A;Status: translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesiduse: 1-526 <BOD>
A;Cross-references: UNIPROT:P25020; UNIPARC:UPI0000135F2A; EMBL:X15345; NID:g61706; PIDN
C;Genetics:
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C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Reyords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; ond
C;Reyords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; ond
C;Reyords: ATP; autophosphorylation; blocked amino end;
F;188-137/Domain: SH3 homology <SH3>
F;148-245/Domain: protein kinase homology <KIN>
F;265-523/Domain: protein kinase ATP-binding motif
F;273-281/Region: protein kinase ATP-binding motif
F;273-281/Region: protein kinase ATP-binding motif
F;285/Active site: myristylated amino end (Gly) (in mature form) #status predicte
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
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                                                                                                                                                                                  protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain H-19)
N;Alternate names: kinase-related דיבוסלרישויה
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C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-.
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-.
C;Accession: S09609
R;Bodor, J.; Poliak, E.; Pichrtova, J.; Geryk, J.; Svoboda, J.
Nucleic Acids Res. 17, 8869, 1989
A;Title: Complete nucleotide sequence of LTR, v-src, LTR provirus H-19.
A;Reference number: S09609; MUID:90067864; PMID:2587228
A;Status: translation not shown
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الاستفادة 9; Conservative
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A,Residues: 1526 <LIUs
A,Cross-references: UNIPROT:064994; UNIPROT:092806; UNIPROT:060567; UNIPROT:007461; UNIP
A,Cross-references: UNIPROT:064994; UNIPROT:092806; UNIPROT:060567; UNIPROT:007461; UNIP
A,Ferperimental source: strain Prague
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989
A,Note: only a list of differences from sequence S09665 is given; however, the list is in R,Ferperimentary, V.J.; Wyke, J.J.
A,Note: only a list of differences from sequence S09665 is given; however, the list is in R,Title: Localization of temperature-sensitive transformation mutations and back mutation A,Reference number: S09665; MUID:86200422; PMID:3009882
A,Reference number: S09665; MUID:86200422; PMID:3009882
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C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
S;Reywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; ond
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
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F;265-523/Domain: protein kinase homology <KIN>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;273-281/Region: protein kinase ATP-binding motif
F;2/Active site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
RESULT 30
S15582
protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague A)
C;Species: Rous sarcoma virus
A;Variety: strain Prague A
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Oct-2004
C;Accession: S15582; 809665
R;Liu, Z.; Hackett, P.B.
Nucleic Acids Res. 17, 3986, 1989
A;Title: Sequence variation of the Rous sarcoma virus PrA src gene.
A;Reference number: S15582; MUID:89282411; PMID:2543959
A;Actus: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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058F01_HUMAN
06156_HUMAN
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Q8N5D7_HUMAN
Q5R3A8_HUMAN
Q5TYU7_BRARE
Q1U6Q5_MOUSE
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Q6ZMB9_CHICK
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028414 FLV
028414 MOUSE
070W10 CIOIN
04R6L8 MACFA
04RAT6 TETNG
STYK1 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OSSLR3 HUMAN
OSSELS HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q53EL3 HUMAN
Q80UT3 MOUSE
CSK CHĪCK
CSK HUMAN
CSK MOUSE
CSK RAT
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Q3TLX4_MOUSE
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                                                                                                                                                                                                                                        Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                              protein search, using sw model
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FLK_RAT
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09BDK8
                                                                June 29, 2006, 08:59:39
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Gapop 10.0 , Gapext 0.5
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1: uniprot sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Query
Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                         OM protein
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Result Š. Sarcom

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NUCLEOTIDE SEQUENCE.

RX STRAIN=CS7BL/6J; TISSUE=Whole body;
RX CATAIN=CS7BL/6J; TISSUE=Whole body;
RX CATAIN=CS7BL/6J; TISSUE=Whole body;
RX CATAIN=CS7BL/6J; TISSUE=Whole body;
RA CATAINCI P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., RA CATAIN R., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Bajic V.B., Brenner S.E., Aldinis V., Allen J.E.,
RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxrer L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA di Bernardo D., Down T., Fruuno M., Futaki S., Gariboldi M.,
R Fletcher C.F., Fukushima P., Gingeras T.R., Golobori T., Green R.E.,
Georgii-Hemming P., Gingeras T.R., Golobori T., Green R.E.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2005, sequence version 2.
07-FRB-2006, entry version 24.
10, 11 days embryo whole body cDNA, RIKEN full-length enriched ilbrary, clone:2810409K13 product:c-src tyrosine kinase, full insert sequence. (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                       2; Length 181;
                                                                                                                      GO; GO: 0005524; F:ATP binding; IEA.
GO; GO: 0004713; F:ATP binding; IEA.
GO; GO: 00004713; F:protein-tyrosine kinase activity; IEA.
GO; GO: 00006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR0019; Prot kinase.
InterPro; IPR001290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase_AS.
Pfam; PF07714; Pkinase_Tyr; 1.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                        181 AA; 20808 MW; 351873AB8DD35188 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                       Score 49; DB 2
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 AA.
                                                        EMBL, M11611, AAA49008.1; -; Genomic_DNA.
PIR; I50406; I50406.
HSSP, P11362; IFGK.
Ensembl; ENSGALG00000008340; Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                          ProDom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
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0
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100.0%;
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nes 9; Conservative
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QEBIS9;
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SEQUENCE
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                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                          MEDLINE=85187981; PubMed=2581127;
Parker R.C., Mardon G., Lebo R.V., Varmus H.E., Bishop J.M.;
"Isolation of duplicated human c-src genes located on chromosomes 1
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Ensembl; ENSG00000000938; Homo sapiens.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000413; F:protein-tyrosine kinase activity; IEA.

GO; GO:000468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR00719; Prot kinase.

R InterPro; IPR001245; Tyr pkinase.

R Pfam; PF07714; Pkinase Tyr; 1.

R PRINTS; PR00109; TYRKINASE.

R ProDom; P000001; Prot kinase; 1.

R PROSTIE; PS50011; PROTEIN KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 49; DB 2;
100.0%; Pred. No. 1.2;
tive 0; Mismatches 0;
                                                                            01-MAY-1997, integrated into UniProtKB/TrEMBL.
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                                             113 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; K03219; AAA60585.1; -; Genomic_DNA.
HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001, sequence version 2.
07-FEB-2006, entry version 28.
Fps proto-oncogene, 3' end. (Fragment).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                             PRT;
                                                                                                                                                                                                                                                                                                                                           Mol. Cell. Biol. 5:831-838(1985).
                                                                                           01-MAY-1997, sequence version 1. 07-FEB-2006, entry version 28. C-src-2 protein (Fragment).
                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
les 9; Conservative
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                                                                                                                                                          Homo sapiens (Human)
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                                            P78483_HUMAN
P78483;
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Gaps

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MEDINE-2235468; PubMed=1246685; DOI=10.1038/nature01266; MEDLINE-22354683; PubMed=1246685; DOI=10.1038/nature01266; MEDLINE-22354683; PubMed=1246685; DOI=10.1038/nature01266; MEDLINE-22354683; PubMed=1246685; DOI=10.1038/nature01266; MEDLINE-22354683; PubMed=1246685; DOI=10.1038/nature01266; MEDLINE-22354683; PubMed=1246685; DOI=10.1038/nature01266; MEDLINE-23161; MEDLINE-23161; MEDLINE-23161; MEDLINE-23161; MEDLINE-23161; MEDLINE-23161; MEDLINE-23166; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE-2316; MEDLINE A Jakt M., Kanapin A., Katch M., Kawasawa Y., Kelso J., Kitamura H., Aktano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Akurochkin I.V., Lazereu L.P., Lazerevic D., Lipovich L., Liu J., Liu J., Akurochkin I.V., Lazerewic D., Lipovich L., Liu J., Liu J., Akurochkin I.V., Maden Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Akuroda N., Nakano N., Nakanoh H., Mg P., Mortagui-Tabar S., Mulder N., Nakano N., Nori F., Ohara O., Akurazai Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G., Petrovsky N., Palaze S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Knan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Sandelin A., Schneider C., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Akanaya S., Stupka E., Sugiura K., Sulener J., Takenaka Y., Takenaka Y., Takenaka Y., Takenaka S., Stupka E., Sugiura K., Sulener J., Tegner J., Teichmann S.A., Amamoishi H., Zabarcvsky E., Zhu S., Tegner J., Yagi K., Yananishi H., Zabarcvsky E., Zhu S., Ximer A., Hide W., Bult C., Amanishi H., Zabarcvsky E., Zhu S., Ximer A., Hide W., Bult C., Mattick J.S., Liu E.T., Brusic V., Quackenbush J., Akananishi H., Zabarcvsky E., Zhu S., Ximer A., Kangashira N., Rawashina T., Kojina M., Kodo S., Konno H., Nakano K., Ninomiya N., Ragami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki E., Nawashi J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawashina J., Kawas Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002). STRAIN=C57BL/6J; TISSUB=Whole body;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005). "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005). NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEOUENCE Hayashizaki Y.;

STRAIN=C57BL/6J; TISSUE=Whole body;
BUDILNES-21085660; PubMed=-11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

NUCLEOTIDE SEQUENCE

PUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUB=Whole body;

Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

Adachi J., Aizawa K., Akahira S., Akimura T., Bukunishi Y., Furuno M.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

Inotani K., Ishii Y., Itoh M., Izawa M., Kabukawa T., Kato H.,

Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

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Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Murametou M., Hayashizaki Y.,

Submitted (UUL-2000) to the EMBL/GenBank/DDBJ databases. A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., A Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Suzuki R., Tomita M., Magner L., Washio T., Balake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J. Bult C., Fletcher C., Fujita M., Gariboldi M., Brownstein M.J., Hume D.A., Kamiya M., Lee N.H. Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Toyo-oka K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Winnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Minning L., Munchioni L., Wanning Y., Kawaji H., Kohtsuki S., Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License STRAIN=C57BL/6J; TISSUE=Whole body; MEDLINE=20499374; PubMed=110421199; DOI=101/GY.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nubata Indexion and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000). STRAIN=CSTBL/6J; TISSUE=Whole body;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

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Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamanoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara B., Watshiwagi K.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RIKEN integrated sequence analysis (RISA) system-384-format

Genome Res. 10:1757-1771(2000). annotation of a full-length mouse cDNA collection."; EMBL; AK013057; BAC25388.2; -; mRNA.
SNR; QBLS9; 1-182.
MGI: MGI: B8537; Csk.
GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
InterPro; IPR00013; Prot kinase.
InterPro; IPR00145; Tyr_Dkinase.
InterPro; IPR00145; Tyr_Dkinase.
InterPro; IPR008266; Tyr_Dkinase.
FRUM: PR00149; PKNIASE.
PR00109; TYRKINASE.
PRODOM; PD000001; PTCK Kinase; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1. Nature 409:685-690(2001). tyrosine phosphate. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE Hayashizaki Y.; "Functional

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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
MEDLINE-2005030; Pubmed-10552041;
Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
"Protein tyrosine kinase CDNAs from amphioxus, hagfish, and lamprey: isoform duplications around the divergence of cyclostomes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MBDLINE=20020330: PubMed=10552041;
Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
"Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:
isoform duplications around the divergence of cyclostomes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gnathostomes.";
J. Mol. Evol. 49:601-608(1999).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                       gnathostomes.";
J. Mol. Evol. 49:601-608(1999).
-!- CATALYTIC ACTVITY: ATP + a protein tyrosine = ADP + a protein
tyrosine phosphate.
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01-MAY-2000, sequence version 1.
07-FBB-2006, entry version 28.
Src-like B (Fragment).
Eptatretus burgari (Inshore hagfish).
Eukaryota; Metazaa; Chordata; Craniata; Hyperotreti; Myxiniformes; Myxinidae; Eptatretinae; Eptatretus.
                                                                                       Lampetra reissneri (Far Eastern brook lamprey).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lethenteron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 49; DB 2; Length 245; 100.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO: 0005524; F:ATP binding; IEA.
GO; GO: 0004713; F:ATP binding; IEA.
GO; GO: 0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO: 0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR00139; Prot kinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PR07114; Pkinase Tyr; 1.
PRINTS; PR00109; TYRKIÑASE.
Probom; PR0000019; Prot kinase; 1.
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                 01-MAY-2000, integrated into UniProtKB/TrEMBL. 01-MAY-2000, sequence version 1. 07-FBB-2006, entry version 28. Src-like B (Fragment).
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NOSSITE, PS50011, PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB025550; BAA84740.1; -; mRNA.
HSSP; P12931; 1FMK.
SMR; Q9PVU9; 1-245.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Berkeley;
Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Membrane, single-pass type I membrane protein (By similarity).
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                 Length 215;
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GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004713; F:Portein-tyrosine kinase activity; IEA.

GO; GO:0006468; P:portein amino acid phosphorylation; IEA.

InterPro; IPR002719; Prot kinase.

InterPro; IPR002290; Ser thr pkinase.

InterPro; IPR00245; Tyr pkinase.

InterPro; IPR002666; Tyr pkinase.

InterPro; IPR0020866; Tyr pkinase AS.

Pfam; PF07714; Pkinase Tyr; 1.
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PRINTS; PR00109; TYRINGSE
ProDom; PD000001; Prot_kinase; 1.
PRODOM; PD000001; Prot_kinase; 1.
PROSTITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
ATP-binding; Developmental protein; Kinase; Membrane; Nucleotide-binding; Receptor; Transferase; Transmembrane; Tyrosine-protein kinase.
Tyrosine-protein kinase.
SEQUENCE 235 AA; 27038 MW; 8B9F65DB2EE15B9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                      215 AA; 24394 MW; 41D8521DE365FE11 CRC64;
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100.0%; Pred. No. 2.5;
ive 0; Mismatches 0
                                                                               100.0%; Score 49; DB 2; 100.0%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                07-DEC-2004, integrated into UniProtKB/TrEMBL. 07-DEC-2004, sequence version 1. 21-FEB-2006, entry version 13.
                                                                                                                                                                                                                                                                                                           235 AA
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                                                                                                                     0; Mismatches
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Kinase; Tyrosine-protein kinase.
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QSU175;
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Src42A;
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SEQUENCE
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RESULT 5 Q9PVU9 LA ID Q9PV

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NCBI_TaxID=7764;
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                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Mol. Evol. 49:601-608(1999).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lampetra reissneri (Far Bastern brook lamprey).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Hyperoartia,
Petromyzontiformes, Petromyzontidae, Lethenteron.
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                                                                                                   Service of GO:0005524; F:1240.

R GO: GO:0005524; F:protein-tyrosine kinase activity; IEA.

GO: GO:0006468; F:protein-tyrosine kinase activity; IEA.

R GO: GO:0006468; F:protein amino acid phosphorylation; IEA.

R InterPro; IPR000129; Prot kinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R PR07714; PR10186; Tyr_pkinase.

R PR00109; TYRKINASE.

R SMART; SM00109; TYRKINASE.

R SMART; SM00109; TYRKINASE.

R PROSITE; PS50011; PROTEIN KINASE DOW; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                    100.0%; Score 49; DB 2; Length 246; 100.0%; Pred. No. 2.6; ive 0; Mismatches 0; Indels
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HSSP; P08631; LAD5.
SMR; O9POVO; 1-246.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004648; P:protein-tyrosine kinase activity; IEA.
GO; GO:000468; P:protein and no acid phosphorylation; IEA.
InterPro; IPR00139; Prot kinase.
InterPro; IPR00139; Prot kinase.
InterPro; IPR00139; Prot Kinase.
InterPro; IPR00148; Tyr pkinase.
InterPro; IPR00148; Tyr pkinase.
InterPro; IPR00148; Tyr pkinase.
InterPro; IPR00148; Tyr pkinase.
InterPro; IPR00148; Tyr pkinase.
FFO7714; Pkinase Tyr; 1.
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01-MAY-2000, sequence version 1.
07-FBB-2006, entry version 28.
Src-like A (Fragment).
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                                                          EMBL; AB025547; BAA84737.1; -; mRNA.
HSSP; P12931; IFMK.
SMR; Q9U8V5; 1-246.
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Matches 9; Conservative
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  tyrosine phosphate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000, integrated into UniProtKB/TrEMBL.
01-MAY-2000, sequence version 1.
07-FEB-2006, entry version 28.
Src-like A (Fragment).
Eptarretus burgeri (Inshore hagfish).
Bukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gnathostomes.";
J. Mol. Evol. 49:601-608(1999).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
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                                                                                                                                                                                             100.0%; Score 49; DB 2; Length 249; 100.0%; Pred. No. 2.6; ive 0; Mismatches 0; Indels
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000413; F:protein-tyrosine kinase activity; IEA.
GO; GO:000418; F:protein amino acid phosphorylation; IEA.
GO; GO:000468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR00119; Prot kinase.
InterPro; IPR001290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001265; Tyr_pkinase_AS.
PEAM: PR00109; TYRKINASE.
                                                                                                                                          SEQUENCE 249 AA; 28627 MW; DAC9DBA041F3D941 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 AA.
SMART; SM00219; TyrKc; 1.
SMOSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
Tyrosine-protein kinase.
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SMART; SM00219; TyrKc; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
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HSSP; P06239; 1QPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QOUBVE EPTBU PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20020330; PubMed=10552041;
                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tyrosine-protein kinase.
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                                                                                                                                                                                                                                                                                                                                                   162 DVWSFGILL 170
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NUCLEOTIDE SEQUENCE
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RESULT 11
Q9U8V3_BRA
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                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wallis J.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ensembl. ENSCO000197122; Homo sapiens.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR000719; Prot kinase.

InterPro; IPR001245; Tyr pkinase.

InterPro; IPR001245; Tyr pkinase.

InterPro; IPR001245; Tyr pkinase.

InterPro; IPR008266; Tyr pkinase AS:

Perm; Proff, Proff, Primase Tyr; 1.
                                                                                                       01-MAR-2001, sequence version 1.
07-MAR-2006, entry version 32.
Hypothetical protein FLJ14219 (OTTHUMP0000030929).
Name=SRC; ORFNames=RP5-823N20.1-004;
Homo sapiens (Human).
                                                                       01-MAR-2001, integrated into UniProtKB/TrEMBL
251 AA
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EMBL; AL133293; CAI22921.1; -; Genomic_DNA
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ProDom; PD000001; Prot kinase; 1.
SMART; SM00219; TYRKC; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
   PRT;
   PRELIMINARY;
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SMR; Q9H7V3; 1-251
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   O9H7V3 HUMAN
   HERE THE SECOND COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR CO
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                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.; "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey: isoform duplications around the divergence of cyclostomes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Mol. Evol. 49:601-608(1999).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
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PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
ATP-binding; Kinase; Membrane; Nucleotide-binding; Receptor;
Transferase; Transmembrane; Tyrosine-protein kinase.
SEQUENCE 251 AA; 28721 WW; ECA7468046D6657A CRC64;
                                                                                                              100.0%; Score 49; DB 2; Length 251; 100.0%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 252;
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GO; GO:0005524; F-ATP binding; IEA.
GO; GO:0004718; F-iprotein-tyrosine kinase activity; IEA.
GO; GO:0004718; F-iprotein amino acid phosphorylation; IEA.
GO; GO:0006468; P-iprotein amino acid phosphorylation; IEA.
InterPro; IPR0002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase_AS.
PEAM: PP07714; PRinase_Tyr; 1.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                               0; Indels
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PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                PRT;
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MEDLINE=20020330; Pubmed=10552041;
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                                                                                                                                       Local Similarity 100.
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Q9U8V3;
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        Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                     GO; GO:0016020; C:membrane; IEA.

RGO; GO:0016021; F:RATP binding; IEA.

GO; GO:0004514; F:receptor activity; IEA.

GO; GO:0004414; F:receptor activity; IEA.

GO; GO:0004414; F:receptor activity; IEA.

RGO; GO:0004414; F:receptor activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. ..;

RO; GO:00169; P:transmembrane receptor protein tyrosine kin. ..;

RO; GO:0007169; P:protein amino acid phosphorylation; IEA.

RINTERPO; IPR001824; RecepttyrkinsIII.

RINTERPO; IPR001824; Recepttyrkinse.

RINTERPO; IPR001245; Tyr_pkinase.

RINTERPO; IPR001245; Tyr_pkinase.

REPODOM; PD0000001; Protein kinase; 2.

REPODOM; PD0000011; Protein kinase; 1.

REPOSITE; PS00119; PROTEIN KINASE DOM; 1.

RECEPTOR; Tyrosine-protein kinase.

TONN_TER.
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Testudines, Cryptodira, Trionychoidea, Trionychidae, Pelodiscus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kuraku S., Ishijima J., Nishida-Umehara C., Agata K., Kuratani S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trionyx sinensis (Chinese softshell turtle) (Pelodiscus sinensis)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 AA; 28776 MW; F1A432566282D951 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 49; DB 2; 100.0%; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-WAR-2006, sequence version 1.
07-MAR-2006, entry version 1.
Fibroblast growth factor receptor 4 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-MAR-2006, integrated into UniProtKB/TrEMBL
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                                                      EMBL; AF347051; AAK31152.1; -; mRNA.
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Q2LGP6;
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                                                                                  HSSP, P11362, 1FGK
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291
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NON TER
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0216F6 TRI
02216F
AC 0216F
DT 07-M9
DT 07-M9
DT 07-M9
DE FIDIC
GN TRIDIC
OC DEWAX
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                                                                                                                                                                                                                                                                 Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T., "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey isoform duplications around the divergence of cyclostomes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001, integrated into UniProtKB/TrEMBL.
01-JUN-2001, sequence version 1.
07-FEB-2006, entry version 24.
Platelet-derived growth factor receptor beta (Fragment).
Sus scrofa (Pig).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Evol. 49:601-608(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remillard P.E., Lacroix D.A., Murphy B.D.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                       Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ATP-binding; Kinase; Membrane; Nucleotide-binding; Transferase;
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:membrane; IEA.

GO; GO:0016022; C:membrane; IEA.

GO; GO:000165; F:nuclectide binding; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:001640; F:transferase activity; IEA.

GO; GO:001640; F:transferase activity; IEA.

R GO; GO:001640; F:protein amino acid phosphorylation; IEA.

R InterPro; IPR000219; Proteiniase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R PRINTS; PR00109; TYRKINASE.

R PRINTS; PR00109; TYRKINASE.

R SMART; SM00219; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 49; DB 2; Length 252; 100.0%; Pred. No. 2.7; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Tyrosine-protein kinase.
SEQUENCE 252 AA; 28798 MW; B331B41E7AFEE2A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB025551; BAA84765.1; -; mRNA.
                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
MEDLINE=20020330; PubMed=10552041;
                                                                            Branchiostoma belcheri (Amphoxius)
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01-MAY-2000, sequence version 1.
07-FEB-2006, entry version 32.
Src-like A-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphate.
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                                                                                                                                                              NCBI_TaxID=7741;
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NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                             gnathostomes.";
                                                                                                                                      Branchiostoma
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Q9BDK8;
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Q9BDK8 PIG
Q9BDK8
AC Q9BDK8
DT 01-JUN-
DT 07-FEB-
DE Platele
OS SUS SUS SCO
OC ENEARY
OC Mammal:
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FLK RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=1549614; DOI=10.1038/nature03025;
PubMed=1549614; DOI=10.1038/nature03025;
PubMed=1549614; DOI=10.1038/nature03025;
A Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozcut-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cutanceau J.-P., Gorzy J., Parra G., Lardler G., Chapple C., McKernan K.J., McEwan P., Bosak S., Rellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J., Lander G., Chapple C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roset Crollius H.; Generals C. C., Contence duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Plays a key role in the control of the eukaryotic cell
ordie. It is required in higher cells for entry into S-phase and
mitosis. Component of the kinase complex that phosphorylates the
repetitive C-terminus of RNA polymerase II. Catalytic component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
SUBUNIT: Forms a stable but non-covalent complex with cyclin B in mature oocytes (By similarity).
                                                                                                                                             19-JUL-2005, sequence version 1.
07-FBB-2006, entry version 6.
Chromosome 14 SCAFIS503, whole genome shotgun sequence. (Fragment).
ORFNames=GSTENG0030294001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPF (By similarity).
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope, Whitehead Institute Centre for Genome Research; submittend (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GC:0005524, F:ATP binding; IEA.
GO:0000166; F:nucleotide binding; IEA.
GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO:0016740; F:transferase activity; IEA.
GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000001; Prot kinase; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Nucleotide-binding; Transferase; Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; CAAE01015003; CAG09110.1; -; Genomic_DNA.
                                                                                                                           19-JUL-2005, integrated into UniProtXB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0000166; F:nucleotide binding; I GO; GO:0004713; F:protein-tyrosine kina GO; GO:0016740; F:protein-tyrosine kina GO; GO:0016468; P:protein amino acid ph InterPro; IPR000719; Prot_kinase. InterPro; IPR001299; Sar thr pkinase. InterPro; IPR001245; Tyr_pkinase. InterPro; IPR001245; Tyr_pkinase. PRINTS; PR00109; TYRKINĀSE.
                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=99883;
                                                                         Q4RR72_TETNG
Q4RR72;
                                                    PETNG
                       RESULT 14
Q4RR72 TET
                                                                                                 WWW WERE BURNESS OF THE STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET
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Distributed under the Creative Commcns Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Letwin K., Yee S.P., Pawson T.;
"Novel protein-tyrosine kinase cDNAs related to fps/fes and eph cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     using anti-phosphotyrosine antibody.";
Oncogene 3:621-627(1988).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine phosphate.
-!- SIMILARITY: Belongs to the Tyr protein kinase family. Fes/fps
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Proton acceptor (By similarity).
ATP (By similarity).
                                         Score 49; DB 2; Length 322;
Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tyrosine-protein kinase FLK./FTId=FRO_000088093.
                                                                                         Indels
322 AA; 36768 MW; EC0ED0B6DB1CBB2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1989, sequence version 1.
07-MAR-2006, entry version 56.
Tyrosine-protein kinase FLK (EC 2.7.1.112) (Fragment).
                                                                                                                                                                                                                                                                                                                                                  01-JUL-1989, integrated into UniProtKB/Swiss-Prot. 01-JUL-1989, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; PS4763; 1JPA.
Ensembl; ENSRNOG0000015898; Rattus norvegicus.
LinkHub; P09760; -.
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                                                                                                                                                                                                                                                                                                    323 AA.
                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATF; 1.
PROSITE; PS50011; PROTEIN KINASE DOK; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50001; SH2; PARTIAL.
PROSITE; PS50002; SH3; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subfamily.
-!- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase_AS.
Pfam; PF07714; Pkinase_Tyr; 1.
Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [MRNA].
STRAIN-Wistar; TISSUE=Brain;
MEDLINE=94167102; PubMed=2485255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X13412; CAA31778.1; -; mRNA.
PIR! S04328; S04328.
                             100.0%; Scu.
100.0%; Pre
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ProDom; PD000001; Prot kinase; 1.
ProDom; PD000093; SH2; 1.
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InterPro; IPR001452; SH3
                                                                                            9; Conservative
                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                   DVWSFGILL 217
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                                              Query Match
Best Local Similarity
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Indels

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9; Conservative
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Q3TLX4;
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    Matches
                                                                                              RESULT 17
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                                                                                             Gaps
  Phosphotyrosine (by autocatalysis) (By
                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
tyrosine phosphate.
                                                                                                                                                                                                                                                                                                        Ciona intestinalis.
Eukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase;
                                                                                             ;
0
                                                                 Score 49; DB 1; Length 323; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                        Coulier F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0005524; F:ATP binding; IEA.
GO:0000166; F:nucleotide binding; IEA.
GO:0000413; F:protein-tyrosine kinase activity; IEA.
GO:0016740; F:transferase activity; IEA.
GO:0007242; P:intracellular signaling cascade; IEA.
GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Leveugle M., Prat K., Popovici C., Birnbaum D., Coulier Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                       D7BA8BDE50C3EAC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24348637494EC157 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ensembl; ENSCING0000005826; Ciona intestinalis.
                                                                                                                                                                                                                                        05-JUL-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                355 AA.
                                                                                            0; Mismatches
                similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00107; PROTEIN KINASE ATP; 1. PROSITE; PS00119; PROTEIN KINASE DOM; 1. PROSITE; PS00109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR000719; Prot kinase.
InterPro: IPR002290; Ser_thr_pkinase.
InterPro: IPR001990; SH2.
InterPro: IPR001452; SH3.
InterPro: IPR001245; Tyr_pkinase.
InterPro: IPR001866; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ534320; CAD58838.1; -; mRNA.
HSSP; P11362: 1acw
                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                   05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 16.
Src protein (Fragment).
                                                                                                                                                                                                                                                                                                                                    Phlebobranchia; Cionidae; Ciona
                                       323 AA; 37104 MW;
                                                                 100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ### PF07714; Pkinase Tyr; 2.
Pfam; PF00017; SH2; 2.
Pfam; PF00018; SH3; 1.
Pfam; PF00018; SH3 II 1.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40337 MW;
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                                                  Query Match
Best Local Similarity luv.
9; Conservative
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  215
                                                                                                                                     SM00326; SH3; 1
                                                                                                                      1 DVWSFGILL 9
                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 AA;
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                          NON TER
SEQUENCE
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 MOD_RES
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Length 355;

DB 2;

Score 49; DB 2 Pred. No. 3.7;

100.0%; 100.0%;

Best Local Similarity

Query Match

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RA Garninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., RA Garninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., RA Bajic V.B., Baralov S., Forrest A.R., Shimokawa K., Baric W.B., Brenner S.E., Batalov S., Forrest A.R., Bainey T.L., RA Bajic V.G., Allen J.E., Aluraliya R.N., Bailey T.L., Ambesi-Impionbato A., Apweiler R., Aluraliya R.N., Bailey T.L., Ambesi-Impionbato A., Apweiler R., Aluraliya R.N., Bailey T.L., Chail K., Bersano T., Bono H., Chalk A.M., RA Grew M.L. Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., A Pletter C.F., Pubushima T., Furuno M., Fadilini M., Faulkner G., A Pletter C.F., Pubushima T., Furuno M., Fadilini M., Faulkner G., RA Fletcher C.F., Pubushima T., Furuno M., Keelso J., Gripcawa N., RA Gustincich S., Harbers M., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Ranppin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Authiniecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakuno H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Larand A., Ishikawa S., Maldar Babu M., Madera M., Marchinoni L., Juni S., Malliama S., Madan Babu M., Madera M., Marchinoni L., Matsucha B., Matsucha S., Maldar B., Nan M., Saweich J., Libovich L., Idu J., Rakano N., Nakano N., Nakauchi H., Ng P., Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P., Mottagui-Tabar S., Rand S., Rade J.F., Rang B.C., Ringal M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schiguchi K., Sandelin A., Schneider C., Schiguchi K., Sandelin A., Schneider C., Rochonbach C., Schiguchi K., Sandelin A., Schneider C., Rochonbach C., Schiguchi K., Sandelin A., Schneider C., Pavan N., Hammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Tammoda M., Teasdale R., Sulwa M., Sulwa J., Hawashima T., Kawashima T., Kawashima T., Kawashima T., Kawashima T., Kawashima T., Kawashima T., Kawashima T., Kawashima T., Watahiki A., Watahiki K., Natahiki A., Okon W., Nakashi Y., Shiraki Y., Rawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi;
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Mammary gland;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency Hayashizaki T.;
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 7.
Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched
library, clone:G830026006 product:lymphocyte protein tyrosine kinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.; "The transcriptional landscape of the mammalian genome.";
                                                                                                                                                                                                                                                                                                                                                   11-OCT-2005, integrated into UniProtKB/TrEMBL
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PubMed=16141072; DOI=10.1126/science.1112014;
                                                                                                                                                                                                                                                                       368 AA.
                                                                                                                                                                                                                                                                   PRT;
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                                                                           273 DVWSFGILL 281
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1 DVWSFGILL
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Genome Res. 10:1617-1630(2000)
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PubMed=16141073; DOI=10.1126/science.1112009;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FAMTOM Consortium;
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Science 309:1564-1566(2005).
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                        Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Komno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshika M., Yonded Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., RIKEN integrated sequence analysis (RISA) system-384-format
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Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
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Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI; MGI:96756; LCK.
GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
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TISSUE=Mammary gland;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
                                                                                                                                                                                                                                                                                                                                   sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771 (2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-2005, integrated into UniProtKB/TrEMBL
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MGI; MGI:96756; Lck.
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PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot_kinase; 1.
ProDom; PD000093; SH2; 1.
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OT-FBB-2006, entry version 7.
LCk_mapped protein (Fragment).
Name=LCk_mapped,
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Matches 9; Conservative
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                                                                                                           MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

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The Month of M. Schein J.E., Jones S.J.M., Marra M.A.;
The Month of M. Intial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH MGC Project;
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Son, Tricko, 1977.

GO; GO:0005524; F:nucleotide binding; IEA.

GO; GO:0000166; F:nucleotide binding; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016469; P:protein amino acid phosphorylation; IEA.

InterPro; IPR002290; Ser thr pkinase.

InterPro; IPR001245; Tyr pkinase.

InterPro; IPR001245; Tyr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 49; DB 2; Length 379; 100.0%; Pred. No. 4; o; Indels ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00252; SH2; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN KINASE_TR; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC099218; AAH99218.1; -; mRNA.
SMR; Q4FZR6; 2-379.
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PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prof. Kinase; 1.
ProDom; PD000093; SH2; 1.
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Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences."
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Best Local Similarity 100.
Matches 9; Conservative
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Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tyrosine phosphate
                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          rissue=Thymus
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                                                                                                                                                                                                                                                                                                                                                                              Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oncogene lacking gamma-actin sequences.";
Oncogene 4:363-372(1989)
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89201884; PubMed-2539576;
Kappes B., Ziemiecki A., Mueller R.G., Theilen G.H., Bauer H.,
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R PIR; S04205; S04205.

R HSSP; P00523; 2PTK.

R SMR; Q28414; 5.390.

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004713; F:proclaide binding; IEA.

GO; GO:0007424; F:proclaide binding; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0007424; P:intracellular signaling cascade; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006469; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR002090; Ser_thr_pkinase.

R InterPro; IPR00195; Tyr_pkinase.

R InterPro; IPR00195; Tyr_pkinase.

R InterPro; IPR00195; Tyr_pkinase.

R Pfam; PF07714; Pkinase Tyr; 1.
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SEQÜENCE 392 AA; 44776 MW; 70CF642A7766F684 CRC64;
                                                                                                                                                                                                                       01-NOV-1996, integrated into UniProtKB/TrEMBL.
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ProDom; PD000093; SH2; 1.
SMART; SM00229; SH2; 1.
SMART; SM00219; TYPKC; 1.
PROSITE; PS001107; PROTEIN KINASE ATP; 1.
PROSITE; PS00110; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                 01-NOV-1996, sequence version 1.
07-FEB-2006, entry version 38.
Gag-onc fusion protein (Fragment)
Feline sarcoma virus.
                                                                                                                                                          PRELIMINARY;
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PRINTS; PR00109; TYRKINASE.
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Best Local Similarity 100.
Matches 9; Conservative
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292 DVWSFGILL 300
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RC STRAIN-G57BL/64) TISSUB-Whole body;
RN PUBCECTIDE STRAIN-G57BL/64) TISSUB-Whole body;
RN PubMed=1614072; DOI=10.1126/Becience.1112014;
RN Bajic V.B. Berner S. Batelbuv S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Berners B., Maidnis V., Allen J.E.,
Ambesi-Impiombato A., Apweller R., Autanis R. N., Bailey T.L.,
And Bansal M., Baxter L., Beisel K. W., Bersano T., Bono H., Chalk A.M.,
And Bansal M., Baxter L., Beisel K. W., Bersano T., Bono H., Chalk A.M.,
And Bensal M., Baxter L., Beisel K. W., Bersano T., Bono H., Chalk A.M.,
And Bensal M., Baxter L., Beisel K. W., Bersano T., Bono H., Chalk A.M.,
And Bensal M., Baxter L., Beisel K. W., Bersano T., Bono H., Chalk A.M.,
And Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
R. Goorgil-Hemming P., Gingeras T.R., Gojobori T., Green R.B.,
Action H., Kalnia B., Marker M., Marchionii L.,
Antenda M., Kanapin A., Katoh M., Kawasawa Y., Keleo J., Kitamura H.,
Antenda H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
Autenda H., Matuazawa S., Mikh H., Mignone F., Miyake S., Morris K.,
Antenda H., Matuazawa S., Mikh H., Mignone F., Miyake S., Morris K.,
Antenda H., Matuazawa S., Mikh H., Mignone F., Miyake S., Morris K.,
Antenda H., Nolland H., Shinkawa S., Nori F., Ohara O.,
Aokazaki Y., Chlando V., Pang K.C., Pawan W.J., Pavesi G., Pescole G.,
Rosaki Y., Chlando V., Pang K.C., Pawan W.J., Pavesi G., Pescole G.,
Antenda H., Van Nimwegen E., Volanda M., Shinclar B.,
Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Shing H. C.,
Anded H.R., van Nimwegen E., Volanda M., Silva D., Sinclari B.,
Andel H.R., van Nimwegen E., Volanda M., Ravasi H., Kawanishi H., Wanishor Y., Sanadishi R.,
Andel H.R., van Nimwegen E., Volanda M., Shinclar R., Hide W., Shincaki T.,
Andel H.R., van Nimwegen E., Waranishi H., Kanamori-Karayama M., Suzuki M., Rawashima T., Kojama M., Kono H., Kanen C., Sasaki D., Tomaru Y.,
Andel B., Kanamori-Karayama M., Suzuki M., Akawashima T., Kojama M., Pakash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Whole body; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninoi P., Hayashizaki Y.; High-efficiency full-length CDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                              QBEG14 MOUSE PRELIMINARY; PRT; 393 AA.
QBEQ14;
QBEQ14;
O1-MAR-2003, integrated into UniProtKB/TrEMBL.
O1-MAR-2003, sequence version 1.
O7-FEB-2006, entry version 24.
7 days embryo whole body cDNA, RIKEN full-length enriched library, clone:C430045019 product:src-related kinase lacking C-terminal regularory tyrosine and N-terminal myristylation sites, full insert sequence. (Fragment).
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RG Genome Nerwork Core Team) and the FANTOM Consortium.

Anticemes Transcription in the Nammalian Transcriptome.";

Anticemes Transcription in the Nammalian Transcriptome.";

(14 mrs 2011564 15651 TISSUE-Whole body, Darlo 10139/nature01266;

RX NORLARE_22518663) PubMed_114466521, Darlo 10139/nature01266;

RX NORLARE_22518663) PubMed_114466521, Darlo 10139/nature01266;

RX NORLARE_22518663) PubMed_114466521, Darlo 10139/nature01266;

RX NORLARE_22518663) PubMed_114466521, Darlo 10139/nature01266;

RX NORLARE_22518663) PubMed_114466521, Darlo 10139/nature01266;

RX NORLARE TRANSPORMENT No. Nature D.A. Quadchenhal J. Condon D.A.

RA Dalla E. Dragan T.A. Patcher C.F. Forter A. Paster K.S.,

RX NORLARE A. Mutchkin T.V., Lee Y. Corbina C. Cochani L.E. Cousin S.,

RX NORLARE T. Numeta K. Oxided T. Pavan M.J. Petree G. Petro C.

RX NORLARE T. Numeta K. Oxided D.J. RRIB B.Z., Ringewald M. And Meglott D.R. Numeta K. Oxided T. Pavan M.J. Petree G. Petro C. P.

RX NORLARE T. Numeta K. Oxided D.J. RRIB B.Z., Ringewald M. A.

RX NORLARE T. Numeta K. Oxided D.J. RRIB B.Z., Ringewald M. A.

RX NORLARE T. Numeta K. Oxided D.J. RRIB B.Z., Ringewald M. A.

RX NORLARE T. Numeta K. Oxided D.J. Ringe T. Ringewald M. A.

RX NORLARE T. Numeta K. A. Manton H. Nakanum M. Salto K. A.

RX NORLARE T. Numeta K. A. Manton H. Nakanum M. Salto K. A.

RX NORLARE T. Numeta K. A. Manton H. Nakanum M. Salto K. A.

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07-FEB-2006, entry version 12.

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                                                                                                                                                                CSTRAIN-CSTBL/62; TISSUE=Whole body;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hayashida K., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Nakamura M.,
Nishi K., Numazaki R., Miyazaki R., Murata M., Nakamura M.,
Sasaki D., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takabashi F., Takaku-Akahira S., Takada Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P. Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda X., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., sequencing pipeline with 384 multicapillary sequencer.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI; MGI:101865; Srms.

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004713; F:Porcein-tyrosine kinase activity; IEA.

GO; GO:0004713; F:porcein-tyrosine kinase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R InterPro; IPR00290; Ser_thr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase_AS.

R Ffam; PF07714; Pkinase_Tyr; 1.
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DT 05-JUL-2004, sequence version 1.
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PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AK049582; BAC33825.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Proc_kinase; 1.
Probom; PD000093; SH2; 1.
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100.0%;
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9; Conservative
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Best Local
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07-FEB-2006, entry version 5.
Testis cDNA, clone: QtsA-17706, similar to human fyn-related kinase
                                                                                                                                                                                                                                                 Leveugle M., Prat K., Popovici C., Birnbaum D., Coulier F., Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                            Ciona intestinalis.
Eukaryota, Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=1594441; DOI=10.1093/molbev/msi187; Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen C.-K.J., Wu C.I., Hashimoto K.; Substitution Rate and Structural Divergence of 5'UTR Evolution: Comparative Analysis Between Human and Cynomolgus Monkey cDNAs."; Mol. Biol. Evol. 22:1976-1982(2005).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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GO; GO: 0004713; F:ATP binding; IEA.
GO; GO: 0004713; F:Protein-tyrosine kinase activity; IEA.
GO; GO: 0004872; F:receptor activity; IEA.
GO; GO: 000468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR001309; I-set.
InterPro; IPR002719; Prot_kinase.
InterPro; IPR00279; Sr_thr pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR00266; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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Fibroblast growth factor receptor (Fragment)
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ProDom; PD000001; Prot_kinase; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PROFILIN KINASE DOW; 1.
PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ534315; CAD58833.1; -; mRNA
HSSP; P11362; 1AGW.
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NON_TER 395 395
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE
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07-FEB-2006,
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the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
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Pubmed-15496914; DOI=10.1038/nature03025;

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"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
   International consortium for macaque cDNA sequencing and analysis; "DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications."; submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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ORFNames=GSTENG00036856001;

Tetracadon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterrygii; Neopterrygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterrygii; Percomorpha; Tetracdontiformes;

Tetradontoidea; Tetracdontidae; Tetracdon.

NCBI_TAXID=99883;
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07-FEB-2006, entry version 6.
Chromosome undetermined SCAF22943, whole genome shotgun sequence.
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GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004713; F:Portein-tyrosine kinase activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR00019; Prot kinase.

InterPro; IPR002290; Ser_thr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.
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                                                                                                                                                                               preliminary data.

FUNCTION: Plays a key role in the control of the eukaryotic cell cycle. It is required in higher cells for entry into S-phase and mitosis. Component of the kinase complex that phosphorylates the repetitive C-terminus of RNA polymerase II. Catalytic component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    tyrosine phosphate.
-!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B mature oocytes (By similarity).
-!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                          MPF (By similarity).
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
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                                                                                                  CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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By GO; GO: 0005524; F: ATP binding; IEA.

GO; GO: 0000166; F: Rucleotide binding; IEA.

GO; GO: 00016713; F: protein-tyrosine kinase activity; IEA.

RO; GO: 0007242; F: protein-tyrosine kinase activity; IEA.

GO; GO: 0007242; F: protein anino acid phosphorylation; IEA.

GO; GO: 0007242; F: protein anino acid phosphorylation; IEA.

RO; GO: 10R000290; Ser_thr_pkinase.

RICEPPO; IPR000290; Ser_thr_pkinase.

RICEPPO; IPR001245; Tyr_pkinase.

RICEPPO; IPR001245; Tyr_pkinase.

RICEPPO; IPR001245; Tyr_pkinase.

RICEPPO; IPR001245; Tyr_pkinase.

RICEPPO; IPR001245; Tyr_pkinase.

RICEPPO; IPR001245; Tyr_pkinase.

RICEPPO; IPR00125; SH3.

RICEPPO; IPR00125; SH3.

REMINTS; PR00109; TYRKINASE.

REDDOM; PD0000001; Prote kinase; 1.

REMART; SM00225; SH2; 1.

REMART; SM00225; SH2; 1.

REMART; SM00219; TyrKc; 1.

REMART; SM00219; TyrKc; 1.

REMART; SM00219; TyrKc; 1.

REMART; SM00219; TyrKc; 1.

REMART; SM00219; TyrKc; 1.

REMOSITE; PS50011; PROTEIN KINASE DOM; 1.

REMOSITE; PS50011; PROTEIN KINASE LYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 49; DB 2; Length 408; 100.0%; Pred. No. 4.3; cive 0; Mismatches 0; Indels
NUCLECTIDE SEQUENCE. Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408 AA; 46231 MW; F6DCC51EBD5B603E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 24
STYK1 HUMAN
ID STYKL HUMAN STANDARD; PRT; 422 AA.
ID STYKL HUMAN STANDARD;
AC Q6J9GÖ; Q9BXY2; Q9NSH1;
DT 26-APR-2005, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; CAAE01022943; CAG14497.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
nes 9; Conservative
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                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine phosphate.
SUBCELLULAR LOCATION: Cytoplasm (By similarity).
TISSUE SPECIFICITY: Widely expressed. Highly expressed in brain, placenta and prostate. Expressed in tumor cells such as hepatoma cells LO2, cervix carcinoma cells HeLa, ovary cancer cells H08910 and chronic myelogenous leukemia cells K562, but not in other tumor cells such as epidermoid carcinoma (4431).
SIMILARITY: Belongs to the Tyr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB=Fetal brain;
PubMed=12841579; DOI=10.1023/A:1023934017174;
Ye X., Ji C., Huang Q., Cheng C., Tang R., Xu J., Zeng L., Dai J.,
Wu Q., Gu S., Xie Y., Mao Y.;
"Isolation and characterization of a human putative receptor protein kinase cDNA STYKI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overexpressed, it can also induce tunor cell invasion as well as metastasis in distant organs. May act by activating both MAP kinase and phosphatidylinositol 3'-kinases (PI3K) pathways (By similarity).

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Amygdala;
PubMed=15150103;
DubMed=15150103;
DibMed=15150103;
Dir V. X. Z. Li T.-S., Song L.-X., Chen P.-L., Suo T.-L.,
Liu L., Wang S.-D., Chen Y., Ren Y.-M., Zhang S.-P., Chang Z.-J.,
Fu X.-Y.;
Ru X.-Y.;
A novel protein tyrosine kinase NOK that shares homology with
platelet-derived growth factor/fibroblast growth factor receptors
induces tumorigenesis and metastasis in nude mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proto-oncogene; Transferase; Transmembrane; Tyrosine-protein kinase.
CHAIN 1 422 Tyrosine protein-kinase STYKI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [MRNA], TISSUE SPECIFICITY, AND VARIANT SER-204
26-APR-2005, sequence version 2.
7-MAR-2006, entry version 16.
Tyrosine protein-kinase STYK1 (EC 2.7 1.112)
(Serine/threonine/tyrosine kinase 1) (Novel oncogene with kinase-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Amygdala;
The German cDNA consortium;
The German cDNA consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Probable tyrosine protein-kinase, which has strong transforming capabilities on a variety of cell lines. When
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR0019; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase_AS.
Pfam; PF07714; Pkinase_Tyr; I.
PRO1714; Pkinase_Tyr; I.
PROSITE; PS00109; PROTEIN KINASE_ATP; FALSE_NGG.
PROSITE; PS00110; PROTEIN KINASE_DOM; I.
PROSITE; PS00109; PROTEIN_KINASE_TYR; I.
ATP-binding; Kinase; Membrane; Mucleotide-binding; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY
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EMBL; AYS63064; AAT01226.1; -; mRNA.
EMBL; AL353940; CAB89250.1; -; mRNA.
PIR; T48680; T48680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Biol. Rep. 30:91-96(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cancer Res. 64:3491-3499(2004).
                                                                                                                                              domain) (Protein PK-unique).
Name=STYK1; Synonyms=NOK;
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
                 Potential.

Protein kinase.

ATP (By similarity).

ATP (By similarity).

G -> S (in dbSNP:3759259).

/FTtd=vAR.022245.

V -> M (in Ref. 3).

R -> S (in Ref. 3).
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                                                                                                                                                                                                                                                100.0%; Score 49; DB 1; Length 422; 100.0%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                        81D1F676DC6F2E26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
FTId=PRO 0000088163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-2005, integrated into UniProtKB/TrEMBL. 24-MAY-2005, sequence version 1. 21-FEB-2006, entry version 12.
                                                                                                                                                                                                                                                                   Pred. No. 4.4;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q52LR3_HUMAN PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine/threonine/tyrosine kinase 1.
                                                                                                                                                                                                          47584 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH93822.1;
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                                                                                                                                                                                                                                                                     Local Similarity 100.
Les 9; Conservative
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128
251
147
204
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422 AA;
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NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=STYK1;
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                                                                              ACT SITE
BINDING
VARIANT
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CONFLICT
SEQUENCE
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ACT SITE
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Ensembl; ENSG0000060140; Homo sapiens.

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GO: 0006468;
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SEQUENCE
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              SP TAMES OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
"Construction and characterization of a full length-enriched and a 5'
end-enriched cDNA library.";
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98038986; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Spleen;
MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Spleen;
Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maruyama K., Sugano S.;
Coligo-capping: a simple method to replace the cap structure of
eucaryotic mRNAs with oligoribonuclectides.";
Gene 138:171-174(1994)
R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

R InterPro; IPR000719; Prot kinase.

R InterPro; IPR002290; Ser thr pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R PRINTS; PR00109; TYRKINASE.

R PROSTIE; PS00101; PROTEIN KINASE DOM; 1.

R PROSTIE; PS00101; PROTEIN KINASE DOM; 1.

R PROSTIE; PS00101; PROTEIN KINASE DOM; 1.

R ATP-binding; Kinase; Membrane; Nucleotide-binding; Receptor;

Transferase; Transmembrane; Tyrosine-protein kinase.

SEQUENCE 422 AA; 47547 MW; B7CDBBC006029D3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 422;
                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ensembl; ENSG0000103653; Homo sapiens.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0017242; P:intracellular signaling cascade; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAY-2005, integrated into UniProtKB/TrEMBL. 24-MAY-2005, sequence version 1. 07-FEB-2006, entry version 7. C-src tyrosine kinase variant (Fragment).
                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449 AA
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                         Score 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 SH3 domain.
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0
                                                                                                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308 DVWSFGILL 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DVWSFGILL 9
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NEDLINES ESQUARE.

STRAIN-FVB.N-3: TISSUE-Mammary tumor. MMTV-LTR/INT3 model. 5 month old mouse. Taken by biopsy.;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Maller G.D., A strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Maller G.D., A strausberg R.L., Feingold E.A., Shemmen C.M., Schuler G.D., A strachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., A stachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., & Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rometein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Maruy D.M., Sodergren B.J., Lu X., Gibbs R.A., A Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Hulting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Huterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E., Abranga M.A.; Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 49; DB 2; Length 449; 100.0%; Pred. No. 4.7; o; Mismatches 0; Indels
P:protein amino acid phosphorylation; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             449 AA; 50617 MW; 45BD3B64B8ABB05E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003, integrated into UniProtKB/TrEMBL.
01-JUN-2003, sequence version 1.
07-FBB-2006, entry version 23.
Fert2 protein (Fragment).
                         InterPro; 1PR002019; Proct kinase.
InterPro; 1PR002090; Ser_thr_pkinase.
InterPro; 1PR001452; SH3.
InterPro; 1PR001452; SH3.
InterPro; 1PR001455; Tyr_pkinase.
InterPro; 1PR00145; Tyr_pkinase.
InterPro; 1PR00145; Tyr_pkinase.
InterPro; 1PR00145; Tyr_pkinase.
Prom; PR00017; SH2; 1.
PRINTS; PR00401; SH2; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD0000001; Proct_kinase; 1.
ProDom; PD0000001; Proct_kinase; 1.
ProDom; PD0000065; SH3; 1.
SWART; SM00225; SH2; 1.
SWART; SM00225; SH3; 1.
PROSITE; PS00107; PROTEIN KINASE_DOM; 1.
PROSITE; PS00101; PROTEIN KINASE_DOM; 1.
PROSITE; PS00101; PROTEIN KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity luv...
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50002; SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
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NUCLEOTIDE SEQUENCE
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MEDLINE=92196083; PubMed=1372437;
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BINDING
MOD_RES
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NP BIND
REGION
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                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
"Generation and initial analysis of more than 15,000 full-length human
                                                    STRAIN=FVB/N-3; TISSUE=Mammary tumor. MMTV-LTR/INT3 model. 5 month old mouse. Taken by biopsy.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                       RGO; GO:0005515; F:protein binding; IPI.
RGO; GO:0005515; F:protein binding; IPI.
RGO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
RGO; GO:00046735; P:chemctaxis; IMP.
RGO; GO:0007242; P:chemctaxis; IMP.
RGO; GO:0007242; P:intracellular signaling cascade; RCA.
RGO; GO:0046777; P:protein amino acid autophosphorylation; IDA.
R InterPro; IPR000199; Prot kinase.
R InterPro; IPR0002290; Ser thr pkinase.
R InterPro; IPR001245; Tyr pkinase.
R InterPro; IPR001245; Tyr pkinase.
R InterPro; IPR001245; Tyr pkinase.
R Pfam; PF00114; Pkinase Tyr; 1.
                                                                                                   + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 49; DB 2; Length 449; 100.0%; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995, integrated into UniProtKB/Swiss-Prot.
01-FEB-1995, sequence version 1.
07-MAR-2006, entry version 45.
Tyrosine-protein kinase CSK (EC 2.7.1.112) (C-SRC kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                       Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   449 AA; 51136 MW; 5463C70B41B1FFC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          SWART; SM00219; TYRC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS500101; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50001; SH2; 1.
ATP-binding; Kinase; Nucleotide-binding; Transferase;
                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                         HSSP, P11362; 1FGK.
Ensembl; ENSMUSG0000000127; Mus musculus.
MGI; MGI:105917; Fert2.
                                                                                                                                                     EMBL; BC051249; AAH51249.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Proc kinase; 1.
ProDom; P0000093; SH2; 1.
SMART; SM0252; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [MRNA].
TISSUE=Brain;
          and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                          tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken)
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                                            SEQUENCE
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                                            NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSK_CHICK
P41239;
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CSK_CHICK
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Sabe H., Knudsen B., Okada M., Nada S., Nakagawa H., Hanafusa H.;
"Molecular cloning and expression of Chicken C-terminal Src kinase:
Tack of stable association with C-Src protein.";
Proc. Natl. Acad. Sci. U.S.A. 89:2190-2194 [1992].
-!- FUNCTION: Specifically phosphorylates a tyrosine on the SRC kinase. This tyrosine acts as a negative regulatory site. Can also act on the LYN and FYN kinases.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding; Kinase; Nucleotide-binding; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Protein kinase.

ATP (By similarity).

Interaction with PTPN8 (By similarity).

Proton acceptor (By similarity).

ATP (By similarity).

Phosphotyrosine (by autocatalysis) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                tyrosine phosphate.
-!- SUBUNIT: Interacts with PTPN8 (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasm (Probable).
-!- SIMILARITY: Belongs to the Tyr protein kinase family. CSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 49; DB 1; Length 450; 100.0%; Pred. No. 4.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tyrosine-protein kinase CSK./FTId=PRO_000088069.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P41240; IBYG.
SMR; P41239; 4-450.
Ensembl; ENSGAGG0000001318; Gallus gallus.
InterPro; IPR00719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001452; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001455; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEAM; PF00018; SH3 1; 1.

PRINTS; PR00401; SH2 1; 1.

PRINTS; PR00401; SH2DOMAIN.

PRINTS; PR00452; SH3DOMAIN.

ProDom; PD0000093; TYRKINASE.

ProDom; PD0000093; SH2; 1.

ProDom; PD000066; SH3; 1.

SMART; SM00252; SH2; 1.

SMART; SM00219; TYRKC; 1.

PROSITE; PSS0010; PROTEIN KINASE ATP; 1.

PROSITE; PSS0010; PROTEIN KINASE DOM; 1.

PROSITE; PSS0010; PROTEIN KINASE DOM; 1.

PROSITE; PSS0010; SH3; 1.
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                                                                                                                                                                                                                                                                                                                              subfamily.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M85039; AAA51436.1; -; mRNA.
PIR; A41973; A41973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF07714; Pkinase Tyr; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3 1; 1.
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209
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PubMed=11433379;
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                                                                                                                                                                                                                                                                                                                AND TYR-304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10]
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry
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Rajkumar N., Willa H.T., Daniels M., Downing T.K., Stanaway I.B.,
Nguyen C.P., Gildersleeve H., Cassidy C.M., Johnson B.J.,
Swanson J.E., McParland I., Yool B., Park C., Nickerson D.A.;
"NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REDILNE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L.L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonadlo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Braeuninger A., Holtrich U., Strebhardt K., Ruebsamen-Waigmann H.; "Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase."; Proc. Natl. Acad. Sci. U.S.A. 88:10411-10415 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLECTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS ASP-287; GLN-398 AND
                                  P41240; OGFCZ6;
01-FEB-1995, integrated into UniProtKB/Swiss-Prot.
01-FEB-1995, sequence version 1.
07-MAR-2006, entry version 62.
Tyrosine-protein kinase CSK (BC 2.7.1.112) (C-SRC kinase) (Protein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLECTIDE SEQUENCE [GENOMIC DNA], AND TISSUE SPECIFICITY.
Whythdeal-1371489; DOI=10.1016/0378-1119(92)90649-A.
Brauninger A., Holtrich U., Strebank K., Rubsamen-Waigmann H.;
"Isolation and characterization of a human gene that encodes a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLECTIDE SEQUENCE [LARGE SCALE MRNA].
Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
Korn B., Zuo D., Hu Y., LaBaer J.;
"Cloning of human full open reading frames in Gateway(TM) system
                                                                                                                                                                                                                                                                                                                                                         Partanen J., Armstrong E., Bergman M., Maekelae T.P., Hirvonen
Huebner K., Alitalo K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruebsamen-Waigmann H.;
                                                                                                                                                                                                                                                                                                                                                                                                "CYL encodes a putative cytoplasmic tyrosine kinase lacking conserved tyrosine autophosphorylation site (Y416src).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                       450 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93241739; PubMed=7683131;
Braeuninger A., Karn T., Strebhardt K., Ruel
"Characterization of the human CSK locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subclass of protein tyrosine kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Lung;
MEDLINE=92073297; PubMed=1720539;
                                                                                                                                                                                                                                                                                                                                      MEDLINE=92050797; PubMed=1945408;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncogene 6:2013-2018(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [MRNA]
                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 110:205-211(1992)
                                                                                                                                                tyrosine kinase CYL)
                                                                                                                                                                                         Homo sapiens (Human)
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                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                       HUMAN
                                                                                                                                                                    Name=CSK
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman M.W., Green E.D., Dickson M.C., Sanchez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=2023345; PubMed=10790433; DOI=10.1084/jem.191.9.1591; Brdicka T., Pavlistova D., Bruyns E., Leo A., Korinek V., Angelisova P., Scherer J., Shevchenko A., Shevchenko A., Hilgert I., Cerny J., Drbal K., Kuramitsu Y., Horejsi V., Schraven B.; Phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), a novel ubjquitously expressed transmembrane adaptor protein, binds the protein tyrosine kinase csk and is involved in regulation of T cell activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- TISSUE SPECIFICITY: Expressed in lung and macrophages.
-!- PTM: Autophosphorylation of Tyr-304 occurs only at abnormally high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION SITES TYR-184 AND TYR-304, AND MUTAGENESIS OF TYR-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brdickova N., Brdicka T., Angelisova P., Horvath O., Spicka J.,
Hilgert I., Paces J., Simeoni L., Kliche S., Merten C., Schraven B.,
Horejsi V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bergman M.;
"Identification of csk tyrosine phosphorylation sites and a tyrosine residue important for kinase domain structure.";
Biochem. J. 322:927-935(1997).
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-!- SUBCELLULAR LOCATION: Mainly cytoplasmic. Also present in lipid
-: STER (By Similarity).
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MEDLINE-94185778; PubMed=7511113; DOI=10.1016/0014-5793(94)80244-0;
Borchert T.V., Mathieu M., Zeelen J.P., Courtneidge S.A.,
Wierenga R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfrepper K.-I., Marie-Cardine A., Simeoni L., Kuramitsu Y., Leo A., Spicka J., Hilgert I., Scherer J., Schraven B.; "Structural and functional dissection of the cytoplasmic domain of transmembrane adaptor protein SIT (SHP2-interacting transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as a negative regulatory site. Can also act on the LYN and FYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a new membrane raft-associated adaptor protein involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOI=10.1002/1521-4141(200106)31:6<1825::AID-IMMU1825>3.0.CO;2-V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Υ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSK concentrations in vitro. SIMILARITY: Belongs to the Tyr protein kinase family. CSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97220407; PubMed-9148770;
Joukov V., Vihinen M., Vainikka S., Sowadski J.M., Alitalo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH LIME1.
PubMed=14610046; DOI=10.1084/jem.20031484;
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Eur. J. Immunol. 31:1825-1836(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exp. Med. 191:1591-1604(2000).
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J. Exp. Med. 198:1453-1462(2003)
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FEBS Lett. 341:79-85(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse cDNA sequences.";
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(p50CSK).

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Cloutier J.-F., Veillette A.; "Association of inhibitory tyrosine protein kinase p50csk with protein "Association of inhibitory tyrosine phosphatase PEP in T cells and other hemopoietic cells."; EMBO J. 15:4908-4918(1996).
                                                                                                                                                                                                Klages S., Adam D., Class K., Fargnoli J., Bolen J.B., Penhallow R.C., "Ctk: a protein-tyrosine kinase related to Csk that defines an enzyme
                                   Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                          Gilardi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.-G., Chestier A., Wilkinson D.G., Charnay P.;
"An Eph-related receptor protein tyrosine kinase gene segmentally expressed in the developing mouse hindbrain.";
                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 91:2597-2601(1994).
                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6; TISSUE=Embryonic brain; MEDLINE=93096484; PubMed=1281307;
                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [MRNA] OF 316-367.
                                                                                                                                                                             WEDLINE=94195789; PubMed=7511815;
                                                                                                                                              NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                  Oncogene 7:2499-2506(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH PTPN8.
 tyrosine kinase MPK-2)
                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=8890164;
                                                                                                                                                              TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kinases
                    Name=Csk;
                                                                                                                                                                                                                                    family
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                          AGO: GO: 0005886; C:plasma membrane; IPI.

R GO: GO: 0005886; C:plasma membrane; IPI.

R GO: GO: 0004713; P:protein C-terminus binding; TAS.

GO: GO: 0004713; P:protein amino acid phosphorylation; TAS.

GO: GO: 000074; P:regulation of progression through cell cycle; TAS.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR0012452; Sar_thr_pkinase.

R InterPro; IPR001452; Tyr_pkinase.

R InterPro; IPR001452; Tyr_pkinase.

R InterPro; IPR001452; Tyr_pkinase.

R InterPro; IPR001345; Tyr_pkinase.

R InterPro; IPR001345; Tyr_pkinase.

R Pfam; PF00714; Pkinase Tyr; 1.

R Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3D-structure, ATP-binding, Kinase, Nucleotide-binding,
Phosphorylation, Polymorphism, SH2 domain, SH3 domain, Transferase,
Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 1; Length 450; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tyrosine-protein kinase CSK./FIId=PRO_000088070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0:
                                                                                                                        EMBL; X60114; CAA42713.1; -; mRNA.

EMBL; X5932; CAA42556.1; -; mRNA.

EMBL; X74765; CAB5862.1; -; Genomic_DNA.

EMBL; CR541960; CAG46758.1; -; mRNA.

EMBL; DQ075211; AAY57329.1; -; Genomic_DNA.

EMBL; BC106073; AAI06074.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                           Ensembl; ENSG0000103653; Homo sapiens.
              -!- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD000001; Prot_kinase; 1. ProDom; PD000093; SH2; 1.
                                                                                                                                                                                                                                                PDB; 1BYG; X-ray; A=173-450.
PDB; 1CSK; X-ray; A/B/C/D=1-71.
SMR; P41240; 4-450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00018; SH3 1; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSS0011; PROTEII
PROSITE; PS00109; PROTEII
PROSITE; PSS0001; SH2; 1
PROSITE; PSS0002; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00219; TyrKc; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 DVWSFGILL 376
                                                                                                                                                                                                                                                                                                                                            HGNC; HGNC:2444; CSK.
MIM; 124095; gene.
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SWART; SM00252; SH2;
SWART; SM00326; SH3;
                                                                                                                                                                                                                                   PIR; JH0559; JH0559.
PDB; 1BYG; X-ray; A=:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             LinkHub; P41240;
subfamily
                                                                                                                                                                                                                                                                                                           OGP; P41240;
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THE WAY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE BY A PRINCE B

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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=12612075; DOI=10.1128/MCB.23.6.2017-2028.2003; Davidson D., Bakinowski M., Thomas M.L., Horejsi V., Veillette A.; "Phosphorylation-dependent regulation of T-cell activation by PAG/Cbp, a lipid raft-associated transmembrane adaptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity). Interacts with PTPN8. Interacts with phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rafts.
-!- TISSUE SPECIFICITY: Ubiquitous, but most abundant in thymus and spleen, as well as in neonatal brain.
-!- SIMILARITY: Belongs to the Tyr protein kinase family. CSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=16166631; DOI=10.1128/MCB.25.19.8486-8495.2005; Xu S., Huo J., Tan J.E.-L., Lam K.-P.; "Cbp deficiency alters CSk localization in lipid rafts but does not affect T-cell development.", Mol. Cell. Biol. 25:6486-8495(2005).

-!- FUNCTION: Specifically phosphorylates Tyr-504 on LCK, which acts as a negative regulatory site. Can also act on the LYN and FYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Mainly cytoplasmic. Also present in lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
                                PubMed=12218089;
Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T., Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
Fyn is essential for tyrosine phosphorylation of Csk-binding protein/phosphoprotein associated with glycolipid-enriched microdomains in lipid rafts in resting T cells.";
J. Immunol. 169:2813-2817(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine phosphate.
SUBUNIT: Interacts with phosphorylated SITL and LIMEL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH PAG1, AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subfamily.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Cell. Biol. 23:2017-2028(2003).
INTERACTION WITH PAG1.
                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION WITH PAG1.
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CSK MOUSE STANDARD; PRT; 450 AA.
P41241; Q03143;
01-FBB-1995, integrated into UniProtKB/Swiss-Prot.
01-FBB-1995, sequence version 1.
01-FAB-2006, entry version 55.
Tyrosine-protein kinase CSK (RC 2.7.1.112) (C-SRC kinase) (Protein-

RESULT 30 CSK_MOUSE

δ g DATAB

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SH2.
Protein kinase.
ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
Phosphotyrosine (By similarity).
Phosphotyrosine (by autocatalysis) (By similarity).
      REMEL; M5244; AAA18766.1; -; mRNA.

R EMEL; M5742; CAA4518.1; -; mRNA.

R PRRIJ; K5742; CAA4518.1; -; mRNA.

R PRRIJ; K5742; CAA4518.1; -; mRNA.

R PDB; JURG; NMR; A=1-83.

R PDB; JURG; NMR; A=1-83.

R PDB; JURG; NMR; A=1-83.

R GO; GO:0005828 (C.Cplasma membrane; TAS.

R GO; GO:0005828 (C.Cplasma membrane; TAS.

R GO; GO:000713; F:protein binding; TAS.

R GO; GO:000713; F:protein binding; TAS.

R GO; GO:0007242; P:intracellular signaling cascade; TAS.

R GO; GO:0007242; P:intracellular signaling cascade; TAS.

R GO; GO:0007242; P:intracellular signaling cascade; TAS.

R GO; GO:000413; F:protein amino acid phosphorylation; TAS.

R GO; GO:000446; P:protein amino acid phosphorylation; TAS.

R GO; GO:000466; P:protein amino acid phosphorylation; TAS.

R InterPro; IPR000129; SH2.

R InterPro; IPR001245; TYT_pkinase.

R InterPro; IPR001245; TYT_pkinase.

R InterPro; IPR001245; TYT_pkinase.

R InterPro; IPR001245; TYT_pkinase.

R InterPro; IPR00145; TYT_pkinase.

R InterPro; IPR00163; SH3: 1.

R PROMIN; PR0011; PRTKINASE.

R ProDom; PD000001; PTCL_kinase; 1.

R PRODOM; PD000004; SH3: 1.

R RPCDOM; PD000004; SH3: 1.

R RPCDIE; PS00010; PROTEIN_KINASE_TYR; 1.

R RPCSITE; PS00010; PROTEIN_KINASE_TYR; 1.

R RPCSITE; PS00010; RPCTEIN_KINASE_TYR; 1.

R RPCSITE; PS00010; PROTEIN_KINASE_TYR; 1.

R RPCSITE; PS00010; SH3: 1.

R RPCSITE; PS00010; SH3: 1.

R RPCSITE; PS00010; SH3: 1.

R PROSITE; PS00010; SH3: 1.

R PROSITE; PS00010; SH3: 1.

R PROSITE; PS00010; SH3: 1.

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R PROSITE; PS00010; SH3: 1.

R PROSITE; PS00010; SH3: 1.

R PROSITE; PS00010; SH3: 1.

R PROSITE; PS00010; SH3: 1.

R PROSITE; PS00010
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Search completed: June 29, 2006, 09:29:37 Job time : 107.942 secs

Ouery Match
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

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